# MOLECULAR CARDIOTOXICOLOGY MODELING

INVENTORS: DONNA MENDRICK, MARK PORTER, KORY JOHNSON, BRANDON HIGGS, ARTHUR CASTLE, AND MICHAEL ELASHOFF

# RELATED APPLICATIONS

[0001] This application claims priority to U.S. Application 10/338,044, filed January 8, 2003, which is a continuation-in-part of U.S. Application 10/191,803, filed June 10, 2002, which claims priority to U.S. Provisional Applications 60/303,819 filed on July 10, 2001; 60/305,623 filed on July 17, 2001; 60/369,351 filed on April 3, 2002; and 60/377,611 filed on May 6, 2002, all of which are herein incorporated by reference in their entirety.

[0002] This application is also related to U.S. Application Nos. 09/917,800; 10/060,087; 10/152,319; and 10/301,856, all of which are also herein incorporated by reference in their entirety.

# SEQUENCE LISTING SUBMISSION ON COMPACT DISC

[0003] The Sequence Listing submitted concurrently herewith on compact disc under Section 801(a)(i) and under 37 C.F.R. §§ 1.821(c) and 1.821(e) is herein incorporated by reference in its entirety. Four copies of the Sequence Listing, one on each of four compact discs are provided. Copy 1, Copy 2 and Copy 3 are identical. Copies 1, 2 and 3 are also identical to the CRF. Each electronic copy of the Sequence Listing was created on January 7, 2004 with a file size of 3952 KB. The file names are as follows: Copy 1- gl 5090 01 wo.txt; Copy 2- gl 5090 01 wo.txt; Copy 3- gl 5090 01 wo.txt; and CRF- gl 5090 01 wo.txt.

# BACKGROUND OF THE INVENTION

[0004] The need for methods of assessing the toxic impact of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism has led to the development of procedures which utilize living organisms as biological monitors. The simplest and most convenient of these systems utilize unicellular microorganisms such as yeast and bacteria, since they are the most easily maintained and manipulated. In addition, unicellular screening systems often use easily detectable changes in phenotype to monitor the effect of test compounds on the cell. Uniceliular organisms, however, are inadequate models for estimating the potential effects of many compounds on complex multicellular animals, in

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part because they do not have the ability to carry out biotransformations to the extent or at levels found in higher organisms.

[0005] The biotransformation of chemical compounds by multicellular organisms is a significant factor in determining the overall toxicity of agents to which they are exposed. Accordingly, multicellular screening systems may be preferred or required to detect the toxic effects of compounds. The use of multicellular organisms as toxicology screening tools has been significantly hampered, however, by the lack of convenient screening mechanisms or endpoints, such as those available in yeast or bacterial systems. In addition, previous attempts to produce toxicology prediction systems have failed to provide the necessary modeling data and statistical information to accurately predict toxic responses (e.g., WO 00/12760, WO 00/47761, WO 00/63435, WO 01/32928, and WO 01/38579).

#### DESCRIPTION OF THE TABLES

[0006] Table 1 provides the GenBank Accession Number for each of the sequences of the invention (see www.ncbi.nlm.nih.gov/), as well as the corresponding SEQ ID NO. in the sequence listing filed with this application. The gene name and Unigene Cluster Title, if known, cardiotoxicity prediction model code and internal reference no. are also provided. [0007] Table 2 lists and describes the metabolic pathways in which the genes of the invention are known to function.

[0008] Table 3 provides the LocusLink and Unigene names and descriptions for the human homologues of the genes listed in Tables 1 and 2.

[0009] Table 4 defines the model codes, each of which corresponds to a table in Tables 5A-5LL. Each of Tables 5A-5LL represents part of a cardiotoxicity prediction model and lists for each toxin, or class of toxins, the genes that are predictors of a toxic effect. For each gene listed, the mean and standard deviation for gene expression levels in Tox-Group and Non-tox Group samples, as well as the linear discriminant analysis score (LDA score), are indicated.

[0010] Table 5A lists the genes that predict a toxic effect in samples treated with adrenergic agonists.

[0011] Table 5B lists the toxicity prediction genes in samples treated with alkylating agents.

[0012] Table 5C lists the toxicity prediction genes in samples treated with adriamycin (120 and 168-hour time point data).

[0013] Table 5D lists the toxicity prediction genes in samples treated with adriamycin (6 and 24-hour time point data).

[0014] Table 5E lists the toxicity prediction genes in samples treated with amphotericin B. [0015] Tables 5F and 5G list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with BI-QT, a proprietary heart and liver toxin.

[0016] Tables 5H and 5I list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with clenbuterol (24-hour time point data).

[0017] Tables 5J and 5K list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with clenbuterol (6-hour time point data).

[0018] Tables 5L and 5M list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with cyclophosphamide.

[0019] Tables 5N and 5O list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with epinephrine (24-hour time point data). [0020] Tables 5P and 5Q list the toxicity prediction genes in an alternate model and in a

core model, respectively, in samples treated with epinephrine (3 and 6-hour time point data).

[0021] Table 5R lists the toxicity prediction genes in samples treated with epirubicin.

[0022] Tables 5S and 5T list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with hydralazine.

[0023] Tables 5U and 5V list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with ifosfamide.

[0024] Tables 5W and 5X list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with isoproterenol (24-hour time point data). [0025] Tables 5Y and 5Z list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with isoproterenol (3 and 6-hour time point

data).

100261 Tables 5AA and 5BB list the toxicity prediction genes in an al

[0026] Tables 5AA and 5BB list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with minoxidil (3 and 6-hour time point data).

[0027] Tables 5CC and 5DD list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with norepinephrine (24-hour time point data).

[0028] Tables 5EE and 5FF list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with norepinephrine (3 and 6-hour time point data).

[0029] Tables 5GG (3-hour time point data) and 5HH (6 and 24-hour time point data) list the toxicity prediction genes in samples treated with phenylpropanolamine.

[0030] Table 5II lists the toxicity prediction genes in samples treated with rosiglitazone.

[0031] Tables 5JJ and 5KK list the toxicity prediction genes in a general model and in a general core model, respectively. The general model is produced by combining data from all the other models and includes, therefore, samples treated with various compounds and data taken at various time points. The general core model combines data from the core models produced using one toxin.

[0032] Table 5LL lists the toxicity prediction genes in samples treated with vasculature agents.

### SUMMARY OF THE INVENTION

[0033] The present invention is based, in part, on the elucidation of the global changes in gene expression in tissues or cells exposed to known toxins, in particular cardiotoxins, as compared to unexposed tissues or cells as well as the identification of individual genes that are differentially expressed upon toxin exposure.

[0634] In various aspects, the invention includes methods of predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, and predicting the cardiotoxicity of a compound. The invention also includes methods of identifying agents that modulate the onset or progression of a toxic response. Also provided are methods of predicting the cellular pathways that a compound modulates in a cell. The invention also includes methods of identifying agents that modulate protein activities.

[0035] In a further aspect, the invention includes probes comprising sequences that specifically hybridize to genes in Tables 1-5LL. Also included are solid supports comprising at least two of the previously mentioned probes. The invention also includes a computer system that has a database containing information identifying the expression level in a tissue or cell sample exposed to a cardiotoxin of a set of genes comprising at least two genes in Tables 1-5LL.

[0036] The invention further provides a core set of genes in Tables 5A-5LL from which propes can be made and attached to solid supports. These core genes serve as a preferred

set of markers of cardiotoxicity and can be used with the methods of the invention to predict or monitor a toxic effect of a compound or to modulate the onset or progression of a toxic response.

## **DETAILED DESCRIPTION**

[0037] Many biological functions are accomplished by altering the expression of various genes through transcriptional (e.g. through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death are often characterized by the variations in the expression levels of groups of genes.

[0038] Changes in gene expression are also associated with the effects of various chemicals, drugs, toxins, pharmaceutical agents and pollutants on an organism or cell(s). For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over-expression of oncogene/protooncogenes after exposure to an agent could lead to tumorgenesis or hyperplastic growth of cells (Marshall (1991), Cell 64: 313-326; Weinberg (1991), Science 254: 1138-1146). Thus, changes in the expression levels of particular genes (e.g. oncogenes or tumor suppressors) may serve as signposts for the presence and progression of toxicity or other cellular responses to exposure to a particular compound.

[0039] Monitoring changes in gene expression may also provide certain advantages during drug screening and development. Often drugs are screened for the ability to interact with a major target without regard to other effects the drugs have on cells. These cellular effects may cause toxicity in the whole animal, which prevents the development and clinical use of the potential drug.

[0040] The present inventors have examined tissue from animals exposed to known cardiotoxins which induce detrimental heart effects, to identify global changes in gene expression and individual changes in gene expression induced by these compounds. These global changes in gene expression, which can be detected by producing or obtaining gene expression profiles (an expression level of one or more genes), provide useful toxicity markers that can be used to monitor toxicity and/or toxicity progression by a test compound. Some of these markers may also be used to monitor or detect various disease or physiological states, disease progression, drug efficacy and drug metabolism.

Identification of Toxicity Markers

[0041] To evaluate and identify gene expression changes that are predictive of toxicity, studies using selected compounds with well characterized toxicity have been conducted by the present inventors to catalogue altered gene expression during exposure *in vivo*. In the present study, cyclophosphamide, ifosfamide, minoxidil, hydralazine, BI-QT, clenbuterol, isoproterenol, norepinephrine, epinephrine, adriamycin, amphotericin B, epirubicin, phenylpropanolamine, and rosiglitazone were selected as known cardiotoxins. Cisplatin, PAN, dopamine, acyclovir, carboplatin, etoposide, temozolomide, vancomycin and compound delivery vehicles were selected as negative controls.

[0042] Cyclophosphamide, an alkylating agent, is highly toxic to dividing cells and is commonly used in chemotherapy to treat non-Hodgkin's lymphomas, Burkitt's lymphoma and carcinomas of the lung, breast, and ovary (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p.1234, 1237-1239, J.G. Hardman et al., Eds., McGraw Hill, New York, 1996). Additionally, cyclophosphamide is used as an immunosuppressive agent in bone marrow transplantation and following organ transplantation. Though cyclophosphamide is therapeutically useful, it is also associated with cardiotoxicity, nephrotoxicity, and hemorrhagic cystitis. Once in the liver, cyclophosphamide is hydroxylated by the cytochrome P450 mixed function oxidase system. The active metabolites, phosphoramide mustard and acrolein, cross-link DNA and cause growth arrest and cell death. Acrolein has been shown to decrease cellular glutathione levels (Dorr and Lagel (1994), Chem Biol Interact 93: 117-128). [0043] The cardiotoxic effects of cyclophosphamide have been partially elucidated. One study analyzed plasma levels in 19 women with metastatic breast carcinoma who had been treated with cyclophosphamide, thiotepa, and carboplatin (Ayash et al. (1992), J Clin Oncol 10: 995-1000). Of the 19 women in the study, six developed moderate congestive heart failure. In another case study, a 10-year old boy, who had been treated with highdose cyclophosphamide, developed cardiac arrhythmias and intractable hypotension (Tsai et al. (1990), Am J Pediatr Hematol Oncol 12: 472-476). The boy died 23 days after the transplantation.

[6644] Another clinical study examined the relationship between the amount of cyclophosphamide administered and the development of cardiotoxicity (Goldberg et al. (1986), Blood 68: 1114-1118). When the cyclophosphamide dosage was ≤1.55 g/m²/d, only 1 out of 32 patients had symptoms consistent with cyclophosphamide cardiotoxicity.

Yet when the dosage was greater than 1.55 g/m²/d, 13 out of 52 patients were symptomatic. Six of the high-dose patients died of congestive heart failure. [0045] In a related study, Braverman et al. compared the effects of once daily low-dose administration of cyclophosphamide (87 +/- 11 mg/kg) and twice-daily high-dose treatment (174 +/- 34 mg/kg) on bone marrow transplantation patients (Braverman et al. (1991), J Clin Oncol 9: 1215-1223). Within a week, the high-dose patients had an increase in left ventricular mass index. Out of five patients who developed clinical cardiotoxicity, four were in the high-dose group.

[0046] Ifosfamide, an oxazaphosphorine, is an analog of cyclophosphamide. Whereas cyclophosphamide has two chloroethyl groups on the exocyclic nitrogen, ifosfamide contains one chloroethyl group on the ring nitrogen and the other on the exocyclic nitrogen. Ifosfamide is a nitrogen mustard and alkylating agent, commonly used in chemotherapy to treat testicular, cervical, and lung cancer, as well as sarcomas and lymphomas. Like cyclophosphamide, it is activated in the liver by hydroxylation, but it reacts more slowly and produces more dechlorinated metabolites and chloroacetaldehyde. Comparatively higher doses of ifosfamide are required to match the efficacy of cyclophosphamide.

[0047] Alkylating agents can cross-link DNA, resulting in growth arrest and cell death. Despite its therapeutic value, ifosfamide is associated with nephrotoxicity (affecting the proximal and distal renal tubules), urotoxicity, venooclusive disease, myelosuppression, pulmonary fibrosis and central neurotoxicity (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p.1234-1240, J.G. Hardman et al., Eds., McGraw Hill, New York, 1996). Ifosfamide can also cause acute severe heart failure and malignant ventricular arrhythmia, which may be reversible. Death from cardiogenic shock has also been reported (Cecil Textbook of Medicine 20<sup>th</sup> ed., Bennett et al. eds., p. 331, W.B. Saunders Co., Philadelphia, 1996).

[0048] Studies of patients with advanced or resistant lymphomas or carcinomas showed that high-dose ifosfamide treatment produced various symptoms of cardiac disease, including dyspnea, tachycardia, decreased left ventricular contractility and malignant ventricular arrhythmia (Quezado et al. (1993), Ann Intern Med 118: 31-36; Wilson et al. (1992), J Clin Oncol 19: 1712-1722). Other patient studies have noted that ifosfamide-induced cardiac toxicity may be asymptomatic, although it can be detected by electrocardiogram and should be monitored (Pai et al. (2000), Drug Saf 22:263-302).

[0049] Minoxidil is an antihypertensive medicinal agent used in the treatment of high blood pressure. It works by relaxing blood vessels so that blood may pass through them more easily, thereby lowering blood pressure. By applying minoxidil to the scalp, it has recently been shown to be effective at combating hair loss by stimulating hair growth. Once minoxidil is metabolized by hepatic sulfotransferase, it is converted to the active molecule minoxidil N-O sulfate (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., pp. 796-797, J.G. Hardman et al., Eds., McGraw Hill, New York, 1996). The active minoxidil sulfate stimulates the ATP-modulated potassium channel consequently causing hyperpolarization and relaxation of smooth muscle. Early studies on minoxidil demonstrated that following a single dose of the drug, patients suffering from left ventricular failure exhibited a slightly increased heart rate, a fall in the mean arterial pressure, a fall in the systemic vascular resistance, and a slight increase in cardiac index (Franciosa and Cohn (1981) Circulation 63: 652-657).

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[0050] Some common side effects associated with minoxidil treatment are an increase in hair growth, weight gain, and a fast or irregular heartbeat. More serious side effects are numbness of the hands, feet, or face, chest pain, shortness of breath, and swelling of the feet or lower legs. Because of the risks of fluid retention and reflex cardiovascular effects, minoxidil is often given concomitantly with a diuretic and a sympatholytic drug. [0051] While minoxidil is effective at lowering blood pressure, it does not lead to a regression of cardiac hypertrophy. To the contrary, minoxidil has been shown to cause cardiac enlargement when administered to normotensive animals (Moravec et al. (1994) J Pharmacol Exp Ther 269: 290-296). Moravec et al. examined normotensive rats that had developed myocardial hypertrophy following treatment with minoxidil. The authors found that minoxidil treatment led to enlargement of the left ventricle, right ventricle, and interventricular septum.

[0052] Another rat study investigated the age- and dose-dependency of minoxidil-induced cardiotoxicity (Herman et al. (1996) Toxicology 110: 71-83). Rats ranging in age from 3 months to 2 years were given varying amounts of minoxidil over the period of two days. The investigators observed interstitial hemorrhages at all dose levels, however the hemorrhages were more frequent and severe in the older animals. The 2 year old rats had vascular lesions composed of arteriolar damage and calcification.

[0053] Hydralazine, an antihypertensive drug, causes relaxation of arteriolar smooth muscle. Such vasodilation is linked to vigorous stimulation of the sympathetic nervous

system, which in turn leads to increased heart rate and contractility, increased plasma renin activity, and fluid retention (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p. 794, J.G. Hardman et al., Eds., McGraw Hill, New York, 1996). The increased renin activity leads to an increase in angiotensin II, which in turn causes stimulation of aldosterone and sodium reabsorption.

[0054] Hydralazine is used for the treatment of high blood pressure (hypertension) and for the treatment of pregnant women suffering from high blood pressure (pre-eclampsia or eclampsia). Some common side effects associated with hydralazine use are diarrhea, rapid heartbeat, headache, decreased appetite, and nausea. Hydralazine is often used concomitantly with drugs that inhibit sympathetic activity to combat the mild pulmonary hypertension that can be associated with hydralazine usage.

[0055] In one hydralazine study, rats were given one of five cardiotoxic compounds (isoproterenol, hydralazine, caffeine, cyclophosphamide, or adriamycin) by intravenous injection (Kemi et al. (1996), J Vet Med Sci 58: 699-702). At one hour and four hours post-dose, early focal myocardial lesions were observed histopathologically. Lesions were observed in the rats treated with hydralazine four hours post-dose. The lesions were found in the inner one third of the left ventricular walls including the papillary muscles.

[0056] Another study compared the effects of isoproterenol, hydralazine and minoxidil on young and mature rats (Hanton et al. (1991), Res Commun Chem Pathol Pharmacol 71: 231-234). Myocardial necrosis was observed in both age groups, but it was more severe in the mature rats. Hypotension and reflex tachycardia were also seen in the hydralazine-treated rats.

[0057] BI-QT has been shown to induce QC prolongation in dogs and liver alterations in rats. Over a four week period, dogs treated with BI-QT exhibited sedation, decreased body weight, increased liver weight, and slightly increased levels of AST, ALP, and BUN. After three months of treatment, the dogs exhibited signs of cardiovascular effects.

[0058] Clenbuterol, a β2 adrenergic agonist, can be used therapeutically as a bronchial dilator for asthmatics. It also has powerful muscle anabolic and lipolytic effects. It has been banned in the United States but continues to be used illegally by athletes to increase muscle growth. In a number of studies, rats treated with clenbuterol developed hypertrophy of the heart and latissimus dorsi muscle (Doheny et al. (1998), Amino Acids 15: 13-25; Murphy et al. (1999), Proc Soc Exp Biol Med 221: 184-187; Petrou et al. (1995), Circulation 92: II483-II489).

[0059] In one study, mares treated with therapeutic levels of clenbuterol were compared to mares that were exercised and mares in a control group (Sleeper et al. (2002), Med Sci Sports Exerc 34: 643-650). The clenbuterol-treated mares demonstrated significantly higher left ventricular internal dimension and interventricular septal wall thickness at end diastole. In addition, the clenbuterol-treated mares had significantly increased aortic root dimensions, which could lead to an increased chance of aortic rupture. [0060] In another study, investigators reported a case of acute clenbuterol toxicity in a human (Hoffman et al. (2001), J Toxicol 39: 339-344). A 28-year old woman had ingested a small quantity of clenbuterol, and the patient developed sustained sinus tachycardia, hypokalemia, hypophosphatemia, and hypomagnesemia. [0061] Catecholamines are neurotransmitters that are synthesized in the adrenal medulla and in the sympathetic nervous system. Epinephrine, norepinephrine, and isoproterenol are members of the catecholamine sympathomimetic amine family (Casarett & Doull's Toxicology, The Basic Science of Poisons 6th ed., p. 618-619, C.D. Klaassen, Ed., McGraw Hill, New York, 2001). They are chemically similar by having an aromatic portion (catechol) to which is attached an amine, or nitrogen-containing group. [0062] Isoproterenol, an antiarrhythmic agent, is used therapeutically as a bronchodilator for the treatment of asthma, chronic bronchitis, emphysema, and other lung diseases. Some side effects of usage are myocardial ischemia, arrhythmias, angina, hypertension, and tachycardia. As a  $\beta$  receptor agonist, isoproterenol exerts direct positive inotropic and chronotropic effects. Peripheral vascular resistance is decreased along with the pulse pressure and mean arterial pressure. However, the heart rate increases due to the decrease

[0063] Norepinephrine, an  $\alpha$  and  $\beta$  receptor agonist, is also known as noradrenaline. It is involved in behaviors such as attention and general arousal, stress, and mood states. By acting on  $\beta$ -1 receptors, it causes increased peripheral vascular resistance, pulse pressure and mean arterial pressure. Reflex bradycardia occurs due to the increase in mean arterial pressure. Some contraindications associated with norepinephrine usage are myocardial ischemia, premature ventricular contractions (PVCs), and ventricular tachycardia. [0064] Epinephrine, a potent  $\alpha$  and  $\beta$  adrenergic agonist, is used for treating bronchoconstriction and hypotension resulting from anaphylaxis as well as all forms of cardiac arrest. Injection of epinephrine leads to an increase in systolic pressure,

in the mean arterial pressure.

and heart rate. Some side effects associated with epinephrine

usage are cardiac arrhythmias, particularly PVCs, ventricular tachycardia, renal vascular ischemia, increased myocardial oxygen requirements, and hypokalemia.

[0065] Anthracyclines are antineoplastic agents used commonly for the treatment of breast cancer, leukemias, and a variety of other solid tumors. However, the usefulness of the drugs are limited due dose-dependent cardiomyopathy and ECG changes (Casarett & Doull's Toxicology, The Basic Science of Poisons 6<sup>th</sup> ed., p. 619, C.D. Klaassen, Ed., McGraw Hill, New York, 2001).

[0066] Adriamycin (doxorubicin) is a cytotoxic anthracycline antiobiotic that inhibits the action of topoisomerase II. It has a wide spectrum of antitumor activity, however dose-related cardiotoxicity is a major side effect. The toxic effects are most likely due to the generation of free radicals (DeAtley et al. (1999), Toxicology 134: 51-62). In one study, rats were given a dose of either adriamycin alone or a dose of adriamycin following a dose of captopril (al-Shabanah et al. (1998), Biochem Mol Biol Int 45: 419-427). Those rats that were only given adriamycin developed myocardial toxicity after 24 hours manifested biochemically by an elevation of serum enzymes such as aspartate transaminase, lactate dehydrogenase, and creatine phosphokinase. The rats that were pre-treated with captopril exhibited a significant reduction in serum enzyme levels as well as restoration of white blood cell counts.

[0067] Epirubicin is a semisynthetic derivative of daunorubicin, an anthracycline, approved for the treatment of breast cancer (Casarett & Doull's Toxicology, The Basic Science of Poisons 6<sup>th</sup> ed., p. 619, C.D. Klaassen, Ed., McGraw Hill, New York, 2001). Yet, it, too, may induce cardiotoxicity. In one observational study, 120 patients with advanced breast cancer were followed before, during, and after treatment with epirubicin (Jensen et al. (2002), Ann Oncol 13: 699-709). Approximately 59% of the patients experienced a 25% relative reduction in left ventricular ejection fraction three years after epirubicin treatment, and of these patients 20% had deteriorated into having congestive heart failure.

[0068] Amphotericin B is a polyene, antifungal antibiotic used to treat fungal infections. Its clinical utility is limited by its nephrotoxicity and cardiotoxicity. Amphotericin B may depress myocardial contractility by blocking activation of slow calcium channels and inhibiting the influx of sodium ions (Casarett & Doull's Toxicology, The Basic Science of Poisons 6<sup>th</sup> ed., p. 621, C.D. Klaassen, Ed., McGraw Hill, New York, 2001). It has been shown to increase the permeability of the sarcolemmal membrane, and patients given

amphotericin B have developed ventricular tachycardia and cardiac arrest. This drug has been shown to induce cardiac arrest in rats as well. In the current study, amphotericin B led to an increase in serum Troponin T levels and some early signs of cardiomyopathy within 24 hours of one intravenous bolus injection.

[0069] Phenylpropanolamine was used in over-the-counter decongestants until recently, but was withdrawn when its association with cardiac deaths became known. It is both a beta-1 and alpha adrenergic receptor agonist and has been shown to induce cardiotoxicity in rats. In one rat study, phenylpropanolamine was shown to cause myocardial contractile depression without altering global coronary artery blood flow (Zaloga et al. (2000), *Crit Care Med* 28: 3679-3683).

[0070] In another study, rats were given single intraperitoneal doses of 1, 2, 4, 8, 16, or 32 mg/kg of phenylpropanolamine (Pentel et al. (1987), Fundam Appl Toxicol 9: 167-172). The animals exhibited dose-dependent increased blood pressure and, following termination, myocardial necrosis.

[0071] Rosiglitazone (Avandia) is a thiazolidinedione medication used to treat Type 2 diabetes. It reduces plasma glucose levels and glucose production and increases glucose clearance (Wagstaff and Goa (2002), *Drugs* 62: 1805-1837). Some side effects associated with rosiglitazone treatment are fluid retention, congestive heart failure, and liver disease. In patients who have heart failure or use insulin, there is a potential for mild-to-moderate peripheral edema with rosiglitazone treatment. It has been shown that patients that do not have heart failure or use insulin can also develop moderate-to-severe edema while using rosiglitazone (Niemeyer and Janney (2002), *Pharmacotherapy* 22: 924-929).

# Toxicity Prediction and Modeling

[0072] The genes, gene expression information (including Tox Group means and standard deviations, Nontox Group means and standard deviations, and LDA scores) and gene expression profiles, as well as the portfolios and subsets of the genes provided in Tables 1-5LL, such as the core toxicity markers in Tables 5A-5LL, may be used to predict at least one toxic effect, including the cardiotoxicity of a test or unknown compound. As used herein, at least one toxic effect includes, but is not limited to, a detrimental change in the physiological status of a cell or organism. The response may be, but is not required to be, associated with a particular pathology, such as tissue necrosis, myocarditis, arrhythmias, tachycardia, myocardial ischemia, angina, hypertension, hypotension, dyspnea, and cardiogenic shock. Accordingly, the toxic effect includes effects at the molecular and

cellular level. Cardiotoxicity is an effect as used herein and includes but is not limited to the pathologies of tissue necrosis, myocarditis, arrhythmias, tachycardia, myocardial ischemia, angina, hypertension, hypotension, dyspnea, and cardiogenic shock. As used herein, a gene expression profile comprises any representation, quantitative or not, of the expression of at least one mRNA species in a cell sample or population and includes profiles made by various methods such as differential display, PCR, hybridization analysis, etc.

[0073] In general, assays to predict the toxicity or cardiotoxicity of a test agent (or compound or multi-component composition) comprise the steps of exposing a cell population to the test compound, assaying or measuring the level of relative or absolute gene expression of one or more of the genes in Tables 1-5LL and comparing the identified expression level(s) to the expression levels disclosed in the Tables and database(s) disclosed herein. Assays may include the measurement of the expression levels of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 50, 75, 100, 200, 500, 1000 or more genes from Tables 1-5LL, or ranges of these numbers, such as about 2-10, about 10-20, about 20-50, about 50-100, about 100-200, about 200-500 or about 500-1000 genes from Tables 1-5LL to create multi-gene expression profiles. Assays for toxicity prediction may also include the measurement of nearly all the genes in Tables 1-5LL. "Nearly all" or "substantially all" the genes or gene information may be considered to mean at least 80%, preferably 85%, 90% or 95%, of the genes or information in any one of or all of Tables 1-5LL. [0074] The genes, gene expression information and databases of the present invention may also be used to predict the absence of a toxic effect, or the non-toxicity of a test compound. Gene expression profiles of cell or tissue samples from subjects or samples exposed to the test compound are prepared or obtained and then compared to those stored in a database of the invention. If the test sample gene expression profiles correlate with gene expression profiles classified as Non-tox Group samples, the test compound may considered not to produce a toxic effect.

[0075] Further, the gene expression information and databases of the present invention may also be used to predict the dosage or level of exposure at which a particular test compound produces a toxic effect. Groups of human or animal subjects may be treated with varying dosages of a test compound for varying lengths of time, or cell or tissue samples may be taken from groups of human or animal subjects and treated with varying dosages of a test compound for varying lengths of time. Alternatively, human or animal

cell cultures may be exposed to varying dosages of a test compound for varying lengths of time. Gene expression profiles may then be prepared or obtained from the set of samples treated with the test compound. These gene expression profiles may subsequently be compared to gene expression profiles stored in a database of the invention. In the sample set, the lowest concentration or dosage of the test compound that produces a gene expression profile that matches a gene expression profile indicating a toxic effect (corresponding to one or more Tox-Group samples in the database) may be determined. This concentration or dosage may be considered to be the threshold level at or above which a toxic response or effect may be predicted.

[0076] In the methods of the invention, the gene expression level for a gene or genes induced by the test agent, compound or compositions may be comparable to the levels found in the Tables or databases disclosed herein if the expression level varies within a factor of about 2, about 1.5 or about 1.0 fold. In some cases, the expression levels are comparable if the agent induces a change in the expression of a gene in the same direction (e.g., up or down) as a reference toxin.

[0077] The cell population that is exposed to the test agent, compound or composition

may be exposed in vitro or in vivo. For instance, cultured or freshly isolated heart cells, in particular rat heart cells, may be exposed to the agent under standard laboratory and cell culture conditions. In another assay format, in vivo exposure may be accomplished by administration of the agent to a living animal, for instance a laboratory rat. [0078] Procedures for designing and conducting toxicity tests in in vitro and in vivo systems are well known, and are described in many texts on the subject, such as Loomis et al., Loomis's Essentials of Toxicology, 4th Ed., Academic Press, New York, 1996; Echobichon, The Basics of Toxicity Testing, CRC Press, Boca Raton, 1992; Frazier, editor, In Vitro Toxicity Testing, Marcel Dekker, New York, 1992; and the like. [0079] In in vitro toxicity testing, two groups of test organisms are usually employed: one group serves as a control and the other group receives the test compound in a single dose (for acute toxicity tests) or a regimen of doses (for prolonged or chronic toxicity tests). Because, in some cases, the extraction of tissue as called for in the methods of the invention requires sacrificing the test animal, both the control group and the group receiving compound must be large enough to permit removal of animals for sampling tissues, if it is desired to observe the dynamics of gene expression through the duration of an experiment.

[0080] In setting up a toxicity study, extensive guidance is provided in the literature for selecting the appropriate test organism for the compound being tested, route of administration. dose ranges, and the like. Water or physiological saline (0.9% NaCl in water) is the solute of choice for the test compound since these solvents permit administration by a variety of routes. When this is not possible because of solubility limitations, vegetable oils such as corn oil or organic solvents such as propylene glycol may be used.

[0081] Regardless of the route of administration, the volume required to administer a given dose is limited by the size of the animal that is used. It is desirable to keep the volume of each dose uniform within and between groups of animals. When rats or mice are used, the volume administered by the oral route generally should not exceed about 0.005 ml per gram of animal. Even when aqueous or physiological saline solutions are used for parenteral injection, the volumes that are tolerated are limited, although such solutions are ordinarily thought of as being innocuous. The intravenous  $LD_{50}$  of distilled water in the mouse is approximately 0.044 ml per gram and that of isotonic saline is 0.068 ml per gram of mouse. In some instances, the route of administration to the test animal should be the same as, or as similar as possible to, the route of administration of the compound to man for therapeutic purposes.

[0082] When a compound is to be administered by inhalation, special techniques for generating test atmospheres are necessary. The methods usually involve aerosolization or nebulization of fluids containing the compound. If the agent to be tested is a fluid that has an appreciable vapor pressure, it may be administered by passing air through the solution under controlled temperature conditions. Under these conditions, dose is estimated from the volume of air inhaled per unit time, the temperature of the solution, and the vapor pressure of the agent involved. Gases are metered from reservoirs. When particles of a solution are to be administered, unless the particle size is less than about 2 µm the particles will not reach the terminal alveolar sacs in the lungs. A variety of apparatuses and chambers are available to perform studies for detecting effects of irritant or other toxic endpoints when they are administered by inhalation. The preferred method of administering an agent to animals is via the oral route, either by intubation or by incorporating the agent in the feed.

[0083] When the agent is exposed to cells in vitro or in cell culture, the cell population to be exposed to the agent may be divided into two or more subpopulations, for instance, by

dividing the population into two or more identical aliquots. In some preferred embodiments of the methods of the invention, the cells to be exposed to the agent are derived from heart tissue. For instance, cultured or freshly isolated rat heart cells may be used.

[0084] The methods of the invention may be used generally to predict at least one toxic response, and, as described in the Examples, may be used to predict the likelihood that a compound or test agent will induce various specific heart pathologies, such as tissue necrosis, myocarditis, arrhythmias, tachycardia, myocardial ischemia, angina, hypertension, hypotension, dyspnea, cardiogenic shock, or other pathologies associated with at least one of the toxins herein described. The methods of the invention may also be used to determine the similarity of a toxic response to one or more individual compounds. In addition, the methods of the invention may be used to predict or elucidate the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin (see Tables 5-5LL).

# Diagnostic Uses for the Toxicity Markers

[0085] As described above, the genes and gene expression information or portfolios of the genes with their expression information as provided in Tables 1-5LL may be used as diagnostic markers for the prediction or identification of the physiological state of a tissue or cell sample that has been exposed to a compound or to identify or predict the toxic effects of a compound or agent. For instance, a tissue sample such as a sample of peripheral blood cells or some other easily obtainable tissue sample may be assayed by the methods described above, and the expression levels from a gene or genes from Tables 5-5LL may be compared to the expression levels found in tissues or cells exposed to the toxins described herein. These methods may result in the diagnosis of a physiological state in the cell, may be used to diagnose toxin exposure or may be used to identify the potential toxicity of a compound, for instance a new or unknown compound or agent that the subject has been exposed to. The comparison of expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described below.

or any metabolite produced by the encoded protein may be monitored or detected in a sample, such as a bodily tissue or fluid sample to identify or diagnose a physiological state

of an organism. Such samples may include any tissue or fluid sample, including urine, blood and easily obtainable cells such as peripheral lymphocytes.

Use of the Markers for Monitoring Toxicity Progression

[0087] As described above, the genes and gene expression information provided in Tables 5-5LL may also be used as markers for the monitoring of toxicity progression, such as that found after initial exposure to a drug, drug candidate, toxin, pollutant, etc. For instance, a tissue or cell sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 5-5LL may be compared to the expression levels found in tissue or cells exposed to the cardiotoxins described herein. The comparison of the expression data, as well as available sequence or other information may be done by a researcher or diagnostician or may be done with the aid of a computer and databases.

Use of the Toxicity Markers for Drug Screening

[0088] According to the present invention, the genes identified in Tables 1-5LL may be used as markers or drug targets to evaluate the effects of a candidate drug, chemical compound or other agent on a cell or tissue sample. The genes may also be used as drug targets to screen for agents that modulate their expression and/or activity. In various formats, a candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of a drug's effects by looking at the number of markers which the drug induces and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs may indicate a similarity of effects.

[0089] Assays to monitor the expression of a marker or markers as defined in Tables 1-5LL may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

[0090] In one assay format, gene chips containing probes to one, two or more genes from Tables 1-5LL may be used to directly monitor or detect changes in gene expression in the treated or exposed cell. Cell lines, tissues or other samples are first exposed to a test agent

and in some instances, a known toxin, and the detected expression levels of one or more, or preferably 2 or more of the genes of Tables 1-5LL are compared to the expression levels of those same genes exposed to a known toxin alone. Compounds that modulate the expression patterns of the known toxin(s) would be expected to modulate potential toxic physiological effects *in vivo*. The genes in Tables 1-5LL are particularly appropriate markers in these assays as they are differentially expressed in cells upon exposure to a known cardiotoxin. Tables 1 and 2 disclose those genes that are differentially expressed upon exposure to the named toxins and their corresponding GenBank Accession numbers. Table 3 discloses the human homologues and the corresponding GenBank Accession numbers of the differentially expressed genes of Tables 1 and 2.

[0091] In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the transcriptional regulatory regions of a gene in Tables 1-5LL and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenical acetyltransferase (Alam et al. (1990), Anal Biochem 188: 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

[0092] Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 5-5LL. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time, and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). [0093] In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cells and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (e.g., a plasmid or viral vector) construct comprising an operable non-translated 5'-

promoter containing end of the structural gene encoding the gene products of Tables 1-5LL fused to one or more antigenic fragments or other detectable markers, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct or other detectable tag. Such a process is well known in the art (see Sambrook *et al.*, *supra*).

[0094] Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells are disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (e.g., ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agentcontacted" sample is then compared with the control samples (no exposure and exposure to a known toxin) where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control is used to distinguish the effectiveness and/or toxic effects of the agent.

Use of Toxicity Markers to Identify Agents that Modulate Protein Activity or Levels [0095] Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables 1-5LL. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

[0096] In one format, the relative amounts of a protein (Tables 1-5LL) between a cell population that has been exposed to the agent to be tested compared to an unexposed control cell population and a cell population exposed to a known toxin may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are

exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

[0097] Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

[0098] As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

[0099] The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see G.A. Grant in: Molecular Biology and Biotechnology, Meyers, ed., pp. 659-664, VCH Publishers, New York, 1995). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

## Nucleic Acid Assay Formats

[00100] As previously discussed, the genes identified as being differentially expressed upon exposure to a known cardiotoxin (Tables 1-5LL) may be used in a variety of nucleic acid detection assays to detect or quantify the expression level of a gene or multiple genes in a given sample. The genes described in Tables 1-5LL may also be used in combination with one or more additional genes whose differential expression is associate with toxicity in a cell or tissue. In preferred embodiments, the genes in Tables 5-5LL may be combined

with one or more of the genes described in prior and related applications 60/303,819 filed on July 10, 2001; 60/305,623 filed on July 17, 2001; 60/369,351 filed on April 3, 2002; and 60/377,611 filed on May 6, 2002; 09/917,800; 10/060,087; 10/152,319; 10/191,803, and 10/301,856, all of which are incorporated by reference.

[00101] Any assay format to detect gene expression may be used. For example, traditional Northern blotting, dot or slot blot, nuclease protection, primer directed amplification, RT- PCR, semi- or quantitative PCR, branched-chain DNA and differential display methods may be used for detecting gene expression levels. Those methods are useful for some embodiments of the invention. In cases where smaller numbers of genes are detected, amplification based assays may be most efficient. Methods and assays of the invention, however, may be most efficiently designed with hybridization-based methods for detecting the expression of a large number of genes.

[00102] Any hybridization assay format may be used, including solution-based and solid support-based assay formats. Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, particles, beads, microparticles or silicon or glass based chips, etc. Such chips, wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755).

[00103] Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000, 400,000 or 1,000,000 or more of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of about a square centimeter. Probes corresponding to the genes of Tables 5-5LL or from the related applications described above may be attached to single or multiple solid support structures, e.g., the probes may be attached to a single chip or to multiple chips to comprise a chip set.

[00104] Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart et al. (1996), Nat Biotechnol 14: 1675-1680; McGall et al. (1996), Proc Nat Acad Sci USA 93: 13555-

13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described in Tables 5-5LL. For instance, such arrays may contain oligonucleotides that are complementary to or hybridize to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70, 100 or more of the genes described herein. Preferred arrays contain all or nearly all of the genes listed in Tables 1-5LL, or individually, the gene sets of Tables 5-5LL. In a preferred embodiment, arrays are constructed that contain oligonucleotides to detect all or nearly all of the genes in any one of or all of Tables 1-5LL on a single solid support substrate, such as a chip. [00105] The sequences of the expression marker genes of Tables 1-5LL are in the public databases. Table 1 provides the GenBank Accession Number for each of the sequences (see www.ncbi.nlm.nih.gov/) as well as a corresponding SEQ ID NO. in the sequence listing filed with this application. Table 3 provides the LocusLink and Unigene names and descriptions for the human homologues of the genes described in Tables 1 and 2. The sequences of the genes in GenBank and/or RefSeq are expressly herein incorporated by reference in their entirety as of the filing date of this application, as are related sequences, for instance, sequences from the same gene of different lengths, variant sequences, polymorphic sequences, genomic sequences of the genes and related sequences from different species, including the human counterparts, where appropriate (see Table 3). These sequences may be used in the methods of the invention or may be used to produce the probes and arrays of the invention. In some embodiments, the genes in Tables 1-5LL that correspond to the genes or fragments previously associated with a toxic response may be excluded from the Tables.

[00106] As described above, in addition to the sequences of the GenBank Accession Numbers disclosed in the Tables 1-5LL, sequences such as naturally occurring variants or polymorphic sequences may be used in the methods and compositions of the invention. For instance, expression levels of various allelic or homologous forms of a gene disclosed in Tables 1-5LL may be assayed. Any and all nucleotide variations that do not significantly alter the functional activity of a gene listed in the Tables 1-5LL, including all naturally occurring allelic variants of the genes herein disclosed, may be used in the methods and to make the compositions (e.g., arrays) of the invention.

[00] 107! Probes based on the sequences of the genes described above may be prepared by any commonly available method. Oligonucleotide probes for screening or assaying a ceii sample are preferably of sufficient length to specifically hybridize only to

appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least about 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases, longer probes of at least 30, 40, or 50 nucleotides will be desirable.

[00108] As used herein, oligonucleotide sequences that are complementary to one or more of the genes described in Tables 1-5LL refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequences of said genes, their encoded RNA or mRNA, or amplified versions of the RNA such as cRNA. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes. [00109] "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

[00110] The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (e.g., the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (e.g. probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

[00111] The phrase "hybridizing specifically to" or "specifically hybridizes" refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA.

[00112] Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 100,000 or 1,000,000 or more different nucleic acid hybridizations.

[00113] As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

[00114] The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

[00115] The terms "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

[90116] While the mismatch(es) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

[00117] The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH.

[00118] Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M Na<sup>+</sup> ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

[00119] The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (e.g. nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

#### Probe design

[00120] One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of test probes that specifically hybridize to the sequences of interest. Probes may be produced from any region of the genes identified in the Tables and the attached representative sequence listing. In instances where the gene reference in the Tables is an EST, probes may be designed from that sequence or from other regions of the corresponding full-length transcript that may be available in any of the sequence databases, such as those herein described. See WO 99/32660 for methods of producing

probes for a given gene or genes. In addition, any available software may be used to produce specific probe sequences, including, for instance, software available from Molecular Biology Insights, Olympus Optical Co. and Biosoft International. In a preferred embodiment, the array will also include one or more control probes.

[00121] High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500, or about 7 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 35 nucleotides in length. In other particularly preferred embodiments, the probes are 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences such as cDNA fragments. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using native nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

[00122] In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes may fall into three categories referred to herein as 1) normalization controls; 2) expression level controls; and 3) mismatch controls.

[00123] Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (e.g., fluorescence intensity) read from all other probes in the array are divided by the signal (e.g., fluorescence intensity) from the control probes thereby normalizing the measurements.

[00124] Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of

the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (i.e., no secondary structure) and do not match any target-specific probes.

[00125] Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typically expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

[00126] Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (e.g., stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a 20 mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (e.g., substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

[00127] Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation, for instance, a mutation of a gene in the accompanying Tables 1-5LL. The difference in intensity between the perfect match and the mismatch probe provides a good measure of the concentration of the hybridized material.

### Nucleic Acid Samples

[00128] Cell or tissue samples may be exposed to the test agent in vitro or in vivo. When cultured cells or tissues are used, appropriate mammalian cell extracts, such as liver cell

extracts, may also be added with the test agent to evaluate agents that may require biotransformation to exhibit toxicity.

[00129] The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may or may not be cloned. The genes may or may not be amplified and cRNA produced. The cloning and/or amplification do not appear to bias the representation of genes within a population. In some assays, it may be preferable, however, to use polyA+ RNA as a source, as it can be used with less processing steps.

[00130] As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24, Hybridization With Nucleic Acid Probes: Theory and Nucleic Acid Probes, P. Tijssen, Ed., Elsevier Press, New York, 1993. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and RNA transcribed from the amplified DNA (cRNA). One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates are used.

[00131] Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a tissue or cell sample that has been exposed to a compound, agent, drug, pharmaceutical composition, potential environmental pollutant or other composition. In some formats, the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom. Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

# Forming High Density Arrays

[00132] Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a single or on multiple solid substrates by a variety of methods, including,

but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung, U.S. Patent No. 5,143,854).

[00133] In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, e.g., a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

[00134] In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in PCT Publication Nos. WO 93/09668 and WO 01/23614. High density nucleic acid arrays can also be fabricated by depositing pre-made or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

# Hybridization

[00135] Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO 99/32660. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (e.g., low temperature and or high salt) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower

stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. [00136] In a preferred embodiment, hybridization is performed at low stringency, in this case in 6x SSPET at 37°C (0.005% Triton X-100), to ensure hybridization and then subsequent washes are performed at higher stringency (e.g., 1x SSPET at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (e.g., down to as low as 0.25x SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (e.g., expression level control, normalization control, mismatch controls, etc.).

[00137] In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

# , Signal Detection

[00138] The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. See WO 99/32660.

#### **Databases**

[00139] The present invention includes relational databases, such as the Gene Logic ToxExpress® database, containing sequence information, for instance, for the genes of Tables 1-5LL, as well as gene expression information from tissue or cells exposed to various standard toxins, such as those herein described (see Tables 5-5LL). Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information (see

Tables 1 and 2), or descriptive information concerning the clinical status of the tissue sample, or the animal from which the sample was derived. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases and computer-readable media to which such databases are saved are widely available, for instance, see U.S. Patent No. 5,953,727, which is herein incorporated by reference in its entirety.

[00140] The databases of the invention may be linked to an outside or external database such as GenBank (www.ncbi.nlm.nih.gov/entrez.index.html); KEGG (www.genome.ad.jp/kegg); SPAD (www.grt.kyushu-u.ac.jp/spad/index.html); HUGO (www.gene.ucl.ac.uk/hugo); Swiss-Prot (www.expasy.ch.sprot); Prosite (www.expasy.ch/tools/scnpsit1.html); OMIM (www.ncbi.nlm.nih.gov/omim); and GDB (www.gdb.org). In a preferred embodiment, as described in Tables 1-3, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI) (www.ncbi.nlm.nih.gov).

[00141] Any appropriate computer platform, user interface, etc. may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or information provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such has those available from Silicon Graphics. Client/server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

[00142] The databases of the invention may be used to produce, among other things, ToxScreen<sup>™</sup> reports and electronic Northerns (E-NORTHERN<sup>™</sup>, Gene Logic, Inc., Gaithersburg, MD) that allow the user to determine the cell type or tissue in which a given gene is expressed or allow determination of the abundance or expression level of a given gene in a particular tissue or cell, for instance, a cell or tissue sample exposed to a test compound.

[00143] The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising one or more of the genes in Tables 5-5LL, comprising the step of comparing the expression level of at least one gene in Tables 5-5LL in a cell or tissue exposed to a test agent to the level of expression of the gene in the database. Such methods may be used to predict the toxic potential of a given compound by comparing the level of expression of a gene or genes in

Tables 5-5LL from a tissue or cell sample exposed to the test agent to the expression levels found in a control tissue or cell samples exposed to a standard toxin or cardiotoxin such as those herein described. Such methods may also be used in the drug or agent screening assays as described herein.

#### Kits

[00144] The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, protein reagents encoded by the genes of the Tables, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to predict or model the toxic response of a test compound, to monitor the progression of heart disease states, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed above.

[00145] The databases packaged with the kits are a compilation of expression patterns from human or laboratory animal genes and gene fragments (corresponding to the genes of Tables 1-5LL). In particular, the database software and packaged information that may contain the databases saved to a computer-readable medium include the expression results of Tables 1-5LL that can be used to predict toxicity of a test agent by comparing the expression levels of the genes of Tables 1-5LL induced by the test agent to the expression levels presented in Tables 5-5LL. In another format, database and software information may be provided in a remote electronic format, such as a website, the address of which may be packaged in the kit.

[00146] Databases and software designed for use with microarrays is discussed in PCT/US99/20449, filed September 8, 1999, Genomic Knowledge Discovery, PCT/IB00/00863, filed June 28, 2000, Biological Data Processing, and in Balaban et al., U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed tables, collected from small or large numbers of microarrays, and 6,185,561, a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee et al., U.S. Patent No. 5,974,164, disclose a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences.

[00147] The kits may be used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

[00148] Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

#### **EXAMPLES**

# **EXAMPLE 1: IDENTIFICATION OF TOXICITY MARKERS**

[00149] The cardiotoxins adriamycin, amphotericin B, epirubicin, phenylpropanolamine, and rosiglitazone were administered to male Sprague-Dawley rats at various time points using administration diluents, protocols, and dosing regimes as indicated in Table 6. The cardiotoxins and control compositions, including cyclophosphamide, ifosfamide, minoxidil, hydralazine, BI-QT, clenbuterol, isoproterenol, norepinephrine, and epinephrine were administered to male Sprague-Dawley rats at various time points using administration diluents, protocols and dosing regimes as previously described in the art and previously described in the priority applications discussed above. The low and high dose level for each compound are provided in the chart below.

Heart Toxin	Low Dose (mg/kg)	High Dose (mg/kg)
Cyclophosphamide	20	200
Ifosfamide	5	100
Minoxidil	12 mg/L	120 mg/L
Hydralazine	2.5	25
BI-QT	10	50
Clenbuterol	0.4	4
Isoproterenol	0.05	0.5
Norepinephrine	0.05	0.5
Epinephrine	0.1	1

Heart Toxin	Low Dose (mg/kg)	High Dose (mg/kg)
Adriamycin	1.3	12.8
Amphotericin B	0.25	2.5
Epirubicin	1.2	12
Phenylpropanolamine	6.4	64
Rosiglitazone	18	180

[00150] After administration, the dosed animals were observed and tissues were collected as described below:

## **Observation of Animals**

[00151] 1. Clinical Observations- Twice daily: mortality and moribundity check. Cage Side Observations - skin and fur, eyes and mucous membrane, respiratory system, circulatory system, autonomic and central nervous system, somatomotor pattern, and behavior pattern. Potential signs of toxicity, including tremors, convulsions, salivation, diarrhea, lethargy, coma or other atypical behavior or appearance, were recorded as they occurred and included a time of onset, degree, and duration.

[00152] 2. Physical Examinations- Prior to randomization, prior to initial treatment, and prior to sacrifice.

[00153] 3. Body Weights- Prior to randomization, prior to initial treatment, and prior to sacrifice.

### Clinical Pathology

[00154] 1. Frequency

Prior to necropsy.

[00155] 2. Number of animals

All surviving animals.

[00156] 3. Bleeding Procedure

Blood was obtained by puncture of the orbital

sinus while under 70% CO<sub>2</sub>/ 30% O<sub>2</sub> anesthesia.

[00157] 4. Collection of Blood Samples Approximately 0.5 mL of blood was collected into EDTA tubes for evaluation of hematology parameters. Approximately 1 mL of blood was collected into serum separator tubes for clinical chemistry analysis.

Approximately 200 µL of plasma was obtained and frozen at ~-80°C for test compound/metabolite estimation. An additional ~2 mL of blood was collected into a 15 mL conical polypropylene vial to which ~3 mL of Trizol was immediately added. The contents were immediately mixed with a vortex and by repeated inversion. The tubes were frozen in liquid nitrogen and stored at ~-80°C.

### iermination Procedures

### Terminal Sacrifice

[00158] At the sampling times indicated in Tables 5A-5LL and Table 6 for each cardiotoxin, and as previously described in the related applications mentioned above, rats were weighed, physically examined, sacrificed by decapitation, and exsanguinated. The animals were necropsied within approximately five minutes of sacrifice. Separate sterile, disposable instruments were used for each animal, with the exception of bone cutters, which were used to open the skull cap. The bone cutters were dipped in disinfectant solution between animals.

[00159] Necropsies were conducted on each animal following procedures approved by board-certified pathologists.

[00160] Animals not surviving until terminal sacrifice were discarded without necropsy (following euthanasia by carbon dioxide asphyxiation, if moribund). The approximate time of death for moribund or found dead animals was recorded.

# Postmortem Procedures

[00161] Fresh and sterile disposable instruments were used to collect tissues. Gloves were worn at all times when handling tissues or vials. All tissues were collected and frozen within approximately 5 minutes of the animal's death. The liver sections and kidneys were frozen within approximately 3-5 minutes of the animal's death. The time of euthanasia, an interim time point at freezing of liver sections and kidneys, and time at completion of necropsy were recorded. Tissues were stored at approximately -80°C or preserved in 10% neutral buffered formalin.

# Tissue Collection and Processing

#### [00162] Liver-

- 1. Right medial lobe snap frozen in liquid nitrogen and stored at ~-80°C.
- 2. Left medial lobe Preserved in 10% neutral-buffered formalin (NBF) and evaluated for gross and microscopic pathology.
- 3. Left lateral lobe snap frozen in liquid nitrogen and stored at ~-80°C.

### [00163] Heart-

A sagittal cross-section containing portions of the two atria and of the two ventricles was preserved in 10% NBF. The remaining heart was frozen in liquid nitrogen and stored at  $\sim$  -80°C.

[00164] Kidneys (both)-

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1. Left – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at  $\sim$  -80°C.

2. Right – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at  $\sim$  -80°C.

[00165] Testes (both)-

A sagittal cross-section of each testis was preserved in 10% NBF. The remaining testes were frozen together in liquid nitrogen and stored at  $\sim$ -80°C.

[00166] Brain (whole)-

A cross-section of the cerebral hemispheres and of the diencephalon was preserved in 10% NBF, and the rest of the brain was frozen in liquid nitrogen and stored at ~ -80°C. [00167] Microarray sample preparation was conducted with minor modifications, following the protocols set forth in the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was ground to a powder using a Spex Certiprep 6800 Freezer Mill. Total RNA was extracted with Trizol (GibcoBRL) utilizing the manufacturer's protocol. The total RNA yield for each sample was 200-500 μg per 300 mg tissue weight. mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen) followed by ethanol precipitation. Double stranded cDNA was generated from mRNA using the SuperScript Choice system (GibcoBRL). First strand cDNA synthesis was primed with a T7-(dT24) oligonucleotide. The cDNA was phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 μg/ml. From 2 μg of cDNA, cRNA was synthesized using Ambion's T7 MegaScript in vitro Transcription Kit.

[00168] To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. Following a 37°C incubation for six hours, impurities were removed from the labeled cRNA following the RNeasy Mini kit protocol (Qiagen). cRNA was fragmented (fragmentation buffer consisting of 200 mM Trisacetate, pH 8.1, 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C. Following the Affymetrix protocol, 55 µg of fragmented cRNA was hybridized on the Affymetrix rat array set for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratorics) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Data was analyzed using Affymetrix GeneChip®

version 2.0 and Expression Data Mining (EDMT) software (version 1.0), Gene Logic's GeneExpress® 2000 software and S-Plus™ software.

[00169] Tables 1 and 2 disclose those genes that are differentially expressed upon exposure to the named toxins and their corresponding GenBank Accession and Sequence Identification numbers, the identities of the metabolic pathways in which the genes function, the gene names if known, and the Unigene Cluster titles. The human homologues of the rat genes in Tables 1 and 2 are indicated in Table 3. The model codes in Tables 1-3 represent the various toxicity or heart pathology states that differential expression of each gene is able to identify, as well as the individual toxin or toxin type associated with differential expression of each gene. The model codes are defined in Table 4. The GLGC ID is the internal Gene Logic identification number.

[00170] Tables 5A-5LL disclose a set of genes, along with the summary statistics for each of the comparisons performed as indicated in these tables, *i.e.*, expression levels of a particular gene in toxicity group samples compared to non-toxicity group samples in response to exposure to a particular toxin, or as measured in a particular disease state. Each of these tables contains a set of predictive genes and creates a model for predicting the cardiotoxicity of an unknown, *i.e.*, untested compound. Each gene is identified by its Gene Logic identification number and can be cross-referenced to a gene name and representative sequence identification number in Tables 1 and 2 or in one or more related applications, as mentioned on page 1.

[00171] For each comparison of gene expression levels between samples in the toxicity group (samples affected by exposure to a specific toxin) and samples in the non-toxicity group (samples not affected by exposure to that same specific toxin), the tox mean (for toxicity group samples) is the mean signal intensity, as normalized for the various chip parameters that are being assayed. The non-tox mean represents the mean signal intensity, as normalized for the various chip parameters that are being assayed, in samples from animals other than those treated with the high dose of the specific toxin. These animals were treated with a low dose of the specific toxin, or with vehicle alone, or with a different toxin. Samples in the toxicity groups were obtained from animals sacrificed at the time point(s) indicated in the Table 5-5LL headings, while samples in the non-toxicity groups were obtained from animals sacrificed at all time points in the experiments. For individual genes, an increase in the tox mean compared to the non-tox mean indicates up-regulation

upon exposure to a toxin. Conversely, a decrease in the tox mean compared to the non-tox mean indicates down-regulation.

[00172] The mean values are derived from Average Difference (AveDiff) values for a particular gene, averaged across the corresponding samples. Each individual Average Difference value is calculated by integrating the intensity information from multiple probe pairs that are tiled for a particular fragment. The normalization multiplies each expression intensity for a given experiment (chip) by a global scaling factor. The intent of this normalization is to make comparisons of individual genes between chips possible. The scaling factor is calculated as follows:

[00173] 1. From all the unnormalized expression values in the experiment, delete the largest 2% and smallest 2% of the values. That is, if the experiment yields 10,000 expression values, order the values and delete the smallest 200 and largest 200.

[00174] 2. Compute the trimmed mean, which is equal to the mean of the remaining values.

[00175] 3. Compute the scale factor SF = 100/(trimmed mean)

[00176] Values greater than 2.0\* SD noise are assumed to come from expressers. For these values, the standard deviation SD log (signal) of the logarithms is calculated. The logarithms are then multiplied by a scale factor proportional to 1/SD log (signal) and exponentiated. The resulting values are then multiplied by another scale factor, chosen so there will be no discontinuity in the normalized values from unscaled values on either side of 2.0\* SD noise. Some AveDiff values may be negative due to the general noise involved in nucleic acid hybridization experiments. Although many conclusions can be made corresponding to a negative value on the GeneChip platform, it is difficult to assess the meaning behind the negative value for individual fragments. Our observations show that, although negative values are observed at times within the predictive gene set, these values reflect a real biological phenomenon that is highly reproducible across all the samples from which the measurement was taken. For this reason, those genes that exhibit a negative value are included in the predictive set. It should be noted that other platforms of gene expression measurement may be able to resolve the negative numbers for the corresponding genes. The predictive ability of each of those genes should extend across platforms, however. Each mean value is accompanied by the standard deviation for the mean. The linear discriminant analysis score (discriminant score, or LDA), as disclosed in

the tables, measures the ability of each gene to predict whether or not a sample is toxic. The discriminant score is calculated by the following steps:

Calculation of a discriminant score

[00177] Let  $X_i$  represent the AveDiff values for a given gene across the non-tox samples, i=1...n.

[00178] Let  $Y_i$  represent the AveDiff values for a given gene across the tox samples, i=1...t.

[00179] The calculations proceed as follows:

[00180] 1. Calculate mean and standard deviation for  $X_i$ 's and  $Y_i$ 's, and denote these by  $m_X$ ,  $m_Y$ ,  $s_X$ ,  $s_Y$ .

[00181] 2. For all  $X_i$ 's and  $Y_i$ 's, evaluate the function  $f(z) = ((1/s_Y)*exp(-0.5*((z-m_Y)/s_Y)^2)) / (((1/s_Y)*exp(-0.5*((z-m_Y)/s_Y)^2)) + ((1/s_X)*exp(-0.5*((z-m_X)/s_X)^2))).$ 

[00182] 3. The number of correct predictions, say P, is then the number of  $Y_i$ 's such that  $f(Y_i) > .5$  plus the number of  $X_i$ 's such that  $f(X_i) < 0.5$ .

[00183] 4. The discriminant score is then P/(n+t).

[00184] Linear discriminant analysis uses both the individual measurements of each gene and the calculated measurements of all combinations of genes to classify samples. For each gene a weight is derived from the mean and standard deviation of the toxic and nontox groups. Every gene is multiplied by a weight and the sum of these values results in a collective discriminate score. This discriminant score is then compared against collective centroids of the tox and nontox groups. These centroids are the average of all tox and nontox samples respectively. Therefore, each gene contributes to the overall prediction. This contribution is dependent on weights that are large positive or negative numbers if the relative distances between the tox and nontox samples for that gene are large and small numbers if the relative distances are small. The discriminant score for each unknown sample and centroid values can be used to calculate a probability between zero and one as to the group in which the unknown sample belongs.

## **EXAMPLE 2: GENERAL TOXICITY MODELING**

[00185] Samples were selected for grouping into tox-responding and non-tox-responding groups by examining each study individually with Principal Components Analysis (PCA) to determine which treatments had an observable response. Only groups where confidence

of their tox-responding and non-tox-responding status was established were included in building a general tox model (Tables 5A-5LL).

[00186] Linear discriminant models were generated to describe toxic and non-toxic samples. The top discriminant genes and/or EST's were used to determine toxicity by calculating each gene's contribution with homo and heteroscedastic treatment of variance and inclusion or exclusion of mutual information between genes. Prediction of samples within the database exceeded 80% true positives with a false positive rate of less than 5%. It was determined that combinations of genes and/or EST's generally provided a better predictive ability than individual genes and that the more genes and/or EST used the better predictive ability. Although the preferred embodiment includes fifty or more genes, many pairings or greater combinations of genes and/or EST can work better than individual genes. All combinations of two or more genes from the selected list (Tables 5A-5LL) could be used to predict toxicity. These combinations could be selected by pairing in an agglomerate, divisive, or random approach. Further, as yet undetermined genes and/or EST's could be combined with individual or combination of genes and/or EST's described here to increase predictive ability. However, the genes and/or EST's described here would contribute most of the predictive ability of any such undetermined combinations. [00187] Other variations on the above method can provide adequate predictive ability. These include selective inclusion of components via agglomerate, divisive, or random approaches or extraction of loading and combining them in agglomerate, divisive, or random approaches. Also the use of composite variables in logistic regression to determine classification of samples can also be accomplished with linear discriminate analysis, neural or Bayesian networks, or other forms of regression and classification based on categorical or continual dependent and independent variables.

## **EXAMPLE 3: MODELING WITH CORE GENE SET**

[00188] As described in Examples 1 and 2, above, the data collected from microarray hybridization experiments were analyzed by LDA and by PCA. The genes in Tables 5G, 5I, 5K, 5M, 5O, 5Q, 5T, 5V, 5X, 5Z, 5BB, 5DD, 5FF, and 5KK constitute a core set of markers for predicting the cardiotoxicity of a compound, whereas the genes in Tables 5H, 5J, 5L, 5N, 5P, 5S, 5U, 5W, 5Y, 5AA, 5CC and 5EE constitute an alternative set of markers. The core marker tables comprise genes that are also found in PCT Application CT/US02/21735, whereas the alternate marker tables do not comprise genes also found in the '735 application. Each gene fragment in Tables 1-5LL is assigned an LDA

score, and those gene fragments in the core set are those with the highest LDA scores. The gene fragments in Tables 5A-5LL were determined to give greater than 80% true positive results and less than 5% false positive results. Gene expression profiles prepared or obtained from expression data for these genes, in the presence and absence of toxin treatment, can be used a controls in assays of compounds whose toxic properties have not been examined. Comparison of data from test compound-exposed and test compound-unexposed animals with the data in Tables 5A-5LL allows the prediction of toxic effects-or no toxic effects- upon exposure to the test compound. Thus, the marker gene sets can be used to examine the biological effects of a compound whose toxic properties following exposure are not known and to predict the toxicity in cardiac tissue of this compound.

## **EXAMPLE 4: MODELING METHODS**

[00189] The above modeling methods provide broad approaches of combining the expression of genes to predict sample toxicity. One could also provide no weight in a simple voting method or determine weights in a supervised or unsupervised method using agglomerate, divisive, or random approaches. All or selected combinations of genes may be combined in ordered, agglomerate, or divisive, supervised or unsupervised clustering algorithms with unknown samples for classification. Any form of correlation matrix may also be used to classify unknown samples. The spread of the group distribution and discriminate score alone provide enough information to enable a skilled person to generate all of the above types of models with accuracy that can exceed discriminate ability of individual genes. Some examples of methods that could be used individually or in combination after transformation of data types include but are not limited to: Discriminant Analysis, Multiple Discriminant Analysis, robust multi-array average (RMA) analysis, partial least squares (PLS) analysis, logistic regression, multiple regression analysis, linear regression analysis, conjoint analysis, canonical correlation, hierarchical cluster analysis, k-means cluster analysis, self-organizing maps, multidimensional scaling, structural equation modeling, support vector machine determined boundaries, factor analysis, neural networks, bayesian classifications, and resampling methods.

## **EXAMPLE 5: INDIVIDUAL COMPOUND MARKERS**

[00190] Samples were grouped into individual pathology classes based on known toxicological responses and observed clinical chemical and pathology measurements or into early and late phases of observable toxicity within a compound (Tables 1-5LL). The

top 10, 25, 50, 100 genes based on individual discriminate scores were used in a model to ensure that combination of genes provided a better prediction than individual genes. As described above, all combinations of two or more genes from this list could potentially provide better prediction than individual genes when selected in any order or by ordered, agglomerate, divisive, or random approaches. In addition, combining these genes with other genes could provide better predictive ability, but most of this predictive ability would come from the genes listed herein.

[00191] Samples may be considered toxic if they score positive in any individual compound represented here or in any modeling method mentioned under general toxicology models based on combination of individual time and dose grouping of individual toxic compounds obtainable from the data. Most logical groupings with one or more genes and one or more sample dose and time points should produce better predictions of general toxicity or similarity to known toxicant than individual genes.

[00192] Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, patent applications and publications referred to in this application are herein incorporated by reference in their entirety.

ABLE	1 &	GonPank A		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Atty. Ref. 44921-5090-01-WO/2105485
EO ID	GIGO	GenBank Ad D No.	XC,	AND LOCAL DESIGNATION OF THE PARTY OF THE PA	and the second of the second o
	GEGU	DINO.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
13	2512	20 A03913	f		
					ESTs, Highly similar to splicing factor 3b, subunit
14		7 AA012709	b		155 kDa [Mus musculus] [M.musculus]
15		8 AA108277	е		The state of the second st
16	2510	3 AA685876	cc,dd		
	1				ESTs, Weakly similar to HS9B_RAT Heat shock
17		4 AA685903	d,e,r		protein HSP 00 bots (USP 04) IP
18	1458	0 AA686870	jj,kk		protein HSP 90-beta (HSP 84) [R.norvegicus] ESTs
					ESTs, Highly similar to mitochondrial carrier
19		2 AA799279	f,g		homolog 2 (Mus museulus) 714
20	1827	2 AA799294	e		homolog 2 [Mus musculus] [M.musculus] ESTs
					ECTs Diable significate LOA
21		6 AA799301	d		ESTs, Highly similar to LIGA_MOUSE Ligatin
22	2199	7 AA799325	jj,kk		[M.musculus]
					ESTs
		1			ESTs, Weakly similar to T47122 cell division prote
23	1839	6 AA799330	a,p,q,y		pelota [imported] - fruit fly (Drosophila
24	1508	2 AA799396	p,q		melanogaster) [D.melanogaster]
24	1508	3 AA799396			ESTs
25		4 AA799397	b,p,q		ESTs
		170 (1 0 0 0 0 0 1	b,I,m		ESTs
26	658	1 AA799412			ESTs, Weakly similar to 167424 hERR-2 homolog -
27		AA799420	е		rat (fragment) [R.norvegicus]
28	20042	AA799423	h,l		ESTs
- 20	2002	AA199423	11	nexilin	nexilin
		}			ESTs, Weakly similar to S68418 protein
20	4740				phosphatase 1M chain M110 isoform - rat
29 30	1/13/	AA799438	ee,ff,jj,kk		(fragment) [R.norvegicus]
		AA799442	cc,dd,gg		ESTs
31	18160	AA799448	е		ESTs
اء					ESTs, Highly similar to TELT_MOUSE Telethonin
32	18706	AA799471	d		(Titin cap protein) [M.musculus]
					(Visit out proton) (Williascalas)
					ESTs, Moderately similar to AD16_HUMAN Protein
33	23294	AA799472	b		AD-016 (Protein CGI-116) (x0009) [H.sapiens]
34	11350	AA799488	cc,dd,ll		ESTs (Fisterin GGF110) (x0009) [H.sapiens]
					ESTs Highly similar to TAGEOD hamathattal
35	8289	AA799494	е		ESTs, Highly similar to T46500 hypothetical protein
36	18290	AA799497	hh		DKFZp434D098.1 - human (fragment) [H.sapiens]
37	17612	AA799511	ln j		ESTs, Weakly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
		-			FSTs Highly similar to hundthall the
					ESTs, Highly similar to hypothetical protein
38	15303	AA799518	w,x		FLJ13725; KIAA1930 protein [Homo sapiens] [H.sapiens]
					[i ::>apiciis]
					ECTo Lilebhaniania a servici
39	16942	AA799520	e		ESTs, Highly similar to ITMB_MOUSE Integral
			<del></del>		membrane protein 2B (E25B protein) [M.musculus]
40	21120	AA799526	p,q,gg		ESTS, Highly similar to RIKEN cDNA 1700043F15
			FIMIBA		[Mus musculus] [M.musculus]
41	17687	AA799531	ام	ļ	ESTs, Weakly similar to M18.3.p [Caenorhabditis
		55001	9		elegans] [C.elegans]
41	17688	AA799531	160	i	ESTs, Weakly similar to M18.3.p [Caenorhabditis
	.,,000	V11 00001	f,g		elegans] [C.elegans]
			į į		ESTs, Highly similar to SFR2_MOUSE Splicing
1	ĺ		ĺ	İ	lactor, arginine/serine-rich 2 (Splicing factor 5035)
			s Ì	]	(00 00) (0 (1)
42	15500	A799538	s,t		(SC-35) (Splicing component, 35 kDa) (PR264

	1	GenBank A	00:1	and the second of the second o	Atty. Ref. 44921-5090-01-WO/2105485
יום:	Gieci	D No.			A Committee of the Comm
ا جاء عاد	GLGC	ייסוועס.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
	j				ESTs, Weakly similar to KEAP_RAT Kelch-like EC
				1	associated protein 1 (Cutes alia t. V.)
43	1759	9 AA799539	c		associated protein 1 (Cytosolic inhibitor of Nrf2) (INrf2) [R.norvegicus]
44	2462	8 AA799542	ii —		ESTs ESTs
45	1135	3 AA799569	d		
			<del>-  </del>	<del>-  </del>	ESTs
46	1721	2 AA799571	in in		
		-100071			Rattus norvegicus mRNA for ribosomal protein L3
	[	ļ			
47	2007	1 AA799576			ESTs, Highly similar to T46259 hypothetical protei
48		2 AA799580	C		DKFZp761E0323.1 - human (fragment) [H.sapiens
49		2 AA799580 2 AA799598	r,jj,kk		ESTs ( ESTs
50			f,g		ESTs
50	2097	AA799599	cc,dd		ESTs
_,		.1			ESTs, Highly similar to hypothetical protein
51		AA799600	ii		DKFZn586l021 (Homo porters) (U.
52		AA799601			DKFZp586l021 [Homo sapiens] [H.sapiens] ESTs
53	1669	AA799607	h,i		ESTS
54	17380	AA799612	W,X	ubiquitin conjugating as-	
			117,1	ubiquitin conjugating enzyme	ubiquitin conjugating enzyme
- 1			1		ESTs, Moderately similar to sirtuin 2 (silent mating
55	18333	AA799614	1_		type information regulation 2, homolog) 2 (S
- 33	10000	AA799014	е		(Cerevisiae) [Raffus norvegicus] (R norvegicus)
50	00000		1.		ESTs, Moderately similar to hypothetical protein
56	20980	AA799633	l,m		MGC13016 [Homo sapiens] [H.sapiens]
57	20981	AA799636	у		ESTs [Figure Sapiens]
1					2010
- 1		ĺ			ECTo Monthly to the American
58	20092	AA799637	r,il		ESTs, Weakly similar to A55071 hydrogen peroxide
					inducible protein hic-5 - mouse [M.musculus]
59	18226	AA799641	li .	1	ESTS, Moderately similar to 153063 testicular tumor
		70 17 000 71	- <del> </del> '		overexpressed protein - mouse IM musculus
		1	ŀ	ł	ESTS, Weakly similar to \$68418 protein
60	20002	A A 700057		1	phosphatase 1M chain M110 isoform - rat
- 60	20962	AA799657	d,e,ii	<u>                                     </u>	(fragment) [R.norvegicus]
04	4====				ESTs, Highly similar to S37488 gene T10 protein -
61	1/759	AA799663	c,hh		mouse [M.musculus]
H					FSTs Highly similar to 027400
61	<u> 17</u> 760	AA799663	lc	ł	ESTs, Highly similar to S37488 gene T10 protein -
			<u> </u>		mouse [M.musculus]
					ESTs, Highly similar to RPB9_HUMAN DNA-
62	20994	AA799717	cc,dd		directed RNA polymerase II 14.5 kDa polypeptide
<del></del>  -		0 (7 007 17	100,00		(RPB9) (RPB14.5) [H.sapiens]
1	1			Phosphodiactoraco AD AAAD	
				Phosphodiesterase 4B, cAMP-	ESTs, Phosphodiesterase 4B, cAMP-specific
00	440=0			specific (dunce (Drosophila)-	ESTs, Phosphodiesterase 4B, cAMP-specific
63	14250	AA799729	j,k	specific (dunce (Drosophila)-	(dunce (Drosophila)-homolog phosphodicateses
64	18061	AA799735	j,k r	specific (dunce (Drosophila)- homolog phosphodiesterase E4)	(dunce (Drosophila)-homolog phosphodiesterase E4)
64 65	18061	AA799729 AA799735 AA799744	Γ	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1
64	18061 18349	AA799735 AA799744	r j,p,q,y,z	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1 ESTs
64 65	18061 18349	AA799735	Γ	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1 ESTs ESTs
64 65 66	18061 18349 17494	AA799735 AA799744 AA799751	r j,p,q,y,z w,x	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1 ESTs ESTs ESTs ESTs, Weakly similar to carboxypeptidase E
64 65 66	18061 18349 17494 17875	AA799735 AA799744 AA799751	r j,p,q,y,z w,x cc,dd	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1 ESTs ESTs ESTs ESTs, Weakly similar to carboxypeptidase E
64 65 66 67 68	18061 18349 17494 17875 4133	AA799735 AA799744 AA799751 AA799755 AA799762	r j,p,q,y,z w,x cc,dd e,p,q,ii	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1 ESTs ESTs
64 65 66 67 68 69	18061 18349 17494 17875 4133 20997	AA799735 AA799744 AA799751 AA799755 AA799762 AA799764	r j,p,q,y,z w,x cc,dd e,p,q,ii hh	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1 ESTs ESTs ESTs, Weakly similar to carboxypeptidase E [Rattus norvegicus] [R.norvegicus]
64 65 66 67 68	18061 18349 17494 17875 4133 20997	AA799735 AA799744 AA799751 AA799755 AA799762	r j,p,q,y,z w,x cc,dd e,p,q,ii hh u,jj,kk	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1 ESTs ESTs ESTs, Weakly similar to carboxypeptidase E [Rattus norvegicus] [R.norvegicus] ESTs
64 65 66 67 68 69 70	18061, 18349, 17494, 17875, 4133, 20997, 18360,	AA799735 AA799744 AA799751 AA799755 AA799762 AA799764 AA799771	r j,p,q,y,z w,x cc,dd e,p,q,ii hh	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1 ESTs ESTs ESTs, Weakly similar to carboxypeptidase E [Rattus norvegicus] [R.norvegicus] ESTs ESTs ESTS
64 65 66 67 68 69	18061, 18349, 17494, 17875, 4133, 20997, 18360,	AA799735 AA799744 AA799751 AA799755 AA799762 AA799764 AA799771	r j,p,q,y,z w,x cc,dd e,p,q,ii hh u,jj,kk a,o,q,y,ee,ff,hh	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4)  RuvB-like protein 1  ESTs  ESTs  ESTs, Weakly similar to carboxypeptidase E  [Rattus norvegicus] [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs
64 65 66 67 68 69 70	18061, 18349, 17494, 17875, 4133, 20997, 18360,	AA799735 AA799744 AA799751 AA799755 AA799762 AA799764	r j,p,q,y,z w,x cc,dd e,p,q,ii hh u,jj,kk	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4)  RuvB-like protein 1  ESTs  ESTs  ESTs, Weakly similar to carboxypeptidase E [Rattus norvegicus] [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Weakly similar to A37098 gelation factor  ABP-280, long form - human [H.saniens]
64 65 66 67 68 69 70 71	18061, 18349, 17494, 17875, 4133, 20997, 18360,	AA799735 AA799744 AA799751 AA799755 AA799762 AA799764 AA799771	r j,p,q,y,z w,x cc,dd e,p,q,ii hh u,jj,kk a,o,q,y,ee,ff,hh ,Jj,kk	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4)  RuvB-like protein 1  ESTs  ESTs  ESTs, Weakly similar to carboxypeptidase E [Rattus norvegicus] [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Weakly similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]  ESTs, Weakly similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]
64 65 66 67 68 69 70 71	18061, 18349, 17494, 17875, 4133, 20997, 18360, 11530,	AA799735 AA799744 AA799751 AA799755 AA799762 AA799764 AA799771 AA799773	r j,p,q,y,z w,x cc,dd e,p,q,ii hh u,jj,kk a,o,q,y,ee,ff,hh ,jj,kk	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4)  RuvB-like protein 1  ESTs  ESTs  ESTs, Weakly similar to carboxypeptidase E [Rattus norvegicus] [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Weakly similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]  ESTs, Weakly similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]
64 65 66 67 68 69 70 71	18061, 18349, 17494, 17875, 4133, 20997, 18360, 11530,	AA799735 AA799744 AA799751 AA799755 AA799762 AA799764 AA799771	r j,p,q,y,z w,x cc,dd e,p,q,ii hh u,jj,kk a,o,q,y,ee,ff,hh ,Jj,kk	specific (dunce (Drosophila)- homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4)  RuvB-like protein 1  ESTs  ESTs  ESTs, Weakly similar to carboxypeptidase E  [Rattus norvegicus] [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Weakly similar to A37098 gelation factor  ABP-280, long form - human [H.saniens]
64 65 66 67 68 69 70 71	18061, 18349, 17494, 17875, 4133, 20997, 18360, 11530, 41531, 6425,	AA799735 AA799744 AA799751 AA799755 AA799762 AA799764 AA799771 AA799773	r j,p,q,y,z w,x cc,dd e,p,q,ii hh u,jj,kk a,o,q,y,ee,ff,hh ,jj,kk a,o,q,z,ff,hh,kk f,aa,bb	specific (dunce (Drosophila)-homolog phosphodiesterase E4) RuvB-like protein 1	(dunce (Drosophila)-homolog phosphodiesterase E4)  RuvB-like protein 1  ESTs  ESTs  ESTs, Weakly similar to carboxypeptidase E [Rattus norvegicus] [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Weakly similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]  ESTs, Weakly similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]

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SEO ID	GL GC:	No.	OC;		Company of the compan
حاا بمبيد	orgoili	JINO.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
		1			ESTs, Weakly similar to JC6554 complement
		1.			subcomponent C1s (EC 3.4.21.42) precursor
74	2099	8 AA799803	b,i,m		[similarity] - rat [R.norvegicus]
75	1450	4 AA799804	f,g,cc,dd		ESTs ESTs
		ŀ			ESTs, Moderately similar to PTN3_HUMAN Protein
					tyrosine phosphotose, not seem the protein the phosphotose and the phosphotose are the phosphotose and the phosphotose are the phosphotose and the phosphotose are the
76	1142	2 AA799812	a,ee,ff,jj,kk		tyrosine phosphatase, non-receptor type 3 (Protein
					tyrosine phosphatase H1) (PTP-H1) [H.sapiens]
		1		1	FSTs Moderately elmilante DTMs Augustin
					ESTs, Moderately similar to PTN3_HUMAN Protein
76	1142	3 AA799812	a,jj,kk,ll	1	tyrosine phosphatase, non-receptor type 3 (Protein
			- 777		tyrosine phosphatase H1) (PTP-H1) [H.sapiens]
					ESTo Highly day 1 Transaction
77	2100	AA799816	h,i		ESTs, Highly similar to T46306 hypothetical protei
78		AA799832	99	<del> </del>	DKFZp434D2411.1 - human (fragment) [H.sapiens
			- 33	<del>                                     </del>	ESTs Control of the c
79	21007	AA799861	d		ESTs, Highly similar to IRF7_MOUSE Interferon
		1	<del></del>	<del>                                     </del>	regulatory factor 7 (IRF-7) [M.musculus]
ł			1		ESTS, Highly similar to nuclear localization signal
80	18378	AA799888	hh		protein absent in velo-cardio-facial patients (Mus
		7 4 1 0 0 0 0 0	11111		[musculus] [M.musculus]
81	15011	AA799893	hh		ESTs, Highly similar to DDRT helix-destabilizing
82		AA799964		·	protein - rat [R.norvegicus]
83	18400	AA799991	h		ESTs
	10400	MA 3333 I	aa,bb		ESTs
- 1				ļ	ESTs, Moderately similar to predicted gene
84	10004	4 4 700000			ICRFP703B1614Q5.6; ICRFP703N2430Q5.6;
04	10001	AA799992	c,h,l,n,o,w,x		C11orf17 [Mus musculus] [M musculus]
- 1					ESTs, ESTs, Moderately similar to predicted gene
أرم	40000	4.470000		1	ICRFP703B1614Q5.6; ICRFP703N2430Q5.6;
<u>84</u> 85		AA799992	c,n,o,kk		C11orf17 [Mus musculus] [M.musculus]
65	16/12	AA800015	е	integrin-linked kinase	integrin-linked kinase
00	00040				ESTs, Weakly similar to Yeast ABD1 protein like
86		AA800016	cc,dd		[Caenorhabditis elegans] [C.elegans]
87		AA800034	s,t		ESTs
88	11352	AA800036	f,jj,kk,ll		ESTs
89	19177	AA800062	li_		ESTs
90	13568	AA800169	h,l		ESTs
					ESTs, Highly similar to NOC4_MOUSE Neighbor of
91	21065	AA800179	s,t		COX4 [M.musculus]
	1	_			ESTs, Highly similar to S37300 glycogen
				HHs:phosphorylase, glycogen;	phosphorylase (EC 2.4.1.1), brain - rat
92		AA800190	a,e,ii,kk	brain	[R.norvegicus]
93		AA800191	f,g		[ESTs
94		AA800197	99		ESTs
95		AA800200	l,m,ee,ff,jj,kk		ESTs
96	21656	AA800202	s,t		ESTs .
97	3692	AA800210	hh,jj,kk		ESTs .
98		A800222	g,bb		ESTS
99		A800298	c,g,kk		
			,,,,,,,		ESTs Moderately shall be ESTs
100	21086	A800305	cc,dd		ESTs, Moderately similar to RB5A_HUMAN Ras-
					related protein Rab-5A [H.sapiens]
					ESTs, Moderately similar to IC1_MOUSE_Plasma
101	24228	A800318	lb m		protease C1 inhibitor precursor (C1 inh) (C1inh)
102		A800549	b,m r,ii		[M.musculus]
103	6892	A800551		Dec I III	ESTs
104		A800613	e,ee,ff,ii	DnaJ-like protein	DnaJ-like protein
	4042	10000	j,k,p,q,y,z f,g		EST
105					ESTs

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SEO ID	GLCC "	GenBank Acc	916.	The state of the s	the facility of the control of the c
PEQ ID.	GLGC IL	JNO.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
	'				ESTs, Moderately similar to A54854 Ras GTPase
					activating protein-related protein - human
106	17997	7 AA800671	u		[H.sapiens]
					ESTs, Highly similar to KIAA0164 gene product
107		7 AA800673	s	1	[Homo sapiens] [H.sapiens]
108		AA800678	a,j,k,jj,kk		ESTs
109	21377	AA800719	w,x		ESTs
					ESTs, Weakly similar to VIL1_MOUSE Villin 1
110	17648	AA800735	cc,dd		[M.musculus]
		_			ESTs, Weakly similar to VIL1_MOUSE Villin 1
110	17649	AA800735	cc,dd		[M.musculus]
111		AA800749	g		ESTs
112		AA800787	aa,bb,ll		ESTs
113	12797	AA800790	p,q		ESTs
					ESTs, Moderately similar to LYOX_RAT Protein-
j		1			lysine 6-oxidase precursor (Lysyl oxidase)
114	22386	AA800844	g	<u>}</u>	[R.norvegicus]
115	17658	AA800853	d,j,k,s,t	<u> </u>	ESTs .
			<del>                                     </del>		
1				1	ESTs, ESTs, Highly similar to MLF2_MOUSE
116	10320	AA800855	b,l,m		Myeloid leukemia factor 2 (Myelodysplasia-myeloi
117	15213	AA800908	hh		leukemia factor 2) [M.musculus] ESTs
118	21416	AA800962	hh		ESTs, Highly similar to S11661 talin - mouse
			<del> </del>	aldehyde dehydrogenase family	[M.musculus]
119	11901	AA801058	d	9, subfamily A1	1,1
120		AA801116	a	9, Subtaining AT	aldehyde dehydrogenase family 9, subfamily A1
			<del> </del>	grouth factor recorded	ESTs
121	16852	AA801130	h,i	growth factor receptor bound protein 2	
122	23115	AA801165	C	Testis-specific histone 2a	growth factor receptor bound protein 2
		7 100 1 100	<del> </del>	resus-specific historie za	Testis-specific histone 2a
. !	!				FOT- 10 11 4 4 4
i			ļ		ESTs, Highly similar to P52K_HUMAN 52 kDa
1			]		repressor of the inhibitor of the protein kinase
					(p58IPK-interacting protein) (58 kDa interferon-
					induced protein kinase-interacting protein)
123	21427	<b>ΔΔ</b> ΩΠ11Ω1	00 44		
123	21427		cc,dd		(P52rlPK) (Death associated protein 4) [H.sapiens]
124	22318	AA801187	h,i		ESIS
	22318				ESTS ESTS
124	22318	AA801187	h,i		ESTs ESTs ESTs, Weakly similar to TAC1_HUMAN
124 125	22318 / 10549 /	AA801187 AA801255	h,i r,kk		ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1
124 125 126	22318 / 10549 / 12399 /	AA801187 AA801255 AA801307	h,i r,kk gg,ll		ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens]
124 125	22318 / 10549 / 12399 /	AA801187 AA801255	h,i r,kk		ESTS ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs
124 125 126 127	22318 / 10549 / 12399 / 16388 /	AA801187 AA801255 AA801307 AA801310	h,l r,kk gg,ll e		ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 IMus
124 125 126	22318 / 10549 / 12399 / 16388 /	AA801187 AA801255 AA801307 AA801310	h,i r,kk gg,ll		ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus]
124 125 126 127 128	22318 / 10549 / 12399 / 16388 / 11166 /	AA801187 AA801255 AA801307 AA801310 AA801346	h,l r,kk gg,ll e n,o		ESTs  ESTs  ESTs, Weakly similar to TAC1_HUMAN  Transforming acidic coiled-coil-containing protein 1 [H.saplens]  ESTs  ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus]  ESTs, Moderately similar to S63540 protein DS 1
124 125 126 127 128	22318/ 10549/ 12399/ 16388/ 11166/	AA801187 AA801255 AA801307 AA801310 AA801346 AA801352	n,i r,kk gg,ii e n,o		ESTs ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.sapiens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.sapiens]
124 125 126 127 128 129 130	22318/ 10549/ 12399/ 16388/ 11166/ 11995/ 24237/	AA801307 AA801310 AA801346 AA801352 AA8013726	n,i r,kk gg,ii e n,o		ESTs ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.sapiens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.sapiens]
124 125 126 127 128 129 130 131	22318 / 10549 / 12399 / 16388 / 11166 / 11995 / 24237 / 18796 /	AA801307 AA801310 AA801310 AA801346 AA801352 AA817726 AA817761	n,i r,kk gg,ii e n,o n,o kk		ESTs ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens] ESTs
124 125 126 127 128 129 130	22318 / 10549 / 12399 / 16388 / 11166 / 11995 / 24237 / 18796 /	AA801307 AA801310 AA801310 AA801346 AA801352 AA817726 AA817761	n,i r,kk gg,ii e n,o		ESTs ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.sapiens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.sapiens] ESTs ESTs ESTs
124 125 126 127 128 129 130 131	22318 / 10549 / 12399 / 16388 / 11166 / 11995 / 24237 / 18796 /	AA801307 AA801310 AA801310 AA801346 AA801352 AA817726 AA817761	n,o n,o kk e a		ESTs ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens] ESTs ESTs ESTs ESTs
124 125 126 127 128 129 130 131	22318 / 10549 / 12399 / 16388 / 11166 / 11995 / 24237 / 18796 /	AA801307 AA801310 AA801310 AA801346 AA801352 AA817726 AA817761	h,l r,kk gg,ll e n,o n,o kk e	-IHs:UDP-Gal:betaGlcNAc beta	ESTs ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens] ESTs ESTs ESTs ESTs ESTs ESTs ESTs, Weakly similar to glycoprotein galactosyltransferase beta 1, 4; beta-1.4-GalT
124 125 126 127 128 129 130 131 132	22318/ 10549/ 12399/ 16388/ 11166/ 11995 A 24237 A 23725 A	AA801307 AA801307 AA801310 AA801346 AA801352 AA817726 AA817761 AA817816	n,o n,o kk e	Hs:UDP-Gal:betaGlcNAc beta	ESTs  ESTs  ESTs, Weakly similar to TAC1_HUMAN  Transforming acidic coiled-coil-containing protein 1 [H.saplens]  ESTs  ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus]  ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Weakly similar to glycoprotein galactosyltransferase beta 1, 4; beta-1,4-GalT; petalactosyltransferase 2 beta 1, 4; B-1,4-GalT; betalactosyltransferase 2 betalactosyl
124 125 126 127 128 129 130 131	22318/ 10549/ 12399/ 16388/ 11166/ 11995 A 24237 A 23725 A	AA801187 AA801255 AA801307 AA801310 AA801346 AA801352 AA817726 AA817761 AA817816	h,i r,kk gg,ii e n,o n,o kk e a	HHs:UDP-Gal:betaGlcNAc beta	ESTs  ESTs  ESTs, Weakly similar to TAC1_HUMAN  Transforming acidic coiled-coil-containing protein 1 [H.saplens]  ESTs  ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus]  ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Weakly similar to glycoprotein galactosyltransferase beta 1, 4; beta-1,4-GalT; petalactosyltransferase 2 beta 1, 4; B-1,4-GalT; betalactosyltransferase 2 betalactosyl
124 125 126 127 128 129 130 131 132	12399 / 16388 / 11166 / 11995 / 24237 / 18796 / 23725 / 23828 /	AA801307 AA801307 AA801310 AA801346 AA801352 AA817726 AA817761 AA817816	h,i r,kk gg,ii e n,o n,o kk e a	HHs:UDP-Gal:betaGlcNAc beta (1,4- galactosyltransferase, bolypeptide 2 potassium channel, subfamily K,	ESTs ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens] ESTs ESTs ESTs ESTs ESTs ESTs ESTs, Weakly similar to glycoprotein galactosyltransferase beta 1, 4; beta-1.4-GalT;
124 125 126 127 128 129 130 131 132	22318/ 10549/ 10549/ 16388/ 11166/ 11995/ 24237/ 18796/ 23725/ 23828/A	AA801187 AA801255 AA801307 AA801310 AA801346 AA801352 AA817726 AA817761 AA817816	h,i r,kk gg,ii e n,o n,o kk e a	HHs:UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, colypeptide 2 cotassium channel, subfamily K,	ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs
124 125 126 127 128 129 130 131 132 132	22318/ 10549/ 10549/ 16388/ 11166/ 11995 A 24237 A 23725 A 23725 A	AA801187 AA801255 AA801307 AA801310 AA801346 AA801352 AA817726 AA817761 AA817816 AA817823 AA817823	h,i r,kk  gg,ii e n,o n,o kk e a	HHs:UDP-Gal:betaGlcNAc beta (1,4- galactosyltransferase, colypeptide 2 cotassium channel, subfamily K, nember 2	ESTs ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.saplens] ESTs ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus] ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs
124 125 126 127 128 129 130 131 132	22318/ 10549/ 10549/ 16388/ 11166/ 11995/ 24237/ 18796/ 23725/ 23828/A	AA801187 AA801255 AA801307 AA801310 AA801346 AA801352 AA81726 AA817761 AA817816 AA817816 AA817823 AA817823 AA817823 AA817824	h,i r,kk gg,ii e n,o n,o kk e a	HHs:UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2 potassium channel, subfamily K, nember 2	ESTs  ESTs  ESTs, Weakly similar to TAC1_HUMAN  Transforming acidic coiled-coil-containing protein 1 [H.saplens]  ESTs  ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus]  ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.saplens]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Weakly similar to glycoprotein galactosyltransferase beta 1, 4; beta-1,4-GalT; galactosyltransferase 2 beta 1, 4; B-1,4-GalT1; beta 1,4-GalT1 [Mus musculus] [M.musculus]

		GenBank A	cc.	gi in the state of the state of the	Atty. Ref. 44921-5090-01-WO/2105485
SEQ:ID	GLGC	D No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
	ĺ		1		ESTs, Highly similar to I48253 beta-N-
			İ		acetylhexosaminidase (EC 3.2.1.52) alpha chain
138	1410	1 AA817867	lii		procures makes (EC 3.2.1.52) alpha chain
				guanine nucleotide binding	precursor - mouse [M.musculus]
139	214	3 AA817892	r	protein beta 2 subunit	
140		0 AA817947	d,jj,kk	protein beta 2 subunit	guanine nucleotide binding protein beta 2 subunit
141		2 AA817999	u,jj,kk		ESIS
142	500	C A A B 4 8 9 9	<u> r</u>		ESTs
142	595	6 AA818065	lii		ESTs
					ESTs, Highly similar to SYG_HUMAN Glycyl-tRN
			İ		synthetase (Chair a IDMAN Glycyl-IRN)
143	1675	6 AA818089	lu	HHs:glycyl-tRNA synthetase	synthetase (Glycine-tRNA ligase) (GlyRS)
144		4 AA818153	-   ii	I II IS. gry Cyr-trovA synthetase	[H.sapiens]
145		5 AA818158	- <del> </del> "		ESTs
		UNAU 10 100	_ -		ESTs
146	CEO				ESTs, Moderately similar to A47318 RNA-binding
146		2 AA818261	r		protein Raly - mouse [M.musculus]
147		7 AA818288	11		ESTs [Wi.musculus]
148	36	7 AA818342	hh		ESTS
				<del> </del>	
149	805	3 AA818475	n,o,w,x		ESTs, Highly similar to RIKEN cDNA 2310008M1
150	622	AA818521			[[Mus musculus] [M.musculus]
151	070	A A D 4 D 2 4 5	_  II		ESTs
		AA818615	h,i		ESTs
152	605	AA818655	t		EST
				Diphtheria toxin receptor	LOI
- 1		ļ	<b>!</b>	(heparin binding epidermal	
- 1		ł		groudh feeter 131	
153	605/	AA818658	2 2 2 2 4	growth factor - like growth	Diphtheria toxin receptor (heparin binding
154	1106/	AA818717	p,q,ee,ff	factor)	epidermal growth factor - like growth factor)
155			W,X		ESTs growth tubioly
		AA818747	r,bb,ll		ESTs
156		AA818761	p,q		ESTs
157	6829	AA818784	lii		
			· · · · · ·		ESTs
158	4491	AA818798	w,x		Rattus norvegicus mRNA for cathepsin Y, partial
159	6073	AA818818			cas
160			С		EST
		AA818820	ji		ESTs
161	13428	AA818861	jj,kk		ESTs
162	6092	AA818897	b		ESTs
163	19729	AA818910	d		
164		AA818911	t		ESTs
165		AA818935	n,o		ESTs
166	6126	AA819086			ESTs
167			cc,dd		ESTs
		AA819111	jj,kk		ESTs
168		AA819220	aa,bb		ESTs
169		AA819332	j,k		
170		AA819367	cc,dd		ESTs
			30,00		ESTs
171	6284	AA819517	1		ESTs, Weakly similar to JC5707 HYA22 protein -
172			hh		human [H.sapiens]
		AA819523	bb		ESTs
173		AA819606	aa,bb		
174	6176	AA819657	V		TECT
T					EST
	ĺ		1 1.	protoin phaset start at	
1	1			protein phosphatase 2 (formerly	
175	16074	A A 040004	2	A), regulatory subunit B (PR	protein phosphatase 2 (formerly 2A), regulatory
175		AA819691	n,o	52), alpha isoform	subunit B (PR 52), alpha isoform
176	11021	AA819767	p.a		ESTs
			24.		ECT- Minter Communication
177	19451	A819788	lc		ESTs, Weakly similar to 28kD interferon alpha
			<del>   </del>		responsive protein [Mus musculus] [M musculus]
		A819891			ESTs, Weakiy similar to B36579 inositol 1,4,5-
178	1 24 7 12 7 1		99		

ABLE		GenBank Ad	oc. F	AND AND AND AND AND AND AND AND AND AND	Atty. Ref. 44921-5090-01-WO/2105485
EQ:ID	GLGC, it	No.	Model Code		Unidana Coques at Other
			., ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	stearoyl-Coenzyme A	Unigene Sequence Cluster Title
179	32	0 AA819905	hh	desaturase 1	
180	981	5 AA848218		uesaturase 1	stearoyl-Coenzyme A desaturase 1
	- 50,	0//040210	p,q	· · · · · · · · · · · · · · · · · · ·	ESTs
181	1761	4 AA848306	l.		ESTs, Weakly similar to DDRT helix-destabilizin
182	2252	1 AA848407	b		[protein - rat [R.norvegicus]
183			h,l		ESTs
100	1110	AA848470	ii		ESTs
					ESTs, Weakly similar to T19253 hypothetical
					protein C14A4.11 - Caenorhabditis elegans
184	2324	AA848545	r		[C.elegans]
					ESTs, Weakly similar to T19253 hypothetical
			i		protein C14A4.11. Connect strutter 1
185	25110	AA848546	cc,dd		protein C14A4.11 - Caenorhabditis elegans [C.elegans]
186	14654	AA848795	jj,kk		ESTs ESTS
			77		ECT CULTURE TO THE PERSON OF T
1				1	ESTs, Highly similar to BTF3_MOUSE Transcrip
187	7749	AA848804	kk		factor BTF3 (RNA polymerase B transcription fac
188	14604	AA848828	C		(3) [M.musculus]
	17004	1.1040020		-	ESTs
189	19109	AA848902		1	ESTs, Weakly similar to S12207 hypothetical
103	12102	AA046902	_ ii		protein (B2 element) - mouse [M.musculus]
j		ĺ		proteasome (prosome,	
400	400=0			macropain) subunit, alpha type	proteasome (prosome, macropain) subunit, alpha
190	186/3	AA849028	t	3	type 3
191	8619	AA849317	jj,kk		ESTs
- 1					ESTs Weakly similar to DDDT half and a table
192	2075	AA849394	u,v	1	ESTs, Weakly similar to DDRT helix-destabilizing
					protein - rat [R.norvegicus]
- 1				1	ESTs, Weakly similar to YLC4_CAEEL Hypothetic
193	18909	AA849426	h,l		81.0 kDa protein C35D10.4 in chromosome III
194	11726	AA849518	+		[C.elegans]
194		AA849518	<del> </del>		ESTs
195		AA849731	00 44		ESTs
	21204	701043731	cc,dd		ESTs
ĺ			İ		
196	24420	AA849766			ESTs, Highly similar to T08750 hypothetical prote
197	24120	AA849766	bb		DKFZp586E1519.1 - human (fragment) [H.sapien
	212/5	AA849796	d		ESTs (reginent) [r.saplen
198	8515	AA849917	b,v		ESTs
199	11355	AA849957	11		ESTs
					ESTs, Moderately similar to 0806162L protein
Suu	22026	AA850060	n,o		LIRES (Mus musculus) 134
					URF5 [Mus musculus] [M.musculus]
200	22028	AA850060	cc,dd		ESTs, Moderately similar to 0806162L protein
201		AA850247	d		URF5 [Mus musculus] [M.musculus]
			<del> </del>		ESTs
202	19071	AA850524	lk l		ESTs, Highly similar to I49257 NF2d9 - mouse
203		AA850563	aa,bb		[M.musculus]
204		A850735			ESTs
205	5660	A850743	e		ESTs
206			jj,kk		ESTs
2001		A850824	li .		ESTs
		A850872	h,l		ESTs
OOC	21/66/	A850916	kk		ESTs
208			]	Rattus norvegicus	
208	J				
				mitochondrial genome.	
i	19424 A	A850922	h,i	mitochondrial genome. 9/22Length = 16.3	dimothyloraining dimethyles
		A850922 A851034	h,l	9/22Length = 16,3	dimethylarginine dimethylaminohydrolase 1
i			h,l  u,v	9/22Length = 16,3	dimethylarginine dimethylaminohydrolase 1 ESTs Rattus norvegicus mRNA for cathepsin Y, partial

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TABLE		GenBank Ac	<del></del>	<u></u>	Atty. Ref: 44921,5090-01-WO/2105485
SEO:ID	GI CC I	Genbank Ac		The second of the second of the	
ישוים ב	GEGC	D No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
					ESTs, Weakly similar to T33304 hypothetical
					protein R01B10.5 - Caenorhabditis elegans
211	416	3 AA851210	gg		[C.elegans]
			- 100		[C.elegans]
		1			ESTs, Moderately similar to exostoses (multiple)
212	2145	6 AA851239	cc,dd		like 2; Exostoses, multiple, like 2 [Homo sanions]
		37 4 100 1200	- CC,QQ		[[H.sapiens]
		1			ESTs, Weakly similar to retinolc acid receptor
213	21/6	5 AA851273	<u>.</u> .		responder (tazarotene induced) 2 [Homo saniens]
214			h,l		[H.sapiens]
	1921	4 AA851364	u,v		ESTs
045	4000				ESTs, Highly similar to RIKEN cDNA 2900010105
215		4 AA851403	b		[Mus musculus] [M.musculus]
216	1362	7 AA851493	aa,bb	claudin 7	claudin 7
				Lutheran blood group (Auberger	
217		3 AA851637	e.r	b antigen included)	
218	21514	AA851660	ee,ff	gon meidaday	Lutheran blood group (Auberger b antigen included ESTs
219		AA851788	e		
220		AA851820	e		ESTs
		100.020	<del> </del>		ESTs
l		İ			ESTs, Moderately similar to T12501 hypothetical
221	10150	AA851953	l		protein DKFZp434O171.1 - human (fragment)
	10100	MU00 1900	u,v		[H.sapiens]
222	45000	4.050540	1_		ESTs, Weakly similar to T51146 ring-box protein 1
222		AA858518	f,g		[imported] - human [H.sapiens]
223		AA858548	a,kk		ESTs
224	23069	AA858572	u,v		ESTs
ĺ					ESTs, Highly similar to mini chromosome
			}	1	maintenance deficient 7 (0)
225	1801	AA858636	n,o		maintenance deficient 7 (S. cerevisiae) [Mus
226	18350	AA858674	p,q,ee,ff		musculus] [M.musculus]
			pjdjoojii		ESTs
					ESTs, Moderately similar to mitochondrial
227	12829	AA858695	00		ribosomal protein S33; mitochondrial 28S ribosoma
	12020	77000000	99		[protein S33 [Homo sapiens] [H sapiens]
1					ESTs, Weakly similar to NTC1 RAT Neurogenic
228	12000	A A 050050	1		locus notch homolog protein 1 precursor (Notch 1)
	13002	AA858853	b,l,m		[R.norvegicus]
000	47000			Tissue inhibitor of	
229	1/236	AA858903	s,t,gg	metalloproteinase 3	Tissue inhibitor of metalloproteinase 3
					ESTs, Moderately similar to SYN_HUMAN
			1		AsparadinyLiRNA syntheteco
230		AA858953	kk		Asparaginyl-tRNA synthetase, cytoplasmic
231		AA858955	j,k	-	(Asparagine—tRNA ligase) (AsnRS) [H.sapiens]
232	17361	AA859114	kk		ESTs
233		AA859284			
234		AA859319	b,l,m		procollagen, type I, alpha 2
235		AA859343	j,k		ESTs
<del></del>		- 1000070	h <sub>iv</sub>		ESTs
İ	1				ESTs, Moderately similar to RP38_HUMAN
236	15160	AA859346	l I		Ribonuclease P protein subunit p38 (RNaseP
237	16244	4A859346 4A859348	u,v		protein p38) [H.sapiens]
	20005	4A050445	p,q		ESTs
238		AA859447	q		ESTs
239		AA859479	f		ESTs
240	13595	AA859508	b,s		ESTs
[					
241	23340	A859519	d,h,l	- i	ESTs, Highly similar to JC6127 RNA-binding protein
242			d,hři		ype 1 - human [H.sapiens]
					57s
243	4809	A859616	gg	[1	ESTs, Weakly similar to FYVE zinc finger
244			99 C	[	Caenorhabditis elegans] [C.elegans]
245					STs
7451			j,k,ll		etiractin

ABLE		GenBank Acc	<del> </del>	4 (1. fe) (1. fe) (1. fe)	Atty. Ref. 44921-5090-01-WO/2105485
		No.	Model Code	Known Gene Name	A. [1] (1) [1] [2] [4] [4] [4] [4] [4] [4] [4] [4] [4] [4
-4:15,	JOSE OF JE	? 110.	Iviogei Code	Known Gene Name	
	Ì				ESTs, Weakly similar to DJA1_MOUSE DnaJ
	1	1			homolog subfamily A member 1 (Heat shock 40 kg
040	4004				protein 4) (DnaJ protein homolog 2) (HSJ-2)
246	1031	AA859648	p,q		[R.norvegicus]
247		AA859680	y,z		ESTs
247	2240	AA859680	s,t		ESTs
					ESTs, Highly similar to AU RNA-binding enoyl-
	i		1	i	coenzyme A hydratase; AU RNA-binding
			1	1	protein/enoyl-coenzyme A hydratase [Mus
248		AA859688	w,hh		musculus] [M.musculus]
249	21440	AA859719	l,m		ESTs
					ESTs Weakly similar to EDE MOURE ETC.
250	22670	AA859750	y,z,hh		ESTs, Weakly similar to ERF_MOUSE ETS-domain transcription factor ERF [M.musculus]
251	2262	AA859757	hh	collagen, type V, alpha 1	collagen, type V, alpha 1
				Tomagon type v, aipna 1	ESTs Moderately alvelled 1 1/2/
					ESTs, Moderately similar to LYOX_RAT Protein-
252	22385	AA859805	g,s,t		lysine 6-oxidase precursor (Lysyl oxidase)
		1	19101		[R.norvegicus]
				1	ESTs, Moderately similar to URK1_MOUSE
253	14213	AA859827	a,y,z,ee,ff		URIDINE KINASE (URIDINE
254	22630	AA859848	gg		MONOPHOSPHOKINASE) [M.musculus]
255		AA859877	h,i,ii		ESTs
256		AA859885			ESTs
257		AA859919	c,r,bb		ESTs
257	15166	AA859919	ļii		ESTs
258			hh		ESTs
200	22340	AA859922	n,o		ESTs
İ					ESTs, Moderately similar to TNP1_HUMAN Tumor
250	40.400	4.4.0			necrosis factor, alpha-induced protein 1, endothelia
259	18468	AA859966	l,m		(B12 protein) [H.sapiens]
					ESTs, Weakly similar to MYOP_RAT Myo-inositol-
1					1(or 4)-monophosphatase (IMPase) (IMP) (Inositol
200				HHs:inositol(myo)-1(or 4)-	monophosphatase) (Lithium-sensitive myo-inositol
260		AA859981	ee,ff,jj,kk	monophosphatase 2	monophosphatase A1) [R.norvegicus]
261	14206	AA859994	a		ESTs
					ESTs, Weakly similar to T50607 hypothetical
			,		protein DKFZp434l1016.1 - human (fragment)
262	23347	AA860015	aa,bb		[H.sapiens]
	Ī				ESTs, Highly similar to EF1G_MOUSE Elongation
- 1					factor 1-gamma (EF-1-gamma) (eEF-1B gamma)
263		AA860024	h,l,w,x		[M.musculus]
264	23585	AA860029	aa		ESTs
T					
265		AA860030	n,o,w,x,ll		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
266			b,l,m		ESTs ESTs
					ESTs, Weakly similar to A60543 protein kinase (EC
267	15884	AA866276	d,f,g,r		2.7.1.37), cAMP-dependent, catalytic chain - rat
			a,j,k,w,x,y,z,jj,		(fragment) [R.norvegicus]
268	17217		kk		TOT-
268			gg,jj,kk		ESTs
-				1 hydroxynhonyl	ESTs
269	17742	A866302		4-hydroxyphenylpyruvic acid	
270				dioxygenase	4-hydroxyphenylpyruvic acid dioxygenase
271		A866364	kk		ESTs
272	11965		d == 4611		ESTs
273	15000/		d,ee,ff,kk		ESTs
		A866426	s,ii		ESTs
274			b		ESTs
275	4000414	A866452	bb,cc,dd /	ctin, alpha, cardiac	2010

TABLE	16	2.10c=b		487	Atty. Ref. 44921-5090-01-WO/2105485
		GenBank A	CC.		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
SEQ ID	GLGC.	D No.	Model Code	Known Gene Name	
276	3	09 AA866460	L		ESTS, Weakly similar to T42737 ap330 protein
210	1	73 AA00046U	b		IDIECUISOF - FALIR MONAGIONEI
	1				ESTs, Moderately similar to COXM_MOUSE
				ĺ	Cytochrome c oxidase polypeptide VIIb,
277	939	1 AA866477	r		mitochandrial program as the
					mitochondrial precursor [M.musculus]
278	1602	9 AA874803	j,k		ESTs, Moderately similar to 0806162L protein
					JUKES Musculus (M musculus)
278	1603	0 AA874803	11.		ESTS, Moderately similar to 08061621, protein
279		O AA874873	J,k		URF5 [Mus musculus] [M.musculus]
213	1007	UAA874873	cc,dd		ESTs
	1	į.			
				j	ESTS Highly similar to ADUN DAT ALCOHOL
			1		ESTs, Highly similar to ADHX_RAT ALCOHOL
		1	1	ł	DEHYDROGENASE CLASS III (ALCOHOL
l		1	- 1		DEHYDROGENASE 2) (GLUTATHIONE-
		1			DEPENDENT FORMALDEHYDE
280	1607	4 4 4 9 7 4 9 7 4			DEHYDROGENASE) (EDH) (EA) DU) (A) COUCL
		4 AA874874	p,q	HMm:alcohol dehydrogenase 5	DEHYDROGENASE-B2) [R.norvegicus]
281	1856	3 AA874875	ii		[Kinorvegicus]
					FSTs Weakly similar to account
į		1		1	ESTs, Weakly similar to segregation of mitotic
		ľ	1	1	chromosomes b; SMC (segregation of mitotic
282	16083	AA874887	lii		John John John Strategy (Veast) (Rattus nonvenious
283	1608	AA874889	- 13		[[R.norvegicus]
	1000	17/10/4009			ESTs
004	0070		A		ESTs, Weakly similar to dual-specificity
284	22/8	AA874926	hh		phosphatase [Mus musculus] [M.musculus]
285	<u>16139</u>	AA874927	cc,dd		ESTs [www.musculus] [w.musculus]
			T		
286	15116	AA874928	f		ESTs, Highly similar to SNX4_HUMAN Sorting
287		AA874952	<del>-                                      </del>	<del></del>	_ nexin 4 [H.sapiens] .
	10111	747074332	- 111		ESTs
288	47202	44074000			ESTs, Weakly similar to RIKEN cDNA
	17303	AA874990	u,v,w,x	1	6330407G11 [Mus musculus] [M.musculus]
289	16192	AA874995	jj,kk		ESTs [Mas mascalds] [Mi.musculds]
1					
				]	ESTs, Highly similar to protein translocation
290	16215	AA874999	h,i,n,o		complex beta; protein transport protein SEC61 beta
		10.00	11,1,11,0		(Subunit [Homo sapiens] [H.sapiens]
291	162/1	AA875019	1	-	ESTS, Highly similar to ZAP3 MOUSE Nuclear
	45570	AA075019	l,m		protein ZAP3 [M.musculus]
292	100/3	AA875023	b,l,m		ESTs
293	16312	AA875032	j,k,p,q,bb,kk		ESTs
1	1				
			Ĭ		ESTs, Highly similar to TCPZ_MOUSE T-complex
294	16319	AA875047	е	1	protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta)
295	16342	AA875060	s,t,jj,kk		[(CCT-zeta-1) [M.musculus]
296	1190	AA875089		0.1	ESTs
	. 100		hh	Calpastatin	Calpastatin
297	16410	A A 075000	1		ESTs, Highly similar to RIKEN cDNA 1110002023
231	10410	AA875098	n,o		[Mus musculus] [M.musculus]
					ESTs, Highly similar to RUXE_HUMAN Small
			1		Duclear thepusions with E / E / E / E
298	16419	4A875102	d		nuclear ribonucleoprotein E (snRNP-E) (Sm protein
			† <del></del>		E) (Sm-E) (SmE) [M.musculus]
299	4339	AA875121	jj,kk	CCAAT binding factor of CBF-	
300	15310	A875123		C/NFY-C	CCAAT binding factor of CBF-C/NFY-C
301	15344	N0/01/23	u,v		EST
	10017	\A875124	li		EST
302	11857	VA875132	d,ii		ESTs
303	14285	A875194	ii		
					ESTs
ļ	1			ļ	ESTs, Highly similar to IF39_HUMAN Eukaryotic
	15372	A875205			translation initiation factor 3 subunit 9 (e1F-3 eta)
3041		V70113/U2	177	1	(-IFO 440) ( IFO (III)
304 305	19907	A875207	y,z	Hemoglobin, beta	(elF3 p116) (elF3 p110) [H.sapiens]

TABLE 1		IGenBank Ass	<del> </del>		Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GLGC II			THE PROPERTY OF A	· 图1987年 1987年 1988年 19
			Model Code	Known Gene Name	Unigene Sequence Cluster Title
306	1538	AA875217	cc,dd		ESTs
007	4500	1		GTP-binding protein (G-alpha-	
307	1588	AA875225	е	i2)	GTP-binding protein (G-alpha ia)
				GTP-binding protein (G-alpha-	
307	15888	AA875225	e,gg	i2)	GTP-binding protein (G-alpha-i2)
308	15402	AA875261	d,jj,kk		ESTs
					ESTs, Highly similar to NUKM_HUMAN NADH-
			1	ì	ubiquinone oxidoreductase 20 kDa subunit,
					mitochondrial precursor (Complex I-20KD) (CI-
309		AA875268	jj,kk	1	20KD) (PSST subunit) [H.saplens]
310		AA875316	h,I		ESTs ESTs
311		AA875327	n,o,s,t		ESTs
312	15510	AA875428	a,s,t,x,ee,ff,II		ESTs
l					ESTs, Weakly similar to synbindin; syndecan
313	15513	AA875431	n,o		binding protoin 2 Mus must all a syndecan
					binding protein 2 [Mus musculus] [M.musculus] ESTs, Highly similar to COP9 (constitutive
i		İ			photomorphogenic) homolog, subunit 7a
					(Arabidopsis thaliana); DNA segment, Chr 6,
			1	1	FRATO Dol 35, everyoned, CODS
			ĺ		ERATO Dol 35, expressed; COP9 complex S7a;
314	18864	AA875470	b		COP9 (constitutive photomorphogenic), subunit 7
315	15412	AA875500	r		(Arabidopsis) [Mus musculus] [M.musculus]
			<del>                                     </del>		ESTs Liberty of the Control of the C
			ł		ESTs, Highly similar to MLES_RAT Myosin light
316	24470	AA875523	aa,bb	İ	chain alkali, smooth-muscle isoform (MLC3SM)
			uu,bb	<del>                                     </del>	[R.norvegicus]
					ESTs, Highly similar to MLES_RAT Myosin light
316	24471	AA875523	lii		chain alkali, smooth-muscle isoform (MLC3SM)
					[R.norvegicus]
i					ESTs, Highly similar to MLES_RAT Myosin light
316	24472	AA875523	ii		chain alkali, smooth-muscle isoform (MLC3SM)
-			<del>"</del>	Rattus norvegicus	[R.norvegicus]
İ				mitochondrial genome.	D.#.
2	6153	AA875531	g,j,k	9/22Length = 16,3	Rattus norvegicus CDK110 mRNA, procollagen,
			91111	5/22Lengur = 10,5	type I, alpha 2
	1				ESTs, Highly similar to SFR2_MOUSE Splicing
- 1					factor, arginine/serine-rich 2 (Splicing factor SC35)
317	15558	AA875537	y,z		(SC-35) (Splicing component, 35 kDa) (PR264
318			hh		protein) [M.musculus]
340	15617	AA875620	ee,ff,jj,kk		ESTS
319	15618		y,z,ee,ff		ESTS
320	15629	AA875629	n,o,ll		ESTs
321			r,gg		ESTs
<del></del> -		07 0000	פפני		ESTs
İ	1				FOT W. I.
	- 1	ļ			ESTs, Weakly similar to FAS_RAT FATTY ACID
	. ]				SYNTHASE [INCLUDES: EC 2.3.1.38; EC 2.3.1.39
322	2848	A875639	a		EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC
		5. 5555	u .		1.3.1.10; EC 3.1.2.14] [R.norvegicus]
!	!		l		ESTs, Highly similar to mitochondria associated
323	15688	A875664	22		granulocyte macrophage CSF signaling molecule
	100007	4 101 0004	aa		[Mus musculus] [M.musculus]
324	15388	A891032	_		EST, Moderately similar to S37488 gene T10
325					protein - mouse [M.musculus]
ا التكان	0304/	A891041	,k,p,q,y,z,kk	un B proto-oncogene	jun B proto-oncogene
226	47053	4004040	İ		ESTs, Highly similar to PFD2_MOUSE Preforan
326	7057	10040-4	C		subunit 2 [M.musculus]
<b>4</b> .			c,p		ESTs
J201		A891108	o,q,y,ee,ff		ESTs
TOPP DEST	18582 A		ı,ee,ff		

SEQ ID			•		Atty. Ref. 44921-5090-01-WO/2105485
SEC ID	01.00.15	GenBank Acc		The state of the s	
	GLGC ID	No:	Model Code	Known Gene Name	Unigene Sequence Cluster Title
					ESTs, Highly similar to interleukin 25; lymphocyte
			j		antigen 6 complex, locus E ligand [Mus musculus]
330	24814	AA891209	n,o,w,x		[M.musculus]
331	21917	AA891220	h,l		ESTs
					ESTs, Weakly similar to A53714 protein kinase (EC
332		AA891302	b,I,m		2.7.1.37) BL44 - human [H.sapiens]
333		AA891423	ii		ESTs Harrian (insapiens)
334		AA891439	С		ESTs
335	13789	AA891476	jj,kk		ESTs
					ESTs, Highly similar to hippocampus abundant
336		AA891535	cc,dd		gene transcript 1 [Mus musculus] [M.musculus]
337		AA891542	d		ESTs
338	21905	AA891546	S		ESTs
339		AA891551	р		ESTs
340		AA891580	е		ESTs
341		AA891595	е		ESTs
342		AA891596	e,aa,bb		ESTs
343		AA891631	ee,ff,jj,kk		ESTs
344		AA891666	cc,dd	melanoma antigen, family D, 1	melanoma antigen, family D, 1
345		AA891677	h,í,íi		ESTs
346		AA891721	w,x		ESTs
347		AA891727	aa		ESTs
348 349		AA891733	a,i,m,ee,ff,jj,kk		ESTs
		AA891734	e,hh		ESTs
350 351	17603	AA891735	S		ESTs
331	17693	AA891737	u,v		ESTs
1					ESTs, Highly similar to endothelial differentiation-
352	CESE	A A BOA 7 4 C			related factor 1; hypothetical protein 1-9 (Mus
332	0000	AA891746	l,m		musculus] [M.musculus]
İ	,		l		
353	18269	AA891769			ESTs, Weakly similar to SC65 synaptonemal
354		AA891774	e I,m		complex protein [Rattus norvegicus] [R.norvegicus]
	- 0000	701031774	6,111		ESTs
			}		ESTs, Highly similar to MRGX_HUMAN
355	21672	AA891789	f,g		Transcription factor-like protein MRGX (MORF-
			9		related gene X protein) [H.sapiens]
	i			1	ESTs, Weakly similar to F22G12.5.p
	[		ĺ	Í	[Caenorhabditis elegans] [C.elegans], ESTs,
					Weakly similar to IPYR_HUMAN inorganic
356	11966	AA891800	hh,jj,kk	]	pyrophosphatase (Pyrophosphate phospho- hydrolase) (PPase) [H.sapiens]
			,,,,,,,,,,		ESTs, Weakly similar to IPYR_HUMAN Inorganic
			]		pyrophosphatase (Pyrophosphate phospho-
356	<u>1</u> 8128	AA891800	n,o		hydrolase) (PPase) [H.sapiens]
	23083	AA891802	cc,dd		ESTs
357					
357 358		AA891803	իի յ	l I	
357		AA891803 AA891824	n,o		ESTs
357 358					ESTs Rattus norvegicus clone ZG52 mRNA sequence
357 358					ESTs Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P)
357 358					ESTs Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor
357 358 359	7050	AA891824			ESTs  Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyrldine nucleotide transhydrogenase)
357 358	7050	AA891824			ESTs  Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
357 358 359	7050	AA891824	п,о		ESTs  Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyrldine nucleotide transhydrogenase)
357 358 359	7050	AA891824	п,о		ESTs  Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) [M.musculus]
357 358 359 360	16023	AA891824 AA891872	п,о		ESTs  Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) [M.musculus]  ESTs, Highly similar to S66254 dolichyl-
357 358 359 360	7050 / 16023 / 19319 /	AA891872 AA891937	m,o w,x		ESTs  Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) [M.musculus]  ESTs, Highly similar to S66254 dolichyldipnosphooligosacchande—protein glycotransterase
357 358 359 360 361 362	7050 / 16023 / 19319 / 1159 /	AA891872 AA891937 AA891949	m,o w,x f kk		ESTs  Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) [M.musculus]  ESTs, Highly similar to S66254 dolichyl-
357 358 359 360	16023 / 19319 / 1159 / 9826 /	AA891872 AA891937 AA891949 AA891950	m,o w,x		ESTs  Rattus norvegicus clone ZG52 mRNA sequence ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) [M.musculus]  ESTs, Highly similar to S66254 dolichyldipnosphooligosacchande—protein glycotransterase (EC 2.4.1.119) 50K chain - human [H.saplens]

	là sy la sa	GenBank Acc	1, 19		Atty. Ref. 44921-5090-01-WO/2105485
EO ID	GI GC in	No.;	Model Code	Known Gene Name	· 机克尔克斯 化二十二甲基酚 电影 (1) 10 10 10 10 10 10 10 10 10 10 10 10 10
rid ip.	OLOO, ID	NO.	IModel Code	Known Gene Name	Unigene Sequence Cluster Title
365	4472	A 4 9 0 4 0 0 5			ESTs, Highly similar to fructosamine 3 kinase [M
366		AA891965	jj,kk		[musculus] [M.musculus]
		AA891969	b,l,m		ESTs
367	1/3/4	AA891978	w,x,jj,kk		ESTs
					ESTs, Weakly similar to T22242 hypothetical
					protein F45G2.10 - Caenorhabditis elegans
368		AA892010	s,t		[C.elegans]
369		AA892014	hh	HLA-B associated transcript 1A	HLA-B associated transcript 1A
370		AA892042	d,t,y,z		ESTs Gallson pt 17
371		AA892094	ii		ESTs
372		AA892120	s,t		ESTs
373	16899	AA892127	u,v		ESTs
374	12010	AA892137	jj,kk		ESTs, Highly similar to open reading frame 12 [N
375		AA892149	C.W		musculus] [M.musculus]
376		AA892238	f,II		ESTs
		7 11002200	1314		ESTs
377	17350	AA892240	l m ::		ESTs, Weakly similar to 2008109A set gene [Ratt
	17000	77032240	l,m,ii		norvegicus] [R.norvegicus]
					ESTs, Highly similar to SYK_HUMAN Lysyl-tRNA
378	ววกกว	A A 0000000	, .		synthetase (Lysine-tRNA ligase) (LysRS)
379		AA892250	d		[H.sapiens]
		AA892273	b		ESTs
380		AA892280	a,s,t,w,x		ESTs
381	11982	AA892284	ii		ESTs
					ESTs, Highly similar to JC7219 nuclear protein SF
382	18209	AA892318	s,t		25 - mouse [M.musculus]
					ESTs, Highly similar to RL3_RAT 60S RIBOSOM
383		AA892367	w,x,cc,dd		PROTEIN L3 (L4) [R.norvegicus]
384	15492	AA892376	f		ESTs
					ESTs, Weakly similar to F13B9.8.p [Caenorhabdi
385	3473	AA892378	le l		elegans] [C.elegans]
<u>-</u>					ESTs Wookly similar to E42D0 0 - 10 - 1 1 1
385	3474	AA892378	e,gg		ESTs, Weakly similar to F13B9.8.p [Caenorhabdi
386	2832	AA892388		CD59 antigen	elegans] [C.elegans] CD59 antigen
			-,-,-		ODOS ANTIGEN
					ESTS Wookly similar to TC47 DAT 71 - 5
-	l		Ì		ESTs, Weakly similar to TC17_RAT Zinc finger
	1				protein 354A (Transcription factor 17) (Renal
387	22868	AA892391	ee,ff		transcription factor Kid-1) (Kidney, ischemia, and
300					developmentally regulated protein-1) [R.norvegicus
389			99	anh da Ad	ESTs
- 000	20104	V1032417	gg	ephrin A1	ephrin A1
390	0254	A A O O O 470			ESTs, Highly similar to S03644 histone H2A.Z - rai
350	9204	AA892470	е		[R.norvegicus]
204	44000	1 4 000 40=		dihydrolipoamide	
391	11992	AA892485	T (	acetyltransferase	dihydrolipoamide acetyltransferase
}					ESTs, Weakly similar to A36690 sucrose alpha-
				·	glucosidase (EC 3.2.1.48) - rat (fragment)
392	1522	AA892486	С		[R.norvegicus]
i.					ESTs, Weakly similar to CD63_RAT CD63 antigen
393		A892498	jj,kk		(AD1 antigen) [R.norvegicus]
394	14066		s,t,u		ESTs
305	11994	A892507	hh		ESTs, Moderately similar to S63540 protein DS 1,
396			w,x		24K - human [H.sapiens]
350			w,x		ESTS
		A892522	r r		ESTs
	M-NAME &				LOTA
397.	65991	U1002022			ESTs
					ESTS, Moderately similar to organic cationic transporter-like 2 [Mus musculus] [M.musculus]

ABLE		GenBank Ac	<u> </u>	Alternative in the second	Atty. Ref., 44921-5090-01-WO/2105485
	GLGC I	D No.	Model Con-	Known Gene Name	N 64 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	1,92001	9 NO. 11111	Woder Code	Known Gene Name	Unigene Sequence Cluster Titte
399	1650	7 AA892547		1	ESTs, Highly similar to hypothetical protein
400		2 AA892554	cc,dd		CL25022 [Homo sapiens] [H.saniens]
400		3 AA892554	-   <u>r</u>		ESTs
401		4 AA892557	j,k		ESTs
70	1337	4 AA692557	jj,kk		ESTs
402	4007	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4			ESTs, Highly similar to RIKEN cDNA 1110001J03
402	1027	4 AA892572	gg,hh		[Mus musculus] [M.musculus]
400	4007	5 4 4 6 6 6 7 6			ESTs, Highly similar to RIKEN cDNA 1110001J03
402	1827	5 AA892572	hh	<u> </u>	[Mus musculus] [M.musculus]
403	451	2 AA892578	j,k,p,q		ESTs
40.4	4500				ESTs, Highly similar to RL8_HUMAN 60S ribosom
404	1587	6 AA892582	g,w,x		protein L8 [R.norvegicus]
					ESTs, Weakly similar to putative nucleotide bindir
		1			protein, estradiol-induced [Homo sapiens]
405	1908	AA892598	j,k,y,z,ee,ff,kk	Í	[H.sapiens]
					FSTs Weakly similar to mutative and all the training
			1		ESTs, Weakly similar to putative nucleotide bindir
405		AA892598	j,k,p,q,y,z	1	protein, estradiol-induced [Homo sapiens] [H.sapiens]
406	2119	AA892607	gg		ESTs
407	4517	AA892642	f		ESTS
408	20068	AA892647	c,d,r	germinal histone H4 gene	
409		AA892773	w,x	germinar historie 114 gene	germinal histone H4 gene
410		AA892775	a,n,x	Lysozyme	ESTs
				Lysozynie	Lysozyme
					ESTs, Highly similar to ERC1_MOUSE DNA
411	21972	AA892791	ii		EXCISION REPAIR PROTEIN ERCC-1
		-	<del>  </del>		[M.musculus]
]			1	Libinary	ESTs, Highly similar to S15892 pyruvate
412	11997	AA892828	6 h 1	HMm:pyruvate dehydrogenase	
	11007	A032020	f,h,i	(lipoamide) beta	rat (R.norvegicus)
ł			1		ESTs, Weakly similar to CAZ3_RAT F-actin capping
413	71/0	AA892842			protein alpha-3 subunit (CAPZ alpha-3)
713	/ 140	AA092042	f,g		[R.norvegicus]
414	47000	4 4 0 0 0 0 4 0			ESTs, Moderately similar to hypothetical protein
415		AA892843	b		FLJ20917 [Homo sapiens] [H.sapiens]
415	17009	AA892851	p,q,s,t		ESTs
410	1/590	AA892851	a,j,k		ESTs
			1		ESTs, Weakly similar to PLO1_RAT Procollagen-
440			[ ]		lysine,2-oxoglutarate 5-dioxygenase 1 precursor
416		AA892859	99		(Lysyl hydroxylase 1) (LH1) [R.norvegicus]
417		AA892860	а		ESTs [K.horvegicus]
418	1031	AA892863	t		ESTs
	i				ESTs, Weakly similar to JC7260 strictosidine
					synthase (EC 4.3.3.2) homolog 2 - fruit fly
419	12848	AA892916	s,t		(Drosophila melanogostos) to melanogostos
420	24279	AA892919		nucleolar phosphoprotein p130	(Drosophila melanogaster) [D.melanogaster] nucleolar phosphoprotein p130
				p. soprioprotein p 130	FSTs Weakly similar to FCO Date To
421	16482	AA892940	gg		ESTs, Weakly similar to EF2_RAT Elongation factor
422	15956		d		2 (EF-2) [R.norvegicus] ESTs
					FSTs Wooldy alegient COVIII
	- 1		ľ		ESTs, Weakly similar to GSHH_RAT Phospholipid
		i			hydroperoxide glutathione peroxidase,
423	19124	AA893022	ii l		mitochondrial precursor (PHGPx) (GPX-4)
424	14360		" h,I		[R.norvegicus]
425					ESTs
426			u,v,ii		ESTs
120		V1030104	m		ESIs
427	17724	A893194			ESTs, Moderately similar to hypothetical protein
428			c,f		MGC10974 [Homo sapiens] [H.sapiens]
429		4000	hh		ESTs

TABLE		GenBank Ac	<u>्र</u> ्र <नः <b>c</b> . ।	The state of the s	Atty. Ref. 44921-5090-01-WO/2105485
SEOID	GLGC II	DINO:			Unigene Sequence Clüster Title
STA ID	OLOG !!	JINO.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
400	207				ESTs, Moderately similar to hypothetical protein
430	387	9 AA893237	е		IMBU32UD IHOMO sanional IU costanal
		1		fatty acid Coenzyme A ligase,	r. c.mo dapiensj [ri.sapiens]
431	2098	5 AA893242	n	long chain 2	fatty acid Coenzyme A ligase, long chain 2
				fatty acid Coenzyme A ligase,	lawy data decirzyme A ligase, long chain 2
431	2098	6 AA893242	11	long chain 2	
432	1775	2 AA893244	ii		fatty acid Coenzyme A ligase, long chain 2
			<u> </u>		
433	2165	2 AA893267	u,v	l .	ESTs, Weakly similar to S46992 protein p130 - rai
					[R.norvegicus]
					ESTs, Moderately similar to ADFP_MOUSE
434	1616	AA893280	a,y,z	1	ADIPOPHILIN (ADIPOSE DIFFERENTIATION-
		1000200	a,y,2		RELATED PROTEIN) (ADRP) [M.musculus]
435	11934	AA893328			ESTS, Moderately similar to C54354 calnexin
	. 1000	777033328	99		precursor - rat [R.norvegicus]
436	22356	AA893338	<b>L</b>	l	Rattus norvegicus hypothetical RNA binding protei
437		AA893357	b,u,v		RDA288 mRNA, complete cds
737		10000000	99		ESTs
438	10540	A A 902 402			ESTs, Highly similar to RL26_RAT 60S
430	10042	AA893493	g		RIBOSOMAL PROTEIN L26 [R.norvegicus]
					ESTs, Highly similar to translocation protein 1;
- 1					Otrp1 protein; membrane protein SEC62,
			]		S.cerevisiae, homolog of [Homo sapiens]
439		AA893515	[R		[H.sapiens]
440		AA893581	f		ESTs
441		AA893607	s,t		ESTs
441		AA893607	b,l,m		ESTs
442	4541	AA893612	е		ESTs
					ESTS Maday I I I
	İ		1		ESTs, Moderately similar to coatomer protein
443	19505	AA893634	r,ii		complex, subunit zeta 1; nonclathrin coat protein
444		AA893663	ji,kk		zeta1-COP [Mus musculus] [M.musculus]
445		AA893664	175	TELLO	ESTs
770	7044	AA033004	h,l	TEMO	TEMO
446	10411	AA893667	1		ESTs, Weakly similar to T46904 hypothetical
447	0004	AA093007	cc,dd		protein DKFZp761D081.1 - human [H saniens]
		AA893717	d		ESTs
448		AA893743	f,g		ESTs
449	4556	AA893811	aa,bb		ESTS
J	1				ESTs, Moderately similar to SYTC_HUMAN
			1		Threonyl-tRNA synthetase, cytoplasmic (Threonine-
450		AA893860 ·	y,z i	Hs:threonyl-tRNA synthetase	tRNA ligase) (ThrRS) [H.sapiens]
451		AA893905	ii	,	ESTs [H.sapiens]
452		AA893970	h,aa,bb		ESTs
453		AA893980	lii		
454		AA893994	b,l,m		ESTS
	-1		-,,,,,,		EST
İ	- 1		1		ESTs, Highly similar to CAPG_MOUSE
	- 1				Macrophage capping protein (Myc basic motif
455	23731	A894004	Inokkii		homolog-1) (Actin-capping protein GCAP39)
456			l,n,o,kk,ii		[M.musculus]
456		A894009	b,l,m		
457			aa,bb,ii		ESTs
		VA894027	Г		
458	10913	A894092	n,o		ESTs
1					ESTs, Weakly similar to T20253 hypothetical
					protein F53E4.1 - Caenorhabditis elegans
459		A894104	jj,kk	4	[C.elegans]
460	9388	40044	C		ESTs
					ESTs, Highly similar to A31568 electron transfer
461	16/3//	A894174	h,l		flavoprotein alpha chain precursor - rat
4011	10404174	/\U34!/4 ·	n.i •		[R.norvegicus]

TABLE 1		I ConPonit Ass	1.	No. 10 A 20 10 10 10 10 10 10 10 10 10 10 10 10 10	Atty. Ref. 44921-5090-01-WO/2105485
פבט וח		GenBank Acc D No.		AND A CHARLES TO A	[7] D. C. C. Aler, M. C. Martin, M. C. A. D. C. Martin, M. C. A. D. C. Martin, M. C. A. D. C. Martin, M. Martin, M. C. Martin
	GLGC	D No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
462	2198	9 AA894188	cc,dd		ESTs
463	213	3 AA894193	r		ESTs
			<del>'</del>	<del></del>	
					ESTs, Highly similar to MLES_RAT Myosin light
464	2447	3 AA894200			chain alkali, smooth-muscle isoform (MLC3SM)
- 707	244/	3 AA694200	b		[R.norvegicus]
405			1		ESTs, Weakly similar to dual-specificity
465		3 AA894207	r	ì	phosphatase [Mus musculus] [M.musculus]
466		9 AA894233	S		ESTs [Mos musculus] [M.musculus]
467	1733	6 AA894297	j,k,s,t		ESTs
			1		
468	391	DAA894345	f,j,k,r,gg		ESTs, Weakly similar to 2021425A MAT1 gene
469		7 AA899109	d		[Mus musculus] [M.musculus]
		74.000100	ļu ———	1	ESTs
470	2422	A A 00000F0	1	Myristoylated alanine-rich	Myristoylated alanine-rich protein kinase C
4/0	2432	AA899253	aa,bb	protein kinase C substrate	substrate
4-4					ESTs, Moderately similar to KIAA1049 protein
471	2249	AA899289	d		[Homo sapiens] [H.sapiens]
					ESTs, Highly similar to SYW_MOUSE Tryptophan
					ItPNA synthetage /Toute-bar in the strain in
472	4636	AA899491	le		tRNA synthetase (Tryptophan–tRNA ligase)
473	22308	AA899535	u,v	<del>-</del>	(TrpRS) [M.musculus]
474	20038	AA899797			ESTs
475	20000	AA899828	bb,II		EST
476	2008	AA000054	l,m		ESTs
4/0	23/10	AA899854	С	topoisomerase (DNA) II alpha	topoisomerase (DNA) II alpha
ŀ					, and the second
			1		ESTs, Highly similar to S30034 translocating chair
477		AA899894	r	İ	associating membrane and it ansiocating chair
478	21639	AA899911	111		associating membrane protein - human [H.sapiens
479		AA899951	cc,dd		ESTs
		7 1000001	CO,UU		ESTs
480	17355	AA899959	l		ESTs, Highly similar to S63993 acrosomal protein
481			l,m		AZ1 - mouse [M.musculus]
401	10090	AA899964	e,r		ESTs
J					
					ESTs, Highly similar to T08712 hypothetical protein
482	11268	AA899969	l,m		DKE7p566C0424.4 hymno (from an and state
				polypyrimidine tract binding	DKFZp566C0424.1 - human (fragment) [H.sapiens
483	3903	AA899986	w,x	protein	
			,	protein	polypyrimidine tract binding protein
484	22480	AA900230			ESTs, Weakly similar to T12B3.4.p [Caenorhabditi
		1000200	u,v	I INA	[elegans] [C.elegans]
ĺ				HMm:carbon catabolite	ESTs, Highly similar to A2MG_RAT ALPHA-2-
405	4	4.4000000		repression 4 homolog (S.	MACROGLOBULIN PRECURSOR (ALPHA-2-M)
485			t,y,z,ee,ff	cerevisiae)	[R.norvegicus]
486	4730	AA900326	d,jj,kk		ESTs
	i				ESTs, Weakly similar to T47146 hypothetical
1					protein DKE76764.0460 4 hours //
487	4732	AA900343	cc,dd		protein DKFZp761C169.1 - human (fragment)
488			u,v		[H.sapiens]
			w) 4		ESTs
1					ESTs, Moderately similar to T50619 hypothetical
489	16752	AA900474			protein DKFZp762M136.1 - human (fragment)
490			W,X		[H.sapiens]
		4 4 4 4 4 4 4	il		ESTs
491	4779	AA900825	u,v		ESTs
1	Ţ				ESTs, Weakly similar to COPP_RAT Coatomer
	ł		l		hota' subusit (Potal and the COPP_KAT Coatomer
492	14712	AA900860	ee,ff		beta' subunit (Beta'-coat protein) (Beta'-COP)
		000000	30,11		(p102) [R.norvegicus]
ľ		i i			Inches to Monthly similar to 1995 State
493	3822	AA900863	k		ESTs, Weakly similar to HE47_RAT Probable ATP- dependent RNA helicase p47 [R.norvegicus]

ABLE		IGenBank As	<del></del>	3.5°C	Atty, Ref. 44921-5090-01-WO/2105485
ייי וה' <del>ו</del>	വര്ര്ഷ	GenBank Ac No.	· .		· 民国 人 经总统 實際 医皮肤 医皮肤病
rdin.	Prop. II	7 NO. ,,	Model Code	Known Gene Name	Unigene Sequence Cluster Title
			,	61 1 606 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	ĺ	Ì	,	Cbp/p300-interacting	}
404	470			transactivator, with Glu/Asp-rich	Cbp/p300-interacting transactivator, with Glu/As
494	4/9	0 AA900875	ee,ff	carboxy-terminal domain, 4	rich carboxy-terminal domain, 4
				branched chain	non ochboxy-terminal domain, 4
495	2303	BAA900881	a,j,k,y,z	aminotransferase 1, cytosolic	branched shelp and a
496	4797	7 AA900967	j,k	The state of the s	branched chain amInotransferase 1, cytosolic ESTs
		1	Ì		ESTs, Highly similar to p34SEI-1; PHD zinc fing
497	22666	AA900974	a,t,y,z,ee,ff		and bromodomain-interacting protein 1 [Mus
498	26075	AA900993	s,t	<del></del>	musculus] [M.musculus]
499		AA901058	99	<u> </u>	
500		AA901069		<u> </u>	ESTs
501	22800	AA901107	j,k		
	22050	MA901107	kk		ESTs
500	4000	440040==			ESTs, Weakly similar to S53358 ubiquitin-
502	4858	AA901238	W,X	<u></u>	conjugating enzyme E2.17kB - rat [R.norvegicus]
503	4861	AA901290	y,z,kk		ESTs ESTs
j			W .		ESTs, Highly similar to sialyltransferase 7 ((alpha
ı			-	1	N-acetylpoursminul 2.2 bates
					N-acetylneuraminyl 2,3-beta-galactosyl-1,3)-N-
504	16976	AA901341	j,k		acetyl galactosaminde alpha-2,6-sialyltransferase
505	4866	AA901350	d		B; ST6GalNAc II [Mus musculus] [M.musculus]
506	4874	AA923850	kk		ESTs
507		AA923996	h,i		ESTs
508		AA924013			EST
509	17644	AA924036	[- 1.1:		ESTs
- 000	17044	AA324030	c,kk		ESTs
510	4007	A 400 400 4			ESTs, Weakly similar to growth supressor 1;
511	4907	AA924091	r		leprecan [Rattus norvegicus] [R.norvegicus]
311	4909	AA924097	jj,kk		ESTs (Carried Hol Voglods) [13.Hol Vegicus]
-40				Tissue inhibitor of	
512	1/231	AA924107	<u>lii</u>	metalloproteinase 3	Tissue inhibitor of metalloproteinase 3
,	i				ESTs, Weakly similar to Y193_HUMAN
513	4917	AA924140	l,m		Lunathatical arreas (NA A CARA TI
514		AA924251	С		Hypothetical protein KIAA0193 [H.sapiens] ESTs
515	22914	AA924335	h,l,ll		
516	12346	AA924346	d,aa,bb		ESTs
			-,,20		ESTs
					ESTs, Weakly similar to Prostatic Acid
517	23096	AA924352	hv		Phosphatase (E.C.3.1.3.2) Complexed With Tartar
540		AA924415	b,v		Acia [R.norvegicus]
519		A924444	n,o		ESTs
<del> </del>	7007/	V104444	u,v		ESTs
520	19254	1004540	<u> </u>		ESTs, Highly similar to RL9_RAT 60S RIBOSOMA
520 521		A924548	jj,kk		PROTEIN L9 [R.norvegicus]
	49/0/	A924571	l,m		ESTs
522	24310	A924578	g,il		ESTs
523		A924598	е		ESTs
524		A924689	ü		ESTs
525		A924794	a,kk		ESTs
526	5030 A	A924802	е		ESTS
527	2238 A	A924902	w,x		
528		A924926	h,l,jj,kk		STs
529		A924943	I,m		STs
530		A924985			STs
531		A925031	- 0		alsequestrin 2
1	2010	Vacano i			STs
532	22472	A00505~		iE	STs, Highly similar to GYRTI cysteine-rich
JJZ!	20113A	A925057	h,l,w,x	lir	ntestinal protein - rat [R.norvegicus]
	İ	j	T	E	STs, Moderately similar to 2118320A
	1				eurodegeneration-associated protein 1 [Rattus
احج	17363 A	A925150 l	11	Ι"	orvegicus] [R.norvegicus]

		GenBank Acc		TREASON PAR	Atty. Ref. 44921-5090-01-WO/2105485
	GLGC ID		Model, Code	Known Gene Name	Unigene Sequence Cluster Title
534	18271	AA925267	е		ESTs
					ESTs, Moderately similar to hypothetical protein
535	23452	AA925289	gg		MGC8974 [Homo sapiens] [H.sapiens]
			100		ESTs, Weakly similar to mitogen activated prot
		1	1	HHs:mitogen-activated protein	kingso kingso kingso tringen activated prot
536	16499	AA925300	p,ee,ff,gg	kinase kinase kinase 3	
537	5129	AA925335	l biociniaa	Kirlase Kirlase S	[R.norvegicus]
		1 102000	<del>-                                     </del>	<del></del>	ESTs
538	5132	AA925342	h,l		ESTs, Highly similar to MYM1_MOUSE Myome
539		AA925352			[1 (Skelemin) [M.musculus]
540	21500	AA925353	kk,ll		ESTs
541	14045	AA925353	w,x,cc,dd		ESTs
	14945	AA925364	n,o		ESTs
542	516/	AA925529	ee,ff		EST
l					ESTs, Moderately similar to WDR1_MOUSE WI
				1	repeat protein 1 (Actin interacting protein 1)
543	4285	AA925708	r,y,z,jj,kk	,	[M.musculus]
544	5206	AA925755	11	Glutaminase	Glutaminase
					Gotaminase
l			1	1	ECTs Wighly similar to 740400
545	3997	AA925771	lii		ESTs, Highly similar to T12483 hypothetical prot
546		AA925876	l,m	<u> </u>	DKFZp564B0769.1 - human (fragment) [H.sapie
-			19111		ESTS
- 1			1		ESTs, Highly similar to cytokine receptor-like fac
547	5227	AA925924	l a kk		1; cytokine receptor like molecule 3 (Mus muscul
548	20245	AA925938	l,o,kk		[M.musculus]
340	20345	AA925938	99		ESTs
E40	5050	4.4.000000			ESTs, Highly similar to KIAA0164 gene product
549	5258	AA926089	t		[Homo sapiens] [H.sapiens]
550	1/15/	AA926129	CC		ESTs
- 1	ł				ESTs, Moderately similar to UCRY_HUMAN
					Ubiquinol-cytochrome C reductase complex 6.4
551	16468	AA926137	hh		protein (Complex III subunit XI) [H.sapiens]
					EST, Weakly similar to ADP-ribosylation factor-li
552	20327	AA926265	cc,dd		E (Pattus parasisus) to ADP-ribosylation factor-li
553	893	AA926305	h,l		5 [Rattus norvegicus] [R.norvegicus]
553		AA926305	h,l,n,o		ESTs
		- 1020000	11,11,11,0	Tyrosine 3-	ESTs
- 1			f l		
				monooxygenase/tryptophan 5-	
554	2017	AA926328		monooxygenase activation	Tyrosine 3-monooxygenase/tryptophan 5-
004	3017	~~320328	p,q	protein, zeta polypeptide	monooxygenase activation protein, zeta polypepti
EEE	0040	A A O 4 O C O =	<u> </u>		ESTS, Highly similar to hypothetical protein
555	9942	AA942697	d		MGC3133 [Homo sapiens] [H.sapiens]
					ESTs, Moderately similar to SUR2_MOUSE Surfe
556	16909	AA942704	g		locus protein 2 (Surf-2) [M.musculus]
					ESTs, Highly similar to hematological and
			1		neurological expressed sequence 1 [Mus musculu
557	6039	A942716	d		[M.musculus]
558				B cell lymphoma 2 like	
559			e,y,z	2 con lymphoma 2 like	B cell lymphoma 2 like
560		A942930	E,y,2		ESTs
561					ESTs
562	3052		cc,dd		ESTs
	22420		U,V		ESTs
563	2213U F	A943020	jj,kk		ESTs
	j				·
	- 1	ļ			ESTs, Highly similar to KFMS_RAT Macrophage
[		[	i		colony stimulating factor i receptor precursor (CST
564			r,w,x		1-R) (Fms proto-oncogene) (c-fms) [R.norvegicus]
			cc,dd		ESTs (Fins proto-oncogene) (c-fms) [R.norvegicus]
565					
565 566	23822 A	A943114	li l		
	23822 A	A943114			EST's EST

ABLE		GenBank Ac	VO. 11.78	T. 17.	Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GLGC.II	DINO.		Known Gene Name	Unigene Sequence Cluster Title
7.5 15	OLOG II	J NOT !	Model code	Known Gene Name	Unigene Sequence Cluster Title
					ESTs, Weakly similar to one twenty two protein
F0/		.1			hypothetical protein FLJ12479 [Homo sapiens]
568		1 AA943240	gg	1	[H.sapiens]
569	2221	8 AA943409	е		ESTs
570	2222	3 AA943440	w,x		EST
571	2199	0 AA943524	b		
572	2224	7 AA943537	y,z	zyxin	ESTs
572	2224	B AA943537	y,z	zyxin	zyxin
573	2226	1 AA943573	d	ZyXIII	zyxin
574	19220	AA943740	jj,kk		ESTs
575		AA943748	- IIII		ESTs
	0000	777343740			ESTs
					ESTs, Moderately similar to ASPG_MOUSE N(4
	ĺ				(beta-N-acetylglucosaminyl)-L-asparaginase
	ł		-		precursor (Glycosylasparaginase)
		İ	-	l	(Aspartylglucosaminidase) (N4-(N-acetyl-beta-
					glucosaminyl) L separatina a-tita - 2 (4 a ti
576	22317	AA943766	j,k		glucosaminyl)-L-asparagine amidase) (AGA) [M.musculus]
577		AA943981	ii		ESTs
577		AA943981	r		
578	16447	AA944188	gg		ESTs
579	22378	AA944212	a,y,z,ee,ff,kk		ESTs
580		AA944216	i,k		ESTs
581		AA944341			ESTs
582	15506	AA944353	u,v		ESTs
583	12200	AA944383	jj,kk		ESTs
- 000	12209	AA944363	99		ESTs ·
ł			1		
584	00705			HMm:heat shock protein, 86	ESTs, Moderately similar to HS9B_RAT Heat sho
304	20795	AA944397	e,ee	kDa 1	protein HSP 90-beta (HSP 84) [R.norvegicus]
- 1					FOR THE SOLUTION OF [IN. HOLVEYICUS]
coc	04000				IES IS. Highly similar to A40457 fibrilla 2 and and
585		AA944398	lgg l		ESTS, Fighly similar to A49457 fibulin-2 precursor
586	22681	AA944413	gg p,q		mouse [M.musculus]
	22681		p,q	Calmodulin III	mouse [M.musculus]  [ESTs]
586	22681	AA944413	p,q	Calmodulin III	mouse [M.musculus]
586	22681	AA944413	p,q	Calmodulin III	ESTS, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTS  Calmodulin III
586	22681	AA944413	p,q	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLI3 RAT SKELETAL
586	22681	AA944413	p,q	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLI3_RAT SKELETAL  MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN
586	22681 15476	AA944413 AA944426	p,q h,i	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALE LIM
586 587	22681 15476	AA944413	p,q	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHI -2) IR populational
586 587	22681 15476	AA944413 AA944426	p,q h,i	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal
586 587	22681 15476 19480	AA944413 AA944426 AA944442	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLI3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68)
586 587 588	22681 15476 19480	AA944413 AA944426 AA944442	p,q h,i	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]
586 587 588	22681 15476 19480	AA944413 AA944426 AA944442	p,q h,l (	Calmodulin III	ESTS, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTS  Calmodulin III  ESTS, Weakly similar to SLI3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTS, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68)  [H.sapiens]
586 587 588	22681 15476 19480	AA944413 AA944426 AA944442	p,q h,l (	Calmodulin III	ESTS, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTS  Calmodulin III  ESTS, Weakly similar to SLI3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTS, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68)  [H.sapiens]
586 587 588	22681 15476 19480	AA944413 AA944426 AA944442	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs
586 587 588 590	22681 15476 19480 21522 22431	AA944413 AA944426 AA944442 AA944449 AA944463	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibringen domain-containing
586 587 588 590	22681 15476 19480 21522 22431	AA944413 AA944442 AA944449 AA944463	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Segum Jectin P36)
586 587 588 590 591 592	22681 15476 19480 21522 22431 44763 A 2661 A	AA944442 AA944449 AA944481 AA944493	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]
586 587 588 590 591 592 593	22681 15476 19480 21522 22431 44763 2661 22438	AA944413 AA944442 AA944449 AA944463 AA944481 AA944493 A944498	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]
586 587 588 590 591 592 593 594	22681 15476 19480 21522 22431 44763 2661 22438 22678	AA944413 AA944442 AA944449 AA944463 AA944481 AA944493 AA944498 AA944498	p.q h,l q	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs
586 587 588 590 591 592 593	22681 15476 19480 21522 22431 44763 2661 22438 22678	AA944442 AA944442 AA944449 AA944463 AA944481 AA944493 AA944498	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  ESTs
586 587 588 590 591 592 593 594	22681 15476 19480 21522 22431 44763 2661 22438 422678 12303	AA944413 AA944442 AA944449 AA944463 AA944481 AA944493 AA944498 AA944498 AA944498 AA944498	p.q h,l q	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  ESTs  ESTs
586 567 588 590 591 592 593 594 595 596	22681 15476 19480 21522 22431 14763 2661 22438 22678 12303 42536	AA944442  AA944442  AA944449  AA944463  AA944481  AA944493  AA944498  AA944556  A944786  A944803	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  ESTs  ESTs  ESTs
586 567 588 590 591 592 593 594 595	22681 15476 19480 21522 22431 14763 2661 22438 22678 12303 42536	AA944442  AA944442  AA944449  AA944463  AA944481  AA944493  AA944498  AA944556  A944786  A944803	p.q h,l q	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs
586 567 588 590 591 592 593 594 595 596 597	22681 15476 19480 21522 22431 22431 2661 A 22438 A 22678 A 12303 A 22536 A 22081 A	AA944442  AA944449  AA944463  AA944481  A944498  A944498  A944556  A944786  A944803  A944818	p,q h,1 ( r,bb gg r P,q d l,m jj,kk t r	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs
586 567 588 590 591 592 593 594 595 596	22681 15476 19480 21522 22431 22431 2661 A 22438 A 22678 A 12303 A 22536 A 22081 A	AA944442  AA944442  AA944449  AA944463  AA944481  AA944498  A944556  A944786  A944803  A944818	p,q h,l (	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  ESTS  ESTs  ESTS  ESTs  ESTS
586 567 588 590 591 592 593 594 595 596 597	22681 15476 19480 21522 22431 22431 2661 A 22438 A 22678 A 12303 A 22536 A 22081 A	AA944442  AA944449  AA944463  AA944481  A944498  A944498  A944556  A944786  A944803  A944818	p,q h,1 ( r,bb gg r P,q d l,m jj,kk t r	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  ESTS  ESTs  ESTS  ESTs  ESTS
586 567 588 590 591 592 593 594 595 596 597	22681 15476 19480 21522 22431 14763 2661 22438 4 22678 4 22536 4 22081 A 21581 A	AA944442 AA944442 AA944449 AA944463 AA944463 AA944493 AA944498 AA944498 AA944498 AA944498 AA944498 AA944498 AA944498 AA944803 AA944803 AA944803	p,q h,l  r,bb  gg r  p,q d l,m jj,kk t r j,k,jj,kk	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs
586 567 588 590 591 592 593 594 595 596 597	22681 15476 19480 21522 22431 14763 2661 22438 4 22678 4 22536 4 22081 A 21581 A	AA944442 AA944442 AA944449 AA944463 AA944463 AA944493 AA944498 AA944498 AA944498 AA944498 AA944498 AA944498 AA944498 AA944803 AA944803 AA944803	p,q h,1 ( r,bb gg r P,q d l,m jj,kk t r	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  E
586 567 588 590 591 592 593 594 595 596 597	22681 15476 19480 21522 22431 14763 2661 22438 4 22678 4 22536 4 22081 A 21581 A	AA944442 AA944442 AA944449 AA944463 AA944463 AA944493 AA944498 AA944498 AA944498 AA944498 AA944498 AA944498 AA944498 AA944803 AA944803 AA944803	p,q h,l  r,bb  gg r  p,q d l,m jj,kk t r j,k,jj,kk	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  E
586 567 588 590 591 592 593 594 595 596 596	22681 15476 19480 21522 22431 14763 2661 22438 22678 4 22536 4 22081 A 21581 A	AA944442  AA944442  AA944449  AA944463  AA944481  A944498  A944498  A944556  A944786  A944803  A944818  A944828	p,q h,l  r,bb  gg r  p,q d l,m jj,kk t r j,k,jj,kk	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs
586 567 588 590 591 592 593 594 595 596 597	22681 15476 19480 21522 22431 14763 2661 22438 4 22678 4 22536 4 22081 A 21581 A	AA944442  AA944442  AA944449  AA944463  AA944481  AA944493  AA944498  AA944498  AA944803  AA944818  AA944828  AA944840	p,q h,l  r,bb  gg r  p,q d l,m jj,kk t r j,k,jj,kk	Calmodulin III	ESTs, Highly similar to A49457 fibulin-2 precursor mouse [M.musculus]  ESTs  Calmodulin III  ESTs, Weakly similar to SLi3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]  ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]  ESTs  ESTs  ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]  ESTs  E

TABLE 1				West and the second	Atty. Ref. 44921-5090-01-WO/2105485
050.15	01.00.15	GenBank Acc.	The state of the state of		[1] 1. [
		No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
601	22556	AA945100	w,x		ESTs
				Rattus norvegicus	
١ .	40404			mitochondrial genome.	
3	19421	AA945152	bb	9/22Length = 16,3	dimethylarginine dimethylaminohydrolase 1
					ESTs, Highly similar to AMPL_HUMAN Cytosol
		1		1	aminopeptidase (Leucine aminopeptidase) (LAP)
000					(Leucyl aminopeptidase) (Proline aminopeptidase)
602		AA945172	е	HHs:leucine aminopeptidase 3	(Prolyl aminopeptidase) [H.sapiens]
603	14352	AA945181	gg		ESTs
004	4000				ESTs, Weakly similar to JC5105 stromal cell-
604		AA945591	n,o,w,x		derived factor 2 - mouse [M.musculus]
605		AA945601	hh		ESTs
605	22267	AA945601	99		ESTs
			1		
606	04504	44045000	l		ESTs, Highly similar to R5RT12 acidic ribosomal
606	24021	AA945636	g,h,l		protein P1, cytosolic [validated] - rat [R.norvegicus]
1					ESTs, Moderately similar to C3L1_MOUSE
					Chitinase-3 like protein 1 precursor (Cartilage
607	22615	AA945643	lele.		glycoprotein-39) (GP-39) (BRP39 protein)
608		AA945679	kk		[M.musculus]
609		AA945679 AA945704	j,k		ESTs
610		AA945704 AA945712	p,q,ee,ff,ii		ESTs
611		AA945737	d roo bb	Chamalian and CODA	ESTs
612		AA945750	d,r,aa,bb	Chemokine receptor (LCR1)	Chemokine receptor (LCR1)
613		AA945878	U,V		ESTs
614		AA945898	gg		ESTs
615	22682	AA945910	cc,dd		ESTs
616		AA945932	+	Annexin A3	ESTS
617		AA945986	jj,kk	Attriexin A3	Annexin A3
618		AA945996	j,k,kk		ESTs
"		701040000	J,N,NN		ESTs
				ļ	ESTs, Highly similar to COXG_MOUSE
619	20832	AA946040	hh		Cytochrome c oxidase polypeptide VIb (AED) [M.musculus]
620		AA946046	l,m		ESTs
			,,,,,		ESTs, Highly similar to ubiquitin-like 3 [Homo
621	22708	AA946063	u,v		sapiens] [H.sapiens]
					ESTs, Highly similar to catenin alpha-like 1; alpha-
					catenin related protein [Mus musculus]
622	22711	AA946072	г,y,z,kk		[M.musculus]
623			n,o		ESTs
624		AA946224	ii		ESTs
625	23027	AA946264	aa,bb		ESTs
					ESTs, Highly similar to AR21_HUMAN ARP2/3
					complex 21 kDa subunit (P21-ARC) (Actin-related
626			а		protein 2/3 complex subunit 3) [H.sapiens]
627	22755	AA946323	ii		ESTs
1 1					ESTs, Highly similar to SNX5_MOUSE Sorting
628			11	<u> </u>	nexin 5 [M.musculus]
629			99		ESTs
630	22771	AA946432	b,l,m	casein kinase I delta	casein kinase I delta
	ا				ESTs, Highly similar to HSRT4 histone H4 - rat
631			d		[R.norvegicus]
632			hh		ESTs
633			e		ESIS
634			j,k,s,t		ESTs
635		AA955206	y,z,ee,ff		ESTs
636			ii		ESTs
637	23498	AA955248	w,x		ESTs

TABLE 1		, in .	:	<b>\$</b> 10	Atty. Ref. 44921-5090-01-WO/2105485
050)D		GenBank Acc.		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
SEQID	GLĆC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
					ESTs, Weakly similar to T46637 transcription factor
638		AA955298	y,z		1, neural - rat [R.norvegicus]
639	23326	AA955415	n,o		ESTs
640		AA955540	p,q		ESTs
			16,14		ESTs, Weakly similar to T21697 hypothetical
				Ī	protein F40E10.6 - Caenorhabditis elegans
641	12928	AA955564			Colorada Valencia
642		AA955684	e s,t		[C.elegans]
- 512	20010	77700004	15,1		ESTs
					EST, ESTs, Highly similar to OKRT2R protein
					kinase (EC 2.7.1.37), cAMP-dependent, type II-
040	-111	4 4 0 5 5 5 5 6	l	1	alpha regulatory chain - rat (fragment)
643	5111	AA955729	f,g,l,m		[R.norvegicus]
					ESTs, Weakly similar to LIS1_MOUSE Platelet-
					activating factor acetylhydrolase IB alpha subunit
				l.	(PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45
				<b>,</b>	kDa subunit) (PAF-AH alpha) (PAFAH alpha)
644	12426	AA955760	u,v	j	(Lissencephaly-1 protein) (LIS-1) [R.norvegicus]
			1 ·		(Lio-1) [K.norvegicus]
			1	1	FSTs Highly similar to TDDD MOUSE TABLES
			1	İ	ESTs, Highly similar to TRBP_MOUSE TAR RNA-
645	6659	AA955857	holm		binding protein 2 (Protamine-1 RNA binding protein)
040	0000	7/1900001	b,c,l,m		(PRM-1 RNA binding protein) [M.musculus]
					EST, EST, Moderately similar to FBRL_MOUSE
			1		Fibrillarin (Nucleolar protein 1) [M.musculus], ESTs,
				]	Highly similar to S38342 fibrillarin - mouse
646	17540	AA955914	a		[M.musculus]
					ESTs, Moderately similar to T43493 hypothetical
647	14327	AA956111	h,l		protein DKFZp434C119.1 - human [H.sapiens]
		1			ESTs, Highly similar to ubiquitin conjugating
648	23357	AA956114	cc,dd		enzyme [Rattus norvegicus] [R.norvegicus]
649		AA956278	aa,bb		ESTs
650		AA956294	e		ESTs
651		AA956550	j,k		ESTs
652		AA956555	r,kk		ESTs
653		AA956689	l,m		EST
654		AA956703	w,x		
655	17/05	AA956733	b		ESTs
656		AA956758			ESTs
- 000	10040	AA30736	l,m		EST
i					ESTs, Highly similar to IF3A_MOUSE
					EUKARYOTIC TRANSLATION INITIATION
ľ					FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3
					P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN)
657			u,v		(CENTROSOMIN) [M.musculus]
658		AA957007	g	glutathione S-transferase, mu 5	glutathione S-transferase, mu 5
659	23952	AA957096	gg		ESTs
					ESTs, Weakly similar to NADE_HUMAN p75NTR-
]					associated cell death executor (Nerve growth factor
	j				receptor associated protein 1) (Ovarian granulosa
660	23957	AA957123	c		Icell 13 0 kDa protota HCDZ4 (II
661			kk		cell 13.0 kDa protein HGR74) [H.sapiens]
662			I,m		ESTS
663					EST
664			p,q,ee,ff		ESTs
004	24012	MA301330	b,d	1	ESTs
1	40500	A A O E 3 O O O		transforming growth factor beta	transforming growth factor beta 1 induced transcript
00-	125291	AA957362	đ	1 induced transcript 1	1
665					
665	-,2020				ESTs, Highly similar to FCEG_RAT High affinity
665	*				immunoglobulin epsilon receptor gamma-subunit
665	*	AA957422			ESTs, Highly similar to FCEG_RAT High affinity immunoglobulin epsilon receptor gamma-subunit precursor (FcERI) (IgE Fc receptor gamma-subunit)

ABLE 1	5 to 2 to 3	GenBank Acc	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2 W 1 W 2 W 2 W 2 W 2 W 3 W 3 W 3 W 3 W 3 W 3	Atty. Ref: 44921-5090-01-WO/2105485
	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
667				Nilown Gene Name	Unigene Sequence Cluster Title
668		AA957452	a,jj,kk		ESTs
000	3005	AA957535	а		ESTs
					ESTs, Weakly similar to RNB6 [Rattus norvegicu
669	23732	AA957653	ee,ff		[R.norvegicus]
					ESTs, Weakly similar to FBL5_RAT Fibulin-5
		]			precursor (FIBL-5) (Developmental arteries and
					neural crost ECE lite and the control of the contro
		1	1		neural crest EGF-like protein) (Dance) (Embryoni
670	24135	AA957736	n,o	Ĭ	vascular EGF repeat-containing protein) (EVEC)
			1.10		[R.norvegicus]
- 1		Ì	İ		ESTs, Weakly similar to SNX9_HUMAN Sorting
671	23644	AA957808		1	nexin 9 (SH3 and PX domain-containing protein 1
672		AA957835	99		(SDP1 protein) [H.sapiens]
673			jj,kk,il		ESTs
0/3	23031	AA963094	d		ESTs
					ESTs, Weakly similar to heterogeneous nuclear
					ribonucleoprotein A/B [Rattus norvegicus]
674		AA963171	cc,dd		[R.norvegicus]
675	23289	AA963173	Jii		ESTs
					ESTs, Moderately similar to A46613 protein 4.1,
676	3953	AA963260	s,t		P4.1 - mouse [M.musculus]
677	2173	AA963627	w,x		For a linease [w.musculus]
					ESTs
					FOT 18 11
					ESTs, Highly similar to P2G4_MOUSE Proliferation
678	24246	AA963703			associated protein 2G4 (Proliferation-associated
679			a		[protein 1) (Protein p38-2G4) [M.musculus]
680		AA963746	r		ESTs
000	02/6	AA963767	b,c,u,v		ESTs
İ					ESTs, Highly similar to S105_MOUSE S100
					calcium-binding protein A5 (S-100D protein)
681		AA963834	l,m	ĺ	[R.norvegicus]
682		AA963838	b		ESTs
683		AA964206	а		ESTs
684	2321	AA964265	11		ESTs
685		AA964362	cc,dd		
686		AA964455	jj,kk		ESTs
			)jjikk		ESTs
687	18830	AA964496			ESTs, Highly similar to ACTB_HUMAN Actin,
688		AA964501	a,z		cytoplasmic 1 (Beta-actin) [R.norvegicus]
- 500	2010	V100400  -	t		ESTs
689	2442	A A O C 4 E O C			ESTs, Weakly similar to C35D10.4.p
690			c		[Caenorhabditis elegans] [C.elegans]
090	2410	AA964589	kk		EST, ESTs
ایم					ESTs, Moderately similar to treacle [Mus musculu
691		AA964595	h,l,s,t		[M.musculus]
692			l,m		ESTs
693		A964617	u,v		ESTs
694		A964755	a,q,y,z,ee,ff		ESTs
695			cc,dd		EST
			,		E01
j					FOT AA I AA A
696	2492	A964866			ESTs, Moderately similar to A49947 interferon
	2702	# 100TOOU	u,v	The second second	gamma receptor beta subunit - mouse [M.musculus
697	17222	A065164		Tissue inhibitor of	
09/	11232 /	A965161	<u>                                     </u>	metalloproteinase 3	Tissue inhibitor of metalloproteinase 3
	0500				ESTs, Moderately similar to RIKEN cDNA
cool	2582 A	A965164	gg		1810017F10 [Mus musculus] [M.musculus]
698					- Inna massarda [wimascarda]
698			i		
					FSTs. Highly similar to T44705 handle it.
698 699 700	15885 A	A965207 A996451			ESTs, Highly similar to T14795 hypothetical protein DKFZp434E171.1 - human (fragment) [H.sapiens]

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ABLE	i ·	GenBank Ac	· 1 · 4 · 1 · 2003.	4	Atty. Ref. 44921-5090-01-WO/2105485
FO ID	GLGC II	No.			a 株計 はどうでは認められていましたが、システィア
LQ ID,	Groc i	J NO.	Model Code	Known Gene Name	
		}			ESTs, Weakly similar to T18768 hypothetical
701	286	1 AA996583	00 ff		protein 80491.7 - Caenorhabditis elegans
702		0 AA996658	ee,ff	<del></del>	[[C.elegans]
		0/2230030	b		EST
703	1020	6 AA996740		1	EST, Moderately similar to A54981 TBD-associated
703	1303	JAA99074U	n,o		lactor 30 - numan [H.saniens]
704	4740		l.		ESTs, Moderately similar to hypothetical protein
705	1749	AA996832	I,m		FLJ11219 [Homo sapiens] [H.sapiens]
	2962	AA996953	u,v		ESTs ESTs
706	16498	AA996955	w,x		ESTs
		ì			EST, Moderately similar to RED_MOUSE Red
-					protein (RER protein) [M.musculus], ESTs, Highly
			Ì		similar to RED_MOUSE Red protein (RER protein
707		AA996993	d		[M.musculus]
708		AA997191	h,l		EST
709	3162	AA997289	gg		ESTs
710	3003	AA997330	e,t,kk		
711	21942	AA997341	e	<u> </u>	ESTs
	-		<del></del>	<del> </del>	ESTs
į		]			ESTs, Weakly similar to S27393 sphingomyelin
712	3165	AA997386	n o	ľ	phosphodiesterase (EC 3.1.4.12), acidic splice
713	14582	AA997412	n,o		form 1 precursor - mouse [M.musculus]
714	3207	AA997466	11.00 #11.		ESTs
715	3242	AA997596	j,k,ee,ff,kk		ESTs
- 110	3242	MA331 330	d		ESTs
716	24440	A A 007055			ESTs, Highly similar to hypothetical protein
716 717	21119	AA997655	b		FLJ14566 [Homo sapiens] [H.sapiens]
	3043	AA997694	jj,kk		ESTs ESTs
718	3250	AA997765	h,l,il	fibrillin-1	fibrillin-1
719	3257	AA997766	ii		ESTs
720	3265	AA997784	u,v		EST
- 1		-			ESTs, Moderately similar to T30249 cell
724	3269	AA997800	C		proliferation entires IV: 67
					proliferation antigen Ki-67 - mouse [M.musculus]
	ł		1	1	ESTs, Weakly similar to A41220 transforming
722	2757	AA997851	bb,ll		growth factor beta receptor type III precursor - rat
723	3290	AA997883	ee,ff		[R.norvegicus]
724	26114	AA997904	aa,bb		ESTs
725	10614	AA997985	cc,dd	<del></del>	
726		AA998006	II		ESTs
<del></del>	3302	1.030000			ESTs
!	İ				ESTs, ESTs, Weakly similar to MOZ_HUMAN
727	3353	A998053	l		Monocytic leukemia zinc finger protein /Zinc finger
121	/ الارزود	-V930033	li		protein 220) [H.sapiens]
720	2544	14000450		brain-specific anglogenesis	brain-specific angiogenesis inhibitor 1-associated
728 729		VA998152	ee,ff	inhibitor 1-associated protein 2	protein 2
129	10033	VA998174	kk		ESTs
720	2000	100045-	]		ESTs, Weakly similar to S37694 gene PC326
730		A998195	u,v		protein - mouse [M.musculus]
731	5789	A998207	b,d		ESTs [M.Mascaids]
732		A998256	y,z		ESTs
733		A998345	w,x		EST
734	3781 A	A998375	b,u,v		ESTs
				adrenergic receptor kinase, beta	LOIS
735 <mark>/</mark>	3505 A	A998430	w,x		
-			,	•	adrenergic receptor kinase, beta 1
i	i	!	ŗ	į	ESTs, Moderately similar to CDNC_MOUSE
	- 1		i	l	CYCLIN-DEPENDENT KINASE INHIBITOR 1C
امتد	2782	A998565	olm		(CYCLIN-DEPENDENT KINASE INHIBITOR P57)
			c,i,m		(P57KIP2) [M.musculus]
	erialiA	naa0000U	1		ESTs

764 15849 A1008074 [r,1] shock protein HSP 90-beta (HSP 84) JR no	othetical	BOY GREEK OF A MAKED BOY	The transfer of the second of	A 100 00 00 00 00 00 00 00 00 00 00 00 00	lGenBank Δcc:	F	
ESTs, Moderately similar to T00051 hyporpotein KIAA0404 - human (fragment)) PL	othetical l.sapiens]		<b>しょしんだちが変異なっしょう かまっちょう</b>		Tombain 100.	0,0000	orodina
ESTs, Moderately similar to T00051 hyporpotein KIAA0404 - human (fragment)) PL	othetical I.sapiens]	Unigene Seguence Cluster Title:	Known Gene Name	Model Code 🔅	No.	GEGCID	SECHO!
25/26   25/2	i.sapiens]	ESTs, Moderately similar to T00051 hypothe					
ESTs, Weakly similar to MAPE_HUMAN antigen preferentially expressed in tumore (Preferentially expressed antigen of method (Preferentially expressed antigen of treatment in the preferential (Preferentially expressed antigen of treatment in translocator of inner mitochondrial membrane antigen preferentially (Preferentially Expressed antigen of treatment in translocator of inner mitochondrial membrane antigen preferentially (Preferentially Expressed antigen of treatment in translocator of inner mitochondrial membrane antigen preferentially (Preferentially Expressed antigen of inner mitochondrial genome assembly protein antigen preferentially (Preferentially Expressed antigen of inner mitochondrial genome assembly protein 1-like 1 apha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin alpha-fodrin		protein KIAA0404 - human (fragment) IH.sar		u,v	AA998979	2526	738
Table							
Table	I Melanom	ESTs, Weakly similar to MAPE_HUMAN Me	}				ł
739	rs	antigen preferentially expressed in tumors					
740   25137   AB005540   Co.,dd   Co.	anoma)	(Preferentially expressed antigen of melanor				10001	
translocator of inner mitochondrial membrane 17 kDa, a	plens]	(OPA-interacting protein 4) (OIP4) [H.saplen					
Translocator of Inner mitochondrial membrane 17 kDa, a   translocator of Inner mitochondrial membrane anchor protein 19 peroxisomal membrane anchor protein 19 peroxisomal membrane anchor protein 19 peroxisomal membrane a	<u></u>			cc,dd	AB005540	25137	740
T41							
T42	orane 17				AD000450	14745	744
T42   21666   AB012214   n.o   methyltransferase 1   methyltransferase (EC 2.1.1.37) - rat (R.n.		kDa, a	kDa, a	hh,jj,kk	AB006450	11/45	741
T42   21666   AB012214   n.o   methyltransferase 1   methyltransferase (EC 2.1.1.37) - rat (R.n.			504 ( )				
17963 AB012231   jj,kk	tosine-5-)-	ESTs, Highly similar to JE0378 DNA (cytosin			A D040044	24666	742
Rattus norvegicus mRNA for G protein-coreceptor, complete cds   Rattus norvegicus mRNA for G protein-coreceptor, complete cds	norvegicus	methyltransferase (EC 2.1.1.37) - rat [R.norv	methyltransferase 1				
15/72   AB015645   Cc,dd   peroxisomal membrane anchor protein   peroxisomal membrane anchor protein   actinin alpha 2 associated LIM   peroxisomal membrane anchor protein   actinin alpha 2 associated LIM   peroxisomal membrane anchor protein   actinin alpha 2 associated LIM   peroxisomal membrane anchor protein   actinin alpha 2 associated LIM   protein   Actinin alpha 2 associated LIM   protein   Protein   Actinin alpha 2 associated LIM   protein   Protein   Actinin alpha 2 associated LIM   Protein   Protein   Actinin alpha 2 associated LIM   Protein   Protein   Protein   P		nuclear factor I/B	nuclear factor I/B	JJ,KK	ADU 1223 1	17803	143
745 22567 AB017544 aa peroxisomal membrane anchor protein actinin alpha 2 associated LIM peroxisomal membrane anchor protein actinin alpha 2 associated LIM peroxisomal membrane anchor protein actinin alpha 2 associated LIM peroxisomal membrane anchor protein actinin alpha 2 associated LIM peroxisomal membrane anchor protein actinin alpha 2 associated LIM protein ARI 19849 AF016387 IJ,kk reflinoid X receptor gamma ( ref	oupled			oo dd	AR015645	15770	744
745   22567   AB017544   aa   protein   actinin alpha 2 associated LIM   actinin alpha 2 associated LIM   actinin alpha 2 associated LIM   actinin alpha 2 associated LIM   actinin alpha 2 associated LIM   protein   protein   protei		receptor, complete cds	porovinemel	cc,aa	ABU 10040	10/12	/ 744
Actinin alpha 2 associated LIM   Potential actinin alpha 2 associated LIM   Potential actinin alpha 2 associated LIM   Potential actinin alpha 2 associated LIM   Potential actinin alpha 2 associated LIM   Potential Actinin   Potential Actinin					AD017544	22567	7/15
746   3799   AF002281   D,U,Vee,Ff,kk,II   protein   actinin alpha 2 associated LIM protein   747   1097   AF016296   e.j.k,cc,dd,kk   retinoid X receptor gamma (		peroxisomal membrane anchor protein		ad	ADU 17 044	2230/	143
T47				Duy oo ff kk li	<b>∆</b> ⊑002284	3700	746
Tellinoid X receptor gamma (		actinin alpha 2 associated LIM protein	protein				
T48	nplete cds	Rattus norvegicus neuropilin mRNA, comple	mathemated V t				
749   23044   AF034218   j,k							
750				72.			
751   2881   AF056034   b,d,u,v   nexilin   nexilin   nexilin   nexilin   nexilin   nexilin   nexilin   nucleosome assembly protein 1- like 1   nucleosome assembly protein   like 1   nucleosome assembly protein 1- like 1   nucleosome assembly p							
Total   Tota							
T52		nexilin		0,0,0,0	AI 000004	2001	701
Total				aa l	AF062594	16006	752
752		flucieosome assembly protein 1-like 1		99	711 00200-1	- 10000	
753   20741   AF084186   S,t   alpha-fodrin   alpha-fodrin   alpha-fodrin   alpha-fodrin   alpha-fodrin   alpha-fodrin   alpha-fodrin   alpha-fodrin   alpha-fodrin   ESTs     754   21957   AF087437   f   core binding factor beta   ESTs     755   18731   AF093139   d   tip associating protein   tip associating protein     756   2947   AF099093   u,v   UBC7   ubiquitin-conjugating enzyme   UBC7     757   25232   AF110508   b   ESTs     758   21757   Al007656   d   ESTs     759   9976   Al007744   e,jj,kk   ESTs     760   4018   Al007770   j,k   ESTs     8   Rattus norvegicus   mitochondrial genome.     9/22Length = 16,3   HGF-regulated tyrosine kinase   HGF-regulated tyrosine kinase substrate     761   10108   Al007857   u,v   substrate   HGF-regulated tyrosine kinase substrate     762   11728   Al007884   t   ESTs     763   11368   Al007948   I,m   ESTs, Highly similar to RIKEN cDNA 150   [Mus musculus] [M.musculus]     764   15849   Al008074   r,li   ESTs, ESTs, Highly similar to HS9B_RAT   shock protein HSP 90-beta (HSP 84) IR not protein HSP 90-beta (HSP		nucleosomo osoombly protein 4 liles 4		hh	AF062594	16007	752
754   21957   AF087437   f   Core binding factor beta   ESTs     755   18731   AF093139   d   tip associating protein   tip associating protein     756   2947   AF099093   u,v   UBC7   Ubiquitin-conjugating enzyme     757   25232   AF110508   b   UBC7   Ubiquitin-conjugating enzyme     758   21757   Al007656   d   ESTs     759   9976   Al007744   e,jj,kk   ESTs     760   4018   Al007770   j,k   ESTs     8		alpha foddin					
755							
756 2947 AF099093 u,v ubiquitin-conjugating enzyme UBC7  757 25232 AF110508 b  758 21757 Al007656 d  759 9976 Al007744 e,jj,kk ESTs  760 4018 Al007770 j,k ESTs  Rattus norvegicus mitochondrial genome.  9/22Length ≈ 16,3  HGF-regulated tyrosine kinase substrate  761 10108 Al007857 u,v Substrate  11368 Al007948 l,m  Fig. 2947 AF099093 u,v Ubiquitin-conjugating enzyme UBC7  ubiquitin-conjugating enzyme UBC7  ESTs  ESTs  HGF-regulated tyrosine kinase substrate  ESTs  ESTs, Highly similar to RIKEN cDNA 150 [Mus musculus] [M.musculus]  ESTs, ESTs, Highly similar to HS9B_RAT shock protein HSP 90-beta (HSP 84) IR not protein HSP 90-beta (HSP							
756   2947   AF099093   U,V   UBC7   Ubiquitin-conjugating enzyme UBC7     757   25232   AF110508   b     ESTs     758   21757   Al007656   d   ESTs     759   9976   Al007744   e,jj,kk   ESTs     760   4018   Al007770   j,k   ESTs     8		up associating protein					
757 25232 AF110508 b  758 21757 Al007656 d  759 9976 Al007744 e,jj,kk ESTs  760 4018 Al007770 j,k ESTs  Rattus norvegicus mitochondrial genome.  4 1804 Al007824 j 9/22i_ength ≈ 16,3  HGF-regulated tyrosine kinase substrate  761 10108 Al007857 u,v substrate  762 11728 Al007884 t ESTs  763 11368 Al007948 l,m ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs, Highly similar to RIKEN cDNA 150 [Mus musculus] [M.musculus]  ESTs, ESTs, Highly similar to HS9B_RAT shock protein HSP 90-beta (HSP 84) IR not have the p		ubiquitin-conjugating on tyme LIBC7			AF099093	2947	756
758   21757   Al007656   d   ESTs     759   9976   Al007744   e,jj,kk   ESTs     760   4018   Al007770   j,k   ESTs     4   1804   Al007824   j   9/22i_ength = 16,3     761   10108   Al007857   u,v   substrate   HGF-regulated tyrosine kinase substrate     762   11728   Al007884   t   ESTs     763   11368   Al007948   I,m   I,m   ESTs, Highly similar to RIKEN cDNA 150     764   15849   Al008074   I,il   ESTs, ESTs, Highly similar to HS9B_RAT     876   STS, ESTS, HIGHLY similar to HS9B_RAT     876   STS, ESTS, HIGHLY similar to HS9B_RAT     876   STS, ESTS, HIGHLY similar to HS9B_RAT     876   STS, ESTS, HIGHLY similar to HS9B_RAT     876   STS, ESTS, HIGHLY similar to HS9B_RAT     876   STS, ESTS, HIGHLY similar to HS9B_RAT     876   STS, ESTS, HIGHLY similar to HS9B_RAT     876   STS, ESTS, HIGHLY similar to HS9B_RAT     876   STS,		abiquian-conjugating enzyme obc/					757
759 9976 Al007744 e,ij,kk ESTs  760 4018 Al007770 j,k ESTs  Rattus norvegicus mitochondrial genome.  9/22Length ≈ 16,3  HGF-regulated tyrosine kinase substrate  761 10108 Al007857 u,v substrate  762 11728 Al007884 t ESTs  763 11368 Al007948 l,m ESTs  Rattus norvegicus mitochondrial genome.  9/22Length ≈ 16,3  HGF-regulated tyrosine kinase substrate  ESTs  ESTs, Highly similar to RIKEN cDNA 150 [Mus musculus] [M.musculus]  ESTs, ESTs, Highly similar to HS9B_RAT shock protein HSP 90-beta (HSP 84) IR not highly shock protei		FSTs		d			758
760 4018 Al007770 j,k ESTs  Rattus norvegicus mitochondriał genome.  9/22i_ength ≈ 16,3  HGF-regulated tyrosine kinase substrate  761 10108 Al007857 u,v substrate  HGF-regulated tyrosine kinase substrate  ESTs  763 11368 Al007948 l,m ESTs, Highly similar to RIKEN cDNA 150 [Mus musculus] [M.musculus]  ESTs, ESTs, Highly similar to HS9B_RAT shock protein HSP 90-beta (HSP 84) IR not protei							759
Rattus norvegicus   mitochondrial genome.   9/22Length = 16,3     T61							760
### description of the image of			Rattus norvegicus				
4 1804 Al007824 j 9/22Length = 16,3  HGF-regulated tyrosine kinase substrate  10108 Al007857 u,v substrate  HGF-regulated tyrosine kinase substrate  HGF-regulated tyrosine kinase substrate  ESTs  ESTs, Highly similar to RIKEN cDNA 150 [Mus musculus] [M.musculus]  ESTs, ESTs, Highly similar to HS9B_RAT shock protein HSP 90-beta (HSP 84) IR not protein H							
Total   10108   Al007857   U,V   HGF-regulated tyrosine kinase   HGF-regulated tyrosine kinase substrate   HGF-regulated tyrosine kinase substrate   HGF-regulated tyrosine kinase substrate   HGF-regulated tyrosine kinase substrate   ESTs					A1007824	1804	4
761   10108   Al007857   U,V   substrate   HGF-regulated tyrosine kinase substrate   ESTs     762   11728   Al007884   t   ESTs     763   11368   Al007948   I,m   [Mus musculus] [M.musculus]     764   15849   Al008074   I,il   Shock protein HSP 90-beta (HSP 84) IR no							
762 11728 Al007884 t ESTs  763 11368 Al007948 I,m ESTs, Highly similar to RIKEN cDNA 150 [Mus musculus] [M.musculus]  ESTs, ESTs, Highly similar to HS9B_RAT shock protein HSP 90-beta (HSP 84) IR not		HGF-regulated tyrosine kinase substrate					
763 11368 Al007948 I,m ESTs, Highly similar to RIKEN cDNA 150 [Mus musculus] [M.musculus]  ESTs, ESTs, Highly similar to HS9B_RAT shock protein HSP 90-beta (HSP 84) IR not		ESTs		t	Al007884	11728	762
763 11368 Al007948   I,m	00000000						
ESTs, ESTs, Highly similar to HS9B_RAT  764 15849 Al008074   r,il   shock protein HSP 90-beta (HSP 84) IR no				l,m	AI007948	11368	763
764 15849 Al008074   r,il   shock protein HSP 90-beta (HSP 84) JR no		4.					- 1
764 15849 A1008074   r,il   shock protein HSP 90-beta (HSP 84) JR no	T Heat	ESTs, ESTs, Highly similar to HS9B_RAT He		ĺ	. 0. 555		
		shock protein HSP 90-beta (HSP 84) [R.norv					
765 4052 A1008095  ]J,KK   ESTs		ESTs		jj,kk	AI008095	4052	765
ESTs, Weakly similar to YJ95_CAEEL		ESTs, Weakly similar to YJ95_CAEEL					
HYPOTHETICAL 52.8 KD PROTEIN T058	E11.5 IN	HYPOTHETICAL 52.8 KD PROTEIN T05E11					
766 2657/Al008275 U,v CHROMOSOME IV [C.elegans]	•	CHROMOSOME IV [C.elegans]					
767 21229 A1008371 r ESTs		ESTs		<u>r</u>	A1008371	21229	767
768 21889 Al008393 U.v ESTs, Highly similar to UBX domain-conta	taining 2	ESTs Highly similar to LIBY domain contain			41000000	04000	700
768  21889 Al008393   u,v   [Mus musculus] [M.musculus]	_			u,v i	A1008393 1	218891/	768

TABLE	1				Atty, Ref. 44921-5090-01-WO/2105485
			cc.		74921-5090-01-WO/2105485
عدقا الأن	IGEGC:	D No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
	1		- 1		ESTs, Weakly similar to DJB1_MOUSE DnaJ
				1	Intribling subtamily B member 1 (Heat shock 40 kg
769	380	8 A1008643			(Protein 1) (rieat shock protein 40) (HSDAN)
770	1130	25 Al008647	p,q,ee,ff		[M.musculus]
- 770	1132	5/A1006047	y,z		ESTs
	İ				ESTs, Weakly similar to TAC1_HUMAN
~~.		_			Transforming soldie selled a lite
771	1239	8 AI008689	s,t		Transforming acidic coiled-coil-containing protein (H.sapiens)
					ECTo Ulable - 1 - 1
					ESTs, Highly similar to ACES_RAT
772	393	1 Al008697	n,o		Acetylcholinesterase precursor (AChE)
773	1603	4 Al008701	u,v		[[R.norvegicus]
774	778	5 AI008758	jj,kk	Dinastidul	ESTs
			JJ,KK	Dipeptidyl peptidase 4	Dipeptidyl peptidase 4
775	1812	5 AI008787			ESTs, Highly similar to \$16788 probable reverse
776	1282	B Al008796	f,g		transcriptase - rat [R.norvegicus]
777			cc,dd		ESTs
- '''	303	2 A1008985	n,o		ESTs
					ESTs, Weakly similar to chimerin (chimaerin) 1
778	3278	A1008988	y,z	HHs:breakpoint cluster region	(Chimaerin) 1
1		1		Family States (Callette	[Rattus norvegicus] [R.norvegicus]
J		1			ESTs, Moderately similar to EAR2_RAT Orphan
İ				1	nuclear receptor EAR-2 (V-erbA related protein EAI
779	16652	Al009019	b	1	2) (Ovalbumin upstream promoter gamma nuclear
			<del></del>	double steer to 1 5014 11 11	receptor rCOUPg) [R.norvegicus]
780	23337	A1009096	l,m	double-stranded RNA-binding	
		711003030	-   5111	protein p74	double-stranded RNA-binding protein p74
- 1		ĺ			protont pr4
781	21622	Al009167		1	ESTs, Highly similar to BAG2_HUMAN BAG-family
701	21032	A1009767	a,y,z,ee,ff		molecular chaperone regulator-2 [H.sapiens]
700	04=0=		1		ESTs, Weakly similar to rhoB gene [Rattus
782	21596	AI009168	j,k		norvegicus] [R.norvegicus]
					ESTs Moderately almitest to the state of the
783	22801	Al009197	е		ESTs, Moderately similar to hypothetical protein
- 1					IMAGE3455200 [Homo sapiens] [H.sapiens]
					ESTs, Highly similar to UNRI_MOUSE UNR-
784	9150	Al009198	h,i		interacting protein (Serine-threonine kinase receptor
785	3755	Al009208	h,i		Jassociated protein) [M.musculus]
			111,1		ESTs
786	7524	AI009350	ا ا		ESTs, Weakly similar to C37H5.3.p
787	3070	AI009368	_d		[Caenorhabditis elegans] [C.elegans]
-:51	0913	71009300	s,t		E318
leer	10000	A 1000 444			ESTs, Highly similar to RS3_MOUSE 40S
788	10820	AI009411	g,h,l		ribosomal protein S3 [R.norvegicus]
					[R.Horvegicus]
789		A1009420	aa,bb	synaptic vesicle alvonrotain 2 h	synaptic vesicle glycoprotein 2 b
790	4154	A1009467	kk	- 10.0 g./ coproteil Z D	EST-
					ESTs
791	9746	1009555	l <sub>r</sub>		Rattus norvegicus dynein light intermediate chain 1
792	10532	1009602	<del> </del>		mrina, complete cds
793		1009614	h,I		ESTs
794		1009654			ESTs
	-,,00/	11000004	]		ESTs
795	16154	1009661	]		ESTs, Moderately similar to AF1Q_MOUSE Protein
796	10104	1000077	a		AF1Q [M.musculus]
	19358 A	1009675	b,c,v		EST
797		1009713	t		ESTs
798	22545 A	1009747	a tr		
799	15089 A	1009752	99		transducer of ERBB2, 1
800:			j,k		EŜTS
		10000	u,v		ESTs
201			u,v		ESTs
<u> </u>	2605 A				
ou∠ <sub>l</sub>	2605 A 26133 A	009843	j,k g		ESTs

TABLE 1		10	<del> </del>		Atty. Ref. 44921-5090-01-WO/2105485
F 1785		GenBank Acc.	[		7y 10.3 10.3 10.3 10.3 10.3 10.3 10.3 10.3
SEQID	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Glüster Title
804	18680	AI010084	l,m		ESTs
805	15988	Al010108	s,t		ESTs
806	4177	Al010123	aa,bb		ESTs
807		AI010237	ii		ESTs
808		Al010241	aa,bb		ESTs
809		AI010256	kk	H3 histone, family 3B	
810		Al010275	li .	no historie, family 3B	H3 histone, family 3B
811		AI010273			ESTs
812		AI010303	g		ESTs
813			l,m		ESTs
013	21020	AI010418	∞,dd		ESTs
			İ		ESTs, Weakly similar to DNA-directed RNA
					polymerase I like [Caenorhabditis elegans]
814	19778	Al010455	W,X		[C.elegans]
815		Al010568	jj,kk	Growth hormone receptor	Growth hormone receptor
816	6936	AI010593	t		ESTs
					ESTs, Moderately similar to S63665 titin protein -
817	18691	AI010605	ь		human (fragment) [H.sapiens]
818		Al010612	n,o,hh		ESTs
819		AI010616	е		ESTs
820		AI010618	ee,ff		ESTS
821		Al010642	jj,kk,ll		
822		A1010660	C		ESTs
022	11221	A10 10000	<u> </u>		ESTs
823	17761	A1040660			ESTs, Highly similar to S37488 gene T10 protein -
		A1010662	c,r		mouse [M.musculus]
824		A1010848	f,g		ESTs
825		AI010865	e,n,o		ESTs
826		AI010917	а		ESTs
827	18438	Al010930	e,r	ribosomal protein L14	ribosomal protein L14
828 829		AI010936	jj,kk		ESTs, Moderately similar to PTN3_HUMAN Protein tyrosine phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1) [H.sapiens] ESTs, Moderately similar to MTM1_MOUSE
		AI011020	11		Myotubularin [M.musculus]
830	5983	Al011070	aa,bb,gg		ESTs
				Rattus norvegicus	
				mitochondrial genome.	ESTs, Moderately similar to 0806162L protein
5	22030	Al011177	h,l	9/22Length = 16,3	URF5 [Mus musculus] [M.musculus]
					ESTs, Highly similar to CU59_HUMAN Protein
831	13787	Al011462	cc,dd		C21orf59 [H.sapiens]
					ESTs, Moderately similar to T00637 hypothetical
					protein H_GS541B18.1 - human (fragment)
832	24022	AI011474	a,ee,ff,ll		[H.sapiens]
			.,,	SWI/SNF related, matrix	[[risapiens]
				associated, actin dependent	SWI/SNF related, matrix associated, actin
				regulator of chromatin,	
833	15917	Al011498	Ь	subfamily d, member 2	dependent regulator of chromatin, subfamily d,
	.0017	711011730	<u> </u>	Sublamily u, member 2	member 2
834	7060	AI044547			ESTs, Highly similar to T47183 hypothetical protein
004	7000	Al011547	b		DKFZp434K1822.1 - human (fragment) [H.sapiens]
	6044	41044855			ESTs, Moderately similar to LMA5_MOUSE
835		Al011598	t,kk		Laminin alpha-5 chain precursor [M.musculus]
836		AI011644	е		ESTs
837		AI011749	cc,dd		ESTs
838		AI011770	y,z		iESTs
839		Al011943	С	Hemoglobin, beta	Hemoglobin, beta
840		Al011949	cc,dd	<u> </u>	ESTs
				Ras homolog gene family,	
841	2531	Al011991	n,o	member G	Pas hamalag gang family mamb 0
					Ras homolog gene family, member G

TABLE				Atty. Ref, 44921-5090-01-WO/2105485		
SEQ ID	GLGC	D No.	Model Code	Known Gene Name		
)	0.000	S INO.	Iviodel Code	Known Gene Name	Unigene Sequence Cluster, Title	
					ESTs, Highly similar to LSP1_MOUSE Lymphocy	
842		8 AI012109	w,x		kDa phosphoprotein) (Lymphocyte-specific antige WP34) (S37 protein) [M.musculus]	
843	234	1 Al012144	d		ESTs	
844	1309	3 Al012177	h,l		ESTs, Highly similar to S14538 transition protein -	
845	1466	8 Al012185	bb		mouse [M.musculus]	
846	1175	2 Al012208	jj,kk		ESTs ESTs	
					ESTs, Weakly similar to intracellular chloride ion	
847	2170	6 Al012221			Channel protein p64H1 (Rattus nonvenious)	
848	393	2 Al012271	a,n,o,x,z,kk		[[R.norvegicus]	
849	660	6 Al012308	a,n,o,x,hh,kk		ESTs	
850	1140	8 AI012353	U,V		ESTs	
851	2420	0 AI012356	j,k,gg	<del>                                     </del>	ESTs ESTs	
852	747	1 Al012379	p,q		ESTS	
050	0000	41040000			ESTs, Weakly similar to hypothetical protein 2443.	
853	23388	Al012380	b		[Homo sapiens] [H.sapiens]	
854	7120	AI012393	1		ESTs, Weakly similar to JE0343 terf protein - rat	
855	2456	AI012393	li v		[[R.norvegicus]	
856	22651	AI012434	e		ESTs	
			<del></del>		ESTs	
					ESTs, Weakly similar to UBP2_MOUSE Ubiquitin	
- 1					carboxyl-terminal hydrolase 2 (Ubiquitin	
0					thiolesterase 2) (Ubiquitin-specific processing protease 2) (Deubiquitinating enzyme 2) (41 kDa	
857	5595	Al012467	u,v	<u> </u>	ubiquitin-specific protease) [M.musculus]	
858	3304	Al012471	131 1.3.		ESTs, Weakly similar to Y48B6A.6.p	
- 000	0004	A1012471	jj,kk		[Caenorhabditis elegans] [C.elegans]	
859	14431	Al012516	h,i	1	ESTS, Weakly similar to T47155 hypothetical	
			<del></del> -	unconventional myosin Myr2 I	protein DKFZp564B0982.1 - human [H.sapiens]	
860	17489	Al012566	d	heavy chain		
204	0000=				unconventional myosin Myr2 I heavy chain ESTs, Weakly similar to T00357 hypothetical	
861	23025	AI012621	j,k		[protein KIAA0685 - human [H sanions]	
l	1				ESTS, Weakly similar to RBMA RAT RNA-binding	
862	6489	AI012636			protein to (RNA binding motif protein 10) (S1-1	
			- <del> "</del>		(protein) [R.norvegicus]	
863		AI012641	l,m		ESTs, Highly similar to I48722 zinc finger protein -	
864		AI012761	cc,dd		mouse (fragment) [M.musculus]	
865		AI012832	ii,II	stannin	stannin	
866 867		AI012958	w,x		ESTs	
<del>- 007</del>	1193/	AI013033	gg		ESTs	
000	3191	AI013075	l,m		ESTs, Moderately similar to hypothetical protein	
8681	7220 /	1013098	t		FLJ14621 [Homo sapiens] [H.sapiens]	
868 869	<del></del>		<del>                                     </del>		ESTs	
869	i i		υ,ν		ESTs, Weakly similar to 163168 gene Ube1x protein - rat (fragment) [R.norvegicus]	
	16686	1013160	1-1.		r-var (rrayment) iK.norvenichsl	
869	16686	1013160			ESTs. Highly similar to EE4C MOUSE 5	
869					ESTs, Highly similar to EF1G MOUSE Florgation	
869		N013160 N013161	aa,bb		ESTs, Highly similar to EF1G_MOUSE Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) [M.musculus]	
869 870 871	16984 A	N013161	aa,bb	Platelet-derived growth factor A	ESTs, Highly similar to EF1G_MOUSE Etongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) [M.musculus]	
869 870 871 872	16984 A		aa,bb	Platelet-derived growth factor A chain amin A	ESTs, Highly similar to EF1G_MOUSE Elongation factor 1-gamma (EF-1-gamma) (EF-1B gamma)	

TABLE		: GenBank Ac	- · · · · · · · · · · · · · · · · · · ·		Atty. Ref. 44921-5090-01-WO/2105485
SEO IO	GLGC I	DINIS		TERM SHIP TO STORY	Unigene Sequence Cluster Title
ع الساعة	GLGC	טומס.	Model Code	Known Gene Name	Unidene Sequence Cluster Title
				heparan sulfate (ducosamine)	3-heparan sulfate (glucosamine) 3-O-sulfotransferas
875	675	8 AI013394	d,jj,kk	O-sulfotransferase 1	3-O-sulfotransferas
876	2614	8 AI013396	cc,dd	o sunotatisterase i	1
877		7 Al013397	ii		
	1040	1 1010331	- 11		ESTs
			ı		ESTs, Highly similar to chromosome 20 open
		1			reading frame 30; HSPC274 protein [Homo saplen
878	2344	4 Ai013448	d		[H.sapiens]
					[[ri.sapiens]
879	2249	3 Al013466	cc,dd	1	ESTs, Moderately similar to KIAA1049 protein
			Cojad		[[Homo sapiens] [H.sapiens]
880	1223	3 A1013474			ESTs, Highly similar to HPS1_HUMAN Protein
881		6 Al013477	y,z,ee,ff		[PHPS1-2 [H.sapiens]
- 001	190	0 AIU 13477	99		Rat VL30 element mRNA
000		1			ESTs, Weakly similar to R10D12.12.p
882		Al013495	u,v,cc,dd		[Caenorhabditis elegans] [C.elegans]
883	726	AI013499	u,v		[Odenomabditis elegans] [C.elegans]
884	955	AI013558	t		EST
			<del> </del>		ESTs
ŀ			1		ESTs, Weakly similar to FIBB_RAT Fibrinogen bet
885	ADE	A1040500	ļ.,,,		chain precursor [Contains: Fibrinopeptide B]
000	420	AI013566	jj,kk		[R.norvegicus]
					ESTs, Weakly similar to T46337 hypothetical
			1		nrotein DKE70434034434
886	3445	Al013724	е		protein DKFZp434O2413.1 - human (fragment)
			<del>-</del>		[H.sapiens]
887	22592	Al013740	DOWY		ESTs, Moderately similar to S32567 A4 protein -
888	1658/	AI013765	n,o,w,x		[numan [H.sapiens]
- 000	10004	AIU 13/05	W,X	Arrestin, beta 2	Arrestin, beta 2
200	040=0		1	3-hydroxyisobutyrate	
889		Al013861	a,h,1	dehydrogenase	3-hydroxyisobutyrate dehydrogenase
890	12802	Ai013865	d		ESTs ESTs
					ESIS
891	2708	AI013882			ESTs, Highly similar to S53612 gene MSSP-2
		7,50 10002	r,y,z		(protein - numan IH.sapiens)
892	7200	A1040044	f. 1		ESTs, Weakly similar to cold inducible RNA-
		Al013911	t		binding protein [Rattus norvegicus] [R.norvegicus]
893		Al013913	ii		ESTs [Fisher to regions] [Runor vegicus]
894	15786	Al013924	b,i,m		ESTs
895	15904	Al013971	l,m	neurofascin	
				10010103011	neurofascin
					ESTs, Weakly similar to PMX1_MOUSE Paired
- 1	į				mesoderm homeobox protein 1 (PRX-1) (Paired
	- 1		1		related homeobox protein 1) (Homeobox protein
000	اء م	1104455-	1		MhoX) (Homeobox protein K-2) (Rhox)
896	/212	A1014065	99		[R.norvegicus]
1	i				FSTs Weakly similar to DDCD CAREE TO
1	I	i	1		ESTs, Weakly similar to DPSD_CAEEL Putative
897	15494	A1014094	s,t	i	phosphatidylserine decarboxylase proenzyme
				Pottus nonceit	[C.elegans]
	l			Rattus norvegicus	
6	10270	NIO4440F	,  n	nitochondrial genome.	
	193/2	AI014135	h 9	/22Length = 16,3	beta-carotene 15, 15'-dioxygenase
	- 1	ĺ	l I	Rattus norvegicus	
1	į		Ìn	nitochondrial genome.	
6	1808	N014135	е,и,у 9		hote coreions 45, 451, 11
				pregulated by 1,25-	beta-carotene 15, 15'-dioxygenase
898	15247	N014169	aa bb		
	//		aa,bb d	ihydroxyvitamin D-3	upregulated by 1,25-dihydroxyvitamin D-3
		1			ESTs, Weakly similar to mitogen activated protein
					kinase kinase kinase 5; MEK kinase 5 [Mus
aas!		1028831	j,k,kk	l'.	musculus] [M.musculus]
899	16631	1028856	,k,y,z		CCT-
900	1000117				ESTs
900		.102887∩ II	hlmuv i		
	12805	1028870	b,l,m,u,v		ESTs
900		1028870	b,l,m,u,v		
900	12805 A	.1028870   1 .1028954   i			ESTs ESTs, Weakly similar to PT0194 protein-tyrosine kinase (EC 2.7.1.112) tyro-12 - rat (fragment)

	12, 11	ICon Pank Ago	·	in the state of th	Atty. Ref. 44921-5090-01-WO/2105485
SEO ID:	GI GC IF	No.			[3] The Proof of the South New York Control of the South State (Section 1997).
יבון גם בי	GLGC IL	NO.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
				Adaptor protein complex AP-1,	
903	17957	Al028975	s,t	beta 1 subunit	Adaptor protein complex AP-1, beta 1 subunit
					ESTs, Weakly similar to sequence-specific single
					stranded-DNA-binding protein [Rattus norvegicus
904		AI028998	u,v		[R.norvegicus]
905		AI029015	ee,ff		ESTs
906	7362	AI029026	kk		ESTS
907	12387	Al029051	e		ESTs
908	9317	Al029174	a,jj,kk		ESTs
909	12662	Al029179	d,ee,ff,jj,kk,ll		ESTs
910	7447	AI029432	u,v		ESTs
911		Al029437	jj,kk		ESTs
			77,144		
					ESTs, Moderately similar to SYEP_HUMAN
		ļ			Bifunctional aminoacyl-tRNA synthetase [Include:
					Glutamyl-tRNA synthetase (Glutamate—tRNA
912	7451	Al029450		l	ligase); Prolyl-tRNA synthetase (ProlinetRNA
913	7/03	Al029608	y,z		ligase)] [H.sapiens]
- 313	7430	A1023000	y,z		ESTs
					ESTs, Weakly similar to S46814 ribosomal protein
914	40005	A100000=			YmS2, mitochondrial - yeast (Saccharomyces
914	16665	Al029827	d		cerevisiae) [S.cerevisiae]
اء	40000				ESTs, Highly similar to CAV1_MOUSE Caveolin-
915			jj,kk		[M.musculus]
916			e		ESTs
917		AI030067	gg		ESTs
918		Al030163	t		ESTs
919		Al030213	cc,dd		ESTs
920		AI030276	u,v		ESTs
921		Al030301	<b>g</b> g		ESTs
922	665	AI030430	Г		ESTs
923		Al030494	ee,ff		ESTs
324	7838	Al030527	u,v		ESTs
925	7715		l,m,ii		ESTs
				nucleosome assembly protein 1-	
926	7665	AI030668	a	like 1	
927			p,q		nucleosome assembly protein 1-like 1 ESTs
928	19257	AI030775	m		Rat (diabetic BB) MHC class II alpha chain RT1.D
929			aa,bb		alpha (u)
930	7760		kk		ESTs
931			J,V		ESTs
			-,-		ESTs FOR White the state of the
932	22614	A1031004	,		ESTs, Weakly similar to B39066 proline-rich prote
			·	translation initiation 5	15 - rat [R.norvegicus]
933	23050	Al031019		translation initiation factor eIF-	
934			s,t	2B alpha-subunit	translation Initiation factor elF-2B alpha-subunit
707	, 042	1001002	aa,bb		ESTs
1				İ	ESTs, Highly similar to GDP-mannose
1			1		pyrophosphorylase B, isoform 2; mannose-1-
035	7044	1004050	. 1		phosphate guanylyltransferase [Homo sapiens]
935	7040	A1031058	1,1		[H.sapiens]
936	/846/	AI031059			ESTs
937	7852	AI043636 a	a,bb,gg		ESTs
أددد			7	phosphoribosyl pyrophosphate	
938	7867	Ai043695 t			phosphoribosyl pyrophosphate amidotransferase
1	1				ESTs, Weakly similar to T17271 hypothetical
939		\1043714 ji		· ·	protein DKFZp434B0335.1 - human [H.sapiens]
040	7584	\!043724 g	g		ESTs
	-				
ار <del>بر</del> ت مورات	6515	\1043798 f, \1043805 ii	g	I	ESTs

TABLE 1		GenRank-A	VCC.   1945 5		Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	GenBank A	Model Code	Known Gene Name	Unigene Sequence Cluster Title
943 944		3 AI043849	ee,ff		ESTs, Weakly similar to ELL_MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) [M.musculus]
945		9 A1043904	u,v		ESTs
945	6/6	6 Al043914	h,l		ESTs
946 947	796°	Al044042 Al044087	l,m		ESTs, Weakly similar to TC17_RAT Zinc finger protein 354A (Transcription factor 17) (Renal transcription factor Kid-1) (Kidney, ischemia, and developmentally regulated protein-1) [R.norvegicus 1557]
948	5371	AI044089	U,V		EST Francisco
949		Al044101	cc,dd		EST
950	5378	Al044101	99		ESTs
951		AI044112	l,m		ESTs
952		AI044124 AI044211	_ lii		ESTs
953		Al044211 Al044253	cc,dd		ESTs
954		AI044253 AI044258	d		EST
955	5/22	AI044258 AI044271	ii .		ESTs
956		AI044271 AI044299	u,v		ESTs
957		AI044299 AI044330	y,z,ee,ff		ESTs
958	5/61	Al044338	cc,dd		ESTs
959	5486	Al044397	a,y,z,kk		ESTs
960	5513	Al044521	gg ii		ESTs
961		Al044539			EST
962		Al044553	C		ESTs
963	5553	AI044632	l,m		ESTs
964		AI044740	l,m u,v		ESTs
965		AI044747	g,kk		ESTs
966		Al044794	j,k		ESTs
967	5322	AI044801	C		ESTs
			<del>- </del>		ESTs
968 969		A1044845 A1044855	cc,dd,gg		ESTs, Weakly similar to T12482 hypothetical protein DKFZp564P0662.1 - human (fragments) [H.sapiens]
970		AI044861	aa,bb		ESTs
971		AI044887	e		ESTs
	0.007	11044007	u,v	fatty acid Coenzyme A ligase,	ESTs
972		1044900	a,h,i,ee,ff,kk	long chair 2	foths asid O
973	5675	1045026	j,k,p,q,ee,ff,kk		fatty acid Coenzyme A ligase, long chain 2 ESTs
974	24290 A	1045040	cc,dd		ESTs, Weakly similar to T15251 hypothetical protein K07B1.4 - Caenorhabditis elegans [C.elegans]
975	5689	1045075	ام		ESTs, Weakly similar to Exonuclease
976		1045075	b,u,v		[Caenorhabditis elegans] [C.elegans]
977		1045378	ee,ff,gg		ESTs
978		1045441	II		ESTs
		1045475	d,jj,kk		ESTs
	10004 A	1045509	gg,ii		ESTs ESTs
981	6808 A	045600	w,x		ESTs, Highly similar to S30034 translocating chain-
982	10020 A	045632	k,y,z	er a	associating membrane protein - human (H sanieng)
					ESIS
983	2662 A	045686	е		ESTs, Weakly similar to CBP_MOUSE CREB- binding protein [M.musculus]
984	10028141	045707	n,o		Journal Droteitt (M.Waschinz)

ABLE 1		GenBank Acc		Tale of the Contract of the Co	Atty. Ref: 44921-5090-01-WO/2105485
EQ ID	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
				Solute carrier family 4, member	onigoige coducince cluster fille.
		I		1, anion exchange protein 1	Solute carrier family 4, member 1, anion exchange
985		AI045744	b,u,v	(kidney band 3)	protein 1 (kidney band 3)
986	5890	AI045836	u,v	, , , , , , , , , , , , , , , , , , , ,	ESTs
987	2360	AI045911	cc,dd		ESTs
988	5913	AI045929	b		ESTs
989	10053	A1045948	n,o		ESTs
990	3319	AI045989	b,l,m		ESTs
991	8012	AI058330	ee,ff,kk	decay-accelarating factor	
			- Company	doody according factor	decay-accelarating factor
992	6828	Al058359	s,t		ESTs, Weakly similar to T46465 hypothetical
993		Al058419	u,v,aa,bb		protein DKFZp434A0530.1 - human [H.sapiens]
994		AI058451	U,V		ESTs
995		Al058453	l,m		ESTs
	0027	711000-100	19114		ESTs
İ					EST, Weakly similar to RRM2_HUMAN Putative
996	10070	A1058505			Inbosomal RNA methyltransferase 2 (rRNA (uridir
- 550	10070	A1000000	u,v		12'-U-)-Methyltransferase) (H sanione)
- 1					ESTS, Highly similar to Nedd4 WW binding# pro-
997	10070	AIOE0E07			4; Nedd4 WW-binding protein 4 [Mus musculus]
998	00/2	AI058507	а		[M.musculus]
	0012	AI058527	٧		ESTs
999		AI058653	u,v		
1000		AI058665	d		ESTs
1001		Al058772	n,o		EST
1002	8158	AI058824	u,v		ESTs
					ESTs, Highly similar to SUI1_MOUSE Protein
1003		AI058869	[l,m		translation factor SUI1 homolog [M.musculus]
1004		AI058890	Γ		ESTs
1005		AI058942	u,v		ESTs
1006		AI059175	е	pericentriolar material 1	pericentriolar material 1
1007	10171	AI059209	u,v		EST Taken a Tracentar I
1006		A1059246	cc,dd		EST
1009	8285	AI059298	cc,dd		ESTs
1010	8290	Al059312	ee,ff		ESTs
1011	8291	AI059313	b		EST
1012	8303	AI059352	s,t		ESTs
1013			p,q		
			PIY		ESTs
Į.	ļ				ESTs, Weakly similar to NCP1_RAT Nck-
ı	j				associated protein 1 (NAP 1) (p125Nap1)
1014	8729	A1059485	w,x		(Membrane-associated protein HEM-2)
		11000 100	W,A		[R.norvegicus]
1015	8347	AI059519			ESTs, Weakly similar to EGRT epidermal growth
	30 71 /		n,o		factor precursor - rat [R.norvegicust
İ					ESTs, Weakly similar to pseudouridylate synthasi
1016	8356	N059543	_		orf, hypothetical protein [Escherichia coli K12]
1017			b		[E.coli]
1018		1059664	l,m		ESTs
1019			1		ESTs
וטו	0423	1059728	cc,dd		EST
1000	400	1050005			EST, Weakly similar to T42092 s-afadin - rat
1020		10.0000	u,v		[R.norvegicus]
1021	6494 A	1059968	a		ESTs
1000					ESTs, Weakly similar to 2205324A lymphotoxin
1022		1059971	a,t	li	peta receptor [Mus musculus] [M.musculus]
1023		1060137	c,dd		EST Teseptor (tildes museurus) (wi.muscurus)
1024	8557 A	J060221 t	1,0		ESTs
بند	6745 A	1069939 t			ESTs
1025		1070068	IH.	Hs:growth arrest and DNA-	STs, Weakly similar to 2104282A Gadd45 gene

ABLE 1	,	GenBank Aco	1 2 19 19 19 19 19 19	1200 January St.	Atty. Ref. 44921-5090-01-WO/2105485
מו ס	GLGC ID	GenBank Acc: No.	Model Code	Known Gene Name	A Company of the Comp
			Model Code	Known Gene Name	Unigene Sequence Cluster Title
1027	2/42	Al070173	а		ESTs
4000	400-				ESTs, Highly similar to JC7218 glia maturation
1028	4967	Al070179	w,x		factor-gamma - rat [R.norvegicus]
					ESTs, Highly similar to T42648 hypothetical prot
1029		Al070195	w,x	ł	DKFZp434C1415.1 - human [H.sapiens]
1030		Al070214	l,m		ESTs [H.sapiens]
1031	8854	A1070285	aa,bb		ESTs
1032		Al070392	b,u,v		ESTs
1033	23277	Al070508	ii		
1034	8938	Al070590	a,ee,ff,kk		ESTs
1035		AI070660	gg		ESTs
1036		Al070697	b,u,v		EST
1037		Al070710			EST
1038	21105	Al070716	d	-	ESTs
1039			h,l		ESTs
		A1070775	a		ESTs
1040		Al071049	d		ESTs
1041		Al071131	u,v		ESTs
1042		Al071166	r		ESTs
1043		A1071174	d		ESTs
1044	9583	Al071185	y,z,kk		ESTs
1045	11017	A1071222	c,r		ESTs
			-		
1046	9604	AI071230	ee,ff,gg		ESTs, Weakly similar to I48842 testin - mouse
1047			ii		[M.musculus]
1048			d		ESTs
1049			r	•	ESTs
10.01	0000/	107 1000	1		ESTs
1050	22020	AI071578	(7)		ESTs, Moderately similar to S29993 P311 protein
1000	22323/	10/15/6	ee,ff,kk		mouse [M.musculus]
1050	20020				ESTs, Moderately similar to S29993 P311 protein
1050			g,jj,kk		mouse [M.musculus]
1051			gg		ESTs
1052	11086	1071698	hh		ESTs
1053	11088	1071703	p,q		ESTs
1054		1071935	b,u,v		ESTs, Highly similar to RIKEN cDNA 1110003N2
1055	9788		b		[Mus musculus] [M.musculus]
	1				ESTs, Moderately similar to T17342 hypothetical
-		ļ	1		protein DKFZp586K1924.1 - human (fragment)
1056	8665	1071965	ee,ff		[H.sapiens], R.norvegicus hsp70.2 mRNA for heat
1057			90,11		ISHOCK Protein 70
1058					ESTs
1059		10-00-	aa,bb		ESTs
1003	3000 A	10/2000	1,0		ESTs
1060	10400	1070000			ESTs, Moderately similar to S11276 alpha-adaptin
1060	18198 A		1,0		- rat [R.norvegicus]
1061	A GRLE	1072088 E	)		ESTs
		1			
		1	1		ESTs, Highly similar to DYNC_HUMAN Dynactin
_			ĺ	•	complex 50 kDa subunit (50 kDa dynein-associate
1062		1072092	,m		polyportido) (Dynamilia) (DOT), so si
1063	10837 A	1072144 V	z,ee,ff		polypeptide) (Dynamitin) (DCTN-50) [H.sapiens]
064		070400	),q		ESTs
065			1,0	· · · · · · · · · · · · · · · · · · ·	ESTs
066			ia,bb		EST
067	10900 A	072594 ii			ESTs
068	6548 41				EST
069	10918 A		,t,kk,ll		ESTs
070	9380 AI				EST
U1 U	330UA	072738 d		-	ESTs
071	10919 AI	0707/4 Ti	,l,w,x		12013

	1 3363 1 3 3 3	: : :IGenBank A	00 1 4		Atty: Ref. 44921-5090-01-WO/2105485
SEQ ID		GenBank A	oc.		Unigene Sequence Cluster Title
			Model Code	Known Gene Name	Unigene Sequence Cluster Title
1072	940	08 Al072835	cc,dd		ESTs
	1				FSTs Moderatoly similar to 200000 in the
1073	940	9 Al072841	Ь	1	ESTs, Moderately similar to S69000 laminin gamm 2 chain - mouse [M.musculus]
1074		30 Al072900	С		EST [W.musculus]
1075		4 Al072992	11		ESTs
1076	961	1 Al073040	а		ESTs
	ļ			ĺ	ESTs, Highly similar to BANP homolog; putative
1077	948	5 Al073109	lu		Italiscription factor: Btg3 associated nulcoar protoic
1078	946	6 Al073135	cc,dd	<del> </del>	[[wids musculus] [M.Musculus]
1079	1097	0 Al073207	n,o		ESTs
1080		1 Al073212	g,j,k		ESTs
1081	1937	1 Al100841	cc'qq		ESTs
	1007	1/1/100041	CC,QQ		ESTs
1082	1510	2 Al101099			ESTs, Highly similar to SMRT2 metallothionein II -
1083	700	2 A1101099	j,k		rat [R.norvegicus]
1003	/00	8 Al101229	jj,kk		ESTs
1004	<b>540</b>	4 440.000		HMm:Rho, GDP dissociation	ESTs, Highly similar to I49687 GDP-dissociation
1084	542	1 Al101270	aa,bb	inhibitor (GDI) beta	inhibitor - mouse [M.musculus]
1085	402	7 Al101330	е		ESTs
1086	11634	4 AI101338	n,o		ESTs
1087		Al101362	hh		ESTs
1088		Al101494	cc,dd		ESTs
1089	6640	AI101500	е		ESTs
1090	22788	Al101659	lgg		ESTs, Weakly similar to dual-specificity
			33	Potassium (K+) channel protein	phosphatase [Mus musculus] [M.musculus]
1091	13267	AI101847	h,i	alpha 5	
1092	4432	AI101851	+	аірпа э	Potassium (K+) channel protein alpha 5
1093	2042	Al101921	s,t		ESIS
1094		Al101924			ESTs
1095		Al102007	r,jj,kk		ESTs
1096	3085	Al102046	h,l		ESTs
1097		Al102046	С		ESTs
1098			r		ESTs
1030	10227	Al102248	kk		ESTs
1000	40500	41400400			ESTs, Weakly similar to S37583 RING finger
1099	16596	Al102486	ee,ff,kk		protein rfp - mouse (fragment) [M.musculus]
				cytochrome c oxidase, subunit	Protest tip mouse (magment) [wi.musculus]
1100	11953	Al102505	hh	VIIIa	cytochrome c oxidase, subunit VIIIa
				cytochrome c oxidase, subunit	Sylvestrictic c oxidase, subunit VIIIa
1100	11954	Al102505	hh	VIIIa	Cytochromo o cyldest
T					cytochrome c oxidase, subunit VIIIa
			]		ESTs, Highly similar to TYRO protein tyrosine
1101	2125	Al102519	n,o,w,x		kinase binding protein; killer cell activating receptor
			1.,1-1.,11		associated protein (Mus musculus) (M musculus)
	1				ESTS, Weakly similar to GABA(A) recentor-
1102	5969	Al102520	b,l,m,bb,kk		associated protein like 2; ganglioside expression
<del></del>			אַלמחיוויוים		factor 2 [Rattus norvegicus] [R norvegicus]
İ	ļ				ESTs, Highly similar to CBX2 MOUSE Chromohox
1103	4102	Al102524			protein homolog 2 (Modifier 3 protein) (M33)
1104			99		[M.musculus]
1104	11003	Al102560	b,e,l,m		ESTs
			j T		
440-	00:00			ļ	ESTs, Highly similar to I49523 tumor necrosis factor
1105		AI102578	e	1	alpha-induced protein 2 - mouse [M.musculus]
1106	19011	Al102618	p,q		ESTs ESTs
4 4 A 7 I	19379	1102711	w,x		ESTs, Highly similar to RIKEN cDNA 0610010:12 [Mus musculus] [M.musculus]
1107					DVIUS ITUSCUIUSI IM MIISCUIUSI
					ECT- Madagadali III
1108	22171	1102734	w,x		ESTs, Moderately similar to JC4965 elk1 protein - mouse [M.musculus]

TABLE	<del> </del>	GenBank Ac			Atty. Ref. 44921-5090-01-WO/2105485
SEO IO	اماددا	_ 1	T 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	的复数 建二级电子	图 的复数操作 医抗肠囊病 化二氯甲基
		<u> </u>	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1110	1172	24 Al102812	c		ESTs
1111		16 Al102819	е		ESTs
1112	1172	23 Al102896	aa,bb		ESTs
1113	2422	9 Al102972	r		
1114		9 Al103059	j,k		ESTs
1115		24 Al103071		<del></del>	ESTs
	012	-7/1103071	s,t,ii		ESTs
1116	224	0 4400004			ESTs, Moderately similar to selective hybridizing
		6 Al103084	hh		clone [Mus musculus] [M.musculus]
1117		4 AI103106	Γ		ESTs
1118	1764	2 Al103357	cc,dd		ESTs
					ESTs, Highly similar to phosphatidylinositol 3-
1119	1172	1 Al103391	ee,ff		kinase, regulatory subunit, polypeptide [Rattus
		-	100,11	Detter	norvegicus] [R.norvegicus]
		1		Rattus norvegicus	
7	1400	0 41400000		mitochondrial genome.	
	1490	0 AI103396	l,m	9/22Length = 16,3	Rattus norvegicus CDK110 mRNA
		1		Rattus norvegicus	The state of the s
ı				mitochondrial genome.	
7	1498	1 AI103396	е	9/22Length = 16,3	Pottus populations ODICAGO
J			1	polypyrimidine tract binding	Rattus norvegicus CDK110 mRNA
1120	390	Al103403	a	protein	
				protein	polypyrimidine tract binding protein
1121	159/	AI103465			ESTs, Moderately similar to RP29 HUMAN
- 1127	1004	A1103405	Ţ.		Ribonuclease P protein subunit p29 [H.sapiens]
4400	4074				ESTs, Highly similar to toll-associated serine
1122	4873	Al103531	II,m,ee,ff		protease [Mus musculus] [M.musculus]
					FSTs Moderately similar to TO (2014)
				1	ESTs, Moderately similar to T24634 hypothetical
1123	7528	Al103548	r	j	protein T07C4.10b - Caenorhabditis elegans
1124	21579	Al103572	p,q		[C.elegans]
1125		Al103738	h,l		ESTs
	10072	71100730	[11,1		ESTs
1126	47700	11100051			ESTs, Highly similar to S37488 gene T10 protein
1120	1//02	Al103854	С		mouse [M.musculus]
- 1					ESTs, Weakly similar to FKB1_RAT FK506-
1					BINDING PROTEIN (FKBP-12) (PEPTIDYL-
j			ì		PROLY CIC TRANS 1991-12) (PEPTIDYL-
1			ł		PROLYL CIS-TRANS ISOMERASE) (PPIASE)
1127	4402	Al103874			(ROTAMASE) (IMMUNOPHILIN FKBP12)
1128		Al103962	1		[R.norvegicus]
1120	11310	A1103902	dd		ESTs
4400	40400			unknown Glu-Pro dipeptide	
1129	10136	Al103983	p,q	repeat protein	unknown Glu-Pro dipeptide repeat protein
1130	26213	Al104113	f,g		dia in dipeptide repeat protein
- 1					Pottuo nomentaria IIII
1131	21927	Al104117	w,x		Rattus norvegicus LIM-domain protein LMP-1
1132		Al104239	99		mRNA, complete cds
1133		Al104278			ESTs
1134			n,o		ESTs
			y,z		ESTs
1135			d		ESTs
1136	2856	Al104349	d		ESTs
	T				
1137	18831	AI104357	bb	ļ	ESTs, Highly similar to ACTB_HUMAN Actin,
				Cytochrome a syldage '	cytoplasmic 1 (Beta-actin) [R.norvegicus]
1138	23574	AI104520	hh	Cytochrome c oxidase subunit	
			int	Vla (liver)	Cytochrome c oxidase subunit VIa (liver)
- 1	ĺ				ESTs, Weakly similar to NADH dehydrogenase
4420	40500			l <sub>i</sub>	(ubiquinone) 1 beta subcomplex, 6 (17kD, B17)
1139			nh i	_ []	[Homo sapiens] [H.sapiens]
1140	4782	AI104570			ESTs
1141	11680	Al104605	j,kk		
1142			,k,l,m		ESTs
1143			(k		ESTs
			NT I	1.	STs

TABLE		GenBank A	00:1: 4: 296		Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	6-21-0 N	Model Code	Known Gene Name	THE REPORT OF THE PARTY OF THE
1144		05 Al104907			Unigene Seguence Cluster Title
1145	92	73 Al104907	9	TEMO	IEMO
1140	- 02	73/A1104908	ii		ESTs
	1				ESTs, Moderately similar to EBNA1 binding prote
	1				2; nucleolar protein p40; homolog of yeast EBNA1
			1		binding protein; nuclear FGF3 binding protein;
4440					EBNA1-binding protein 2 [Homo sapiens]
1146	243	'5 Al104979	j,k	1.	[H.sapiens]
					Rattus populations 250 LD
1147		2 Al105044	gg	ļ	Rattus norvegicus 250 kDa estrous-specific proteir mRNA, partial cds
1148		1 Al105161	d		ESTs ESTS
1149	219	6 Al105243	jj,kk		ESTs
ŀ					
				HHs:glutaryl-Coenzyme A	ESTs, Highly similar to GCDH_MOUSE Glutaryl-
1150	2359	6 Al105435	bb	dehydrogenase	COA denydrogenase, mitochondrial precursor
1151	1519	7 Al105444	d,kk	derrydrogeriase	(GCD) [M.musculus]
			Gill	multiple in calls) and the	ESTs
1152	1529	1 Al111401	hh	multiple inositol polyphosphate	multiple inositol polyphosphate histidine
1153	447	9 Al111599		histidine phosphatase 1	_phosphatase 1
1154	1843	9 Al111877	j,k,jj,kk		ESTs
	1040	AITTIOTT	<u></u>	ribosomal protein L14	ribosomal protein L14
- 1		1	1	-	ESTs, Weakly similar to FKB5_MOUSE 51 kDa
		1			FK506-binding protein (FKBP51) (Peptidyl-prolyl cis
1155	050	1			trans isomerase) (PPiase) (Rotamase)
1100	253	Al111960	e,kk		[M.musculus]
4450					ESTs, Highly similar to JC5556 adhalin - mouse
1156	12887	Al112095	hh		[M.musculus]
1157	4143	Al112107	gg		ESTs
1158	14434	Al112291			ESTs, Weakly similar to T46612 multi PDZ domain
1159	22744	Al112512	h,l		Throreit 1 - Lat IK Volkedichs
1160	12969	Al112969	p,q		ESTs
			1,,,		ESTs
					ESTs, Highly similar to SAP3_MOUSE Ganglioside
1					GIVIZ activator precursor (GM2-AP) (Cerebrosido
1161	2296	Al112979	w,x		(Shingolipid activator protein)
			111/1		(protein 3) (SAP-3) (M.musculus)
1162	4969	Al113008	l,k,n,o		ESTs, Weakly similar to vitropectin (Rattus
			7,1,1,0		norvegicusi IR.norvegicusi
1163	23428	Al113320	In 1		ESTs, Moderately similar to JC4365 arginine_tRNA
1164		Al136516			ligase (EC 6.1.1.19) - human [H.sapiens]
1165	21010	A1136547	r,kk		ESTs
<del></del>	- 1019	A) 13034/	y,z		ESTs
1166	40700	A1400555	1 1		Rattus norvegicus mRNA for Castration Induced
1100	10/50	Al136555	С		Prostatic Apoptosis Related protein-1 (CIPAR-1)
1167	24040	* 1400m /=			ESTs, Highly similar to H33_HUMAN Histone H3.3
1157		AI136747	cc,dd		(H3.A) (H3.B) (H3.3Q) [M.musculus]
1168	13080	AI136842	е		ESTs
1					
			1	Į,	ESTs, Weakly similar to T34013 hypothetical
1169	13082	N136848	c	1:	protein Y4C6B.5 - Caenorhabditis elegans
					C.elegans]
1170	13090	J136977	cc,dd	· /	STs, Highly similar to S14538 transition protein -
1171	12878	1137114	hh		nouse [M.musculus]
			<del>    -   -   -   -   -   -   -   -</del>		STs
į	- 1	i		[E	STs, Moderately similar to S21976 probable RNA-
ł	- 1			Į¢.	lifected DNA polymerase (EC 2.7.7.49) (done
1/2	13/77/14	in 37131		lv.	MH2C) - rat retrotransposon L1 (fragment)
173	13201		n,o		R.norvegicus]
	102011A	113/200	ee,ff		STs
÷,	seen .	1137302	cc,dd	16	STs, Weakly similar to ZF37_RAT Zinc finger

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SECTIO	GEGOTI	7	Model Code	Known Gene Name	Unigene Sequence Glüster Title
					ESTo Madamatali, 1, 1
1175	916	A1137406	kk	į.	ESTs, Moderately similar to A55945 endothelial c
		71107400	INN .		IDIOIGIA C receptor precursor - mouse M musculus
1176	1123	Al137410	#	İ	ESTS, Woderately similar to hypothetical protein
1170	17230	A1137410	ee,ff		FLJ12888 [Homo saplens] [H saplens]
		1	]		ESTS, Weakly similar to GPV RAT Platelet
44	=10				glycoprotein V precursor (GPV) (CD42D)
1177	/122	AI137468	99		[R.norvegicus]
		į.			ESTs, Highly similar to H2A1_RAT Histone H2A.1
1178	18943	Al137495	d		[R.norvegicus]
				Transforming growth factor beta	[[Turorvegicos]
1179	17402	Al137553	ee,ff	stimulated clone 22	Transforming growth facts to the
1180	6638	Al137579	bb	Carrial at Carria Control 22	Transforming growth factor beta stimulated clone
			-		ESTs
·					ESTs, Highly similar to IMB3_HUMAN Importin be
1181	7/1/	Al137586			3 subunit (Karyopherin beta-3 subunit) (Ran-bindin
	7713	71107000	а		(protein 5) [H.sapiens]
i		1			ESTs, Highly similar to MG15_HUMAN
1		1			Transcription factor-like protein MRG15 (MORF-
4400	400= :				related gene 15 protein) (MSL3-1 protein) (Protein
1182		Al137864	cc,dd		HSPC008/HSPC061) [H.sapiens]
1183		Al137925	hh		ESTs
1184		Al137931	l,m		ESTs
1185	23687	Al137958	g		ESTs
			3		
1186	14524	Al137974	d		ESTs, Highly similar to 157019 H3 histone - rat
1187	11372	Al137995	c		[R.norvegicus]
1188		Al138093			ESTs
1189		Al144948	g		ESTs
1190			r		ESTs
		Al145058	<b>g</b> g		ESTs
1191			kk		ESTs
1192	13/86	AI145106	hh		ESTs
					ESTs, Weakly similar to NUCL_RAT Nucleolin
1193		Al145282	a,jj,kk		(Protein C23) [R.norvegicus]
1194		AI145362	ll .		ESTs
1195	13375	Al145454	cc,dd		ESTs
1196	11331	Al145556	1		
1197	23631		,k		ESTs
			1100		ESTs
ſ	I	ŀ			ESTs, Weakly similar to T21659 hypothetical
1198	8330	Al145761			protein F32D8.4 - Caenorhabditis elegans
1199	5504	A1145/01	w,x		[C.elegans]
1199	2231	AI145859			ESTs
			T		ESTs, Highly similar to RB6K_MOUSE Rabkinesin-
			ł	j.	6 (RAB6-interacting kinesin-like protein) (Kinesin-
1200	11337	Al145968	,m	li di di di di di di di di di di di di di	like protein 174) [M.musculus]
T					mo protein 174) [withusculus]
					ESTe Highly similar to TAGGGG Law
1201	11346	A1145991 j	j,kk	12	ESTs, Highly similar to T46266 hypothetical protein
			,,	<u> </u>	DKFZp761A179.1 - human (fragment) [H.sapiens]
1202	11363	Al145997	nh	Į!	ESTs, Moderately similar to 2206377B MHR23B
	1,000/	11170001	<u> </u>	<del></del> [9	gene (Mus musculus) (M.musculus)
- 1	- 1	i		ļi	STs, Weakly similar to Yeast hypothetical 52.9
1202	10470	1460075	.	<u> </u>	(D protein like [Caenorhabditis elegans]
1203	104/2/	N168975 j	,k		C.elegans]
					STs, Weakly similar to Yeast hypothetical 52.9
. 1	. I			ļi.	CD protein like [Caenorhabditis elegans]
1203	18473	\I168975 j	k,kk,ll	*   16	C.elegansi
T					STo Highly similar to A00774
1204	21523	N169104 e	, 1	]*	STs, Highly similar to A26774 platelet factor 4
		10	·	ir	orecursor - rat [R.norvegicus]

		GenBank A	CC T TO THE A	ale i	Atty: Ref. 44921-5090-01-WO/2105485
	GLGC I	DINO	Madeira	Known Gehe Name	[10] [10] [10] [10] [10] [10] [10] [10]
3E Q 1B	02001	J 140.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
	İ				ESTs, Moderately similar to VATE_MOUSE
		İ			Vacualar ATP our thoras authority Transport
				HMm:ATPase, H+ transporting	Vacuolar ATP synthase subunit E (V-ATPase E
1205	1791	4 Al169159	hh	lysosomal 31kDa, V1 subunit E	
				HHs:eukaryotic translation	ATPase 31 kDa subunit) (P31) [M.musculus]
1206	2315	2 AI169170	l <sub>r</sub>	initiation factor 4A, isoform 2	15015, righly similar to \$00985 translation initiation
		1	<del>-   </del>	initiation factor 4A, isoform 2	lactor eir-4A     - mouse   M musculus
1207	1297	9 AI169177	20047	ľ	ESTS, Highly similar to S33363 glv96 protein
			a,p,q,y,z		IMOUSE IM. musculusi
1208	260	7 AI169211	i.	Į.	ESTs, Highly similar to A47318 RNA-hinding prote
		1/1109211			Raly - mouse [M.musculus]
				ATPase, H+ transporting,	
1209	2266	1 4140000		lysosomal (vacuolar proton	ATPase, H+ transporting, lysosomal (vacuolar
		Al169265	gg	pump), subunit 1	proton pump), subunit 1
1210		Al169272	cc,dd		ESTs -
1211	13240	Al169311	j,k		ESTs
1212	1452	AI169512	d		ESTs
1213	<u> </u>	AI169591	r		ESTs, Highly similar to S57447 HPBRII-7 protein -
1214	4480	AI169601	hh		Inuman [H.sapiens]
			<del></del>	vesicle-associated membrane	ESTs
		1		protoin constitute membrane	
1215	6888	AI169615	le t	protein, associated protein A (3)	3 vesicle-associated membrane protein, associated
			s,t	kDa)	(33 kDa)
j		1			ESTs, Highly similar to chromosome 11
1216	22440	A14 COC40			hypothetical protein ORF3 [Homo sapiens]
1210	23110	Al169640	_t		[H.sapiens]
4047	04440				ESTs. Weakly similar to ATD binding and the
1217	24146	Al169668	ii		ESTs, Weakly similar to ATP-binding cassette, sub
					family F, member 2 [Homo sapiens] [H.sapiens]
1218	21660	Al169751	a,kk		Rattus norvegicus Interferon-inducible protein
,					variant 10 mRNA, complete cds
1219	804	AI169756	j,k,p,q		ESTs, Highly similar to G33_RAT GENE 33
1220	13427	Al169993	aa,bb		POLYPEPTIDE [R.norvegicus]
1221	21185	Al170056	a		ESTs
1222	21254	Al170059	d		ESTs
			<del>  -  </del>		ESTs
1223	6969	Al170244	hh		ESTs, Moderately similar to g1-related zinc finger
1224		A1170244 A1170251			protein (Mus musculus) (M.musculus)
17	22342	71110201	aa,bb		ESTs
1225	25.47	A 1470070	]		ESTs, Weakly similar to S54303 zinc transport
1226		A1170279	ii		protein ZnT-1 - rat [R.norvegicus]
		Al170313	gg		ESTs
1227		AJ170363	e,j,k,t,ee,ff		ESTs
1225		AI170379	a,p,q,y,z		ESTs ESTs
1229		AJ170384	cc,dd		ESTS
1230		AI170406	h,l		
1231		AI170407	d,kk		ESTs
			-7		ESTs
1				Mmighton and 11	ESTs, Weakly similar to A35362 UDPglucose-
1232	11585	1170502	<u> </u>	minigrycogen synutase 3,	glycogen glucosyltransferase (EC 2.4.1.11), henatic
1223		1170525	<u> </u>	run .	- rat [R.norvegicus]
1234			ii		ESTs
		1170561	cc,dd		ESTs
1235	2534	1170632	aa,bb,ii		STs
أمما			H	Hs:sterol regulatory element	STs. Weakly similar to A49005
1236		1170663	cc,dd b		STs, Weakly similar to A48085 transcription factor
1237	13305 A	1170676	ee,ff		ADD1 - rat [R.norvegicus]
238	3973 A	I170687	hh		SIS
1			<del>                                     </del>		STs
~ *	60821	1170793	kk	ĮE	STs, Weakly similar to DCC_MOUSE Tumor
Lib,	UJUZIA				uppressor protein DCC precursor [M.musculus]

	1 180 ) 10	GenBank Acc	<u> </u>		Atty. Ref. 44921-5090-01-WO/2105485
	GLGC I	No.			121 (*12), 1 1 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	020011	7110.	Model Code;	Known Gene Name	Unigene Sequence Cluster Title
1240	2120	1 41470040			ESTS, Weakly similar to A57291 cytoking indusing
1240	2120	4 AI170842	hh		Illucied Diolein C193 - hilman (U capional
1241	4000	141470040			ESTs, Moderately similar to A57641 G protein-
1242	1209	AI170948	q		coupled receptor 4 - human [H.sapiens]
1242		AI171019	aa,bb		ESTs [Final Final
1243		AI171064	n,o		ESTs
1244	22033	Al171165	aa,bb		ESTs
					ESTs, Weakly similar to 2118320A
4045	4==00				neurodegeneration-associated protein 1 [Rattus
1245	17783	Al171206	ee,ff		norvegicus] [R.norvegicus]
1246	21771	Al171209	n,o		ESTs ESTS
40.4~				amino acid transporter system	
1247	5953	Al171231	s,t	A2	amino acid transporter system A2
					ESTs, Highly similar to S38342 fibrillarin - mouse
1248	22432	Al171263	a,z		[M.musculus]
					[withdscolds]
					ESTs Moderately similar to David Lungary
					ESTs, Moderately similar to PTN3_HUMAN Protein
1249	11426	Al171305	a,jj,kk		tyrosine phosphatase, non-receptor type 3 (Protein
			T		tyrosine phosphatase H1) (PTP-H1) [H.sapiens]
ĺ			1		ESTs Highly similarly Charles on
ŀ		•			ESTs, Highly similar to SWI/SNF related, matrix
J				guanine nucleotide binding	associated, actin dependent regulator of chromatin
				protein (G protein), beta	subfamily b, member 1; integrase interactor 1 [Mus
1250	14960	AI171319	w,x	polypeptide 2-like 1	musculus] [M.musculus], guanine nucleotide
1251	14117	Al171350	e,p,q	polypeptide 2-like 1	binding protein (G protein), beta polypeptide 2-like
			Cibid		ESIS
1252	18047	Al171359	bb		ESTs, Weakly similar to DnaJ-like protein [Rattus
			100		[norvegicus] [R.norvegicus]
1253	16599	Al171366	ee,ff,jj,kk		ESTs, Weakly similar to S37583 RING finger
			GE,II,JJ,KK		protein rfp - mouse (fragment) (M musculue)
j					ESTS, Moderately similar to MEA6 HUMAN
1254	22958	Al171374	lna.		Meningioma-expressed antigen 6/11 (MFA6)
		117 1074	p,q,t		(MEA11) [H.sapiens]
- 1	ì				
	1		}		ESTs, Weakly similar to HCD2_RAT 3-hydroxyacyl
- 1	i		1		CoA dehydrogenase type II (Type II HADH)
1255	17520	1171460	h.		(Endoplasmic reticulum-associated amyloid beta-
1255 1256	17529	N171460	h,l		(Endoplasmic reticulum-associated amyloid beta-
1256	13453	N171518	г		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs
1256 1257	13453 A	N171518 N171521	r c		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs
1256 1257 1258	13453 A 17220 A 11761 A	M171518 M171521 M171526	r c d		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs
1256 1257 1258 1259	13453 A 17220 A 11761 A 5292 A	M171518 M171521 M171526 M171607	r c d		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs ESTs
1256 1257 1258 1259 1260	13453 A 17220 A 11761 A 5292 A 6667 A	M171518 M171521 M171526 M171607 M171646	r c d t		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs
1256 1257 1258 1259	13453 A 17220 A 11761 A 5292 A 6667 A	M171518 M171521 M171526 M171607 M171646	r c d		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs ESTs
1256 1257 1258 1259 1260 1261	13453 / 17220 / 11761 / 5292 / 6667 / 2795 /	N171518 N171521 N171526 N171607 N171646 N171655	r c d t		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs ESTs ESTs ESTs ESTs
1256 1257 1258 1259 1260 1261	13453 / 17220 / 11761 / 5292 / 6667 / 2795 / 11696 /	N171518 N171521 N171526 N171607 N171646 N171655	r c d t gg e		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs
1256 1257 1258 1259 1260 1261 1262 1263	13453 / 17220 / 11761 / 5292 / 6667 / 2795 / 11696 / 15449 /	N171518 N171521 N171526 N171607 N171646 N171655	r c d t t gg e		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs
1256 1257 1258 1259 1260 1261 1262 1263 1264	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A	N171518 N171521 N171526 N171607 N171646 N171655 N171774 N171779	r c d t gg e		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs
1256 1257 1258 1259 1260 1261 1262 1263	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A	N171518 N171521 N171526 N171607 N171646 N171655	r c d t t gg e		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs
1256 1257 1258 1259 1260 1261 1262 1263 1264 1265	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A 4420 A	N171518 N171521 N171526 N171607 N171646 N171655 N171774 N171779 N171799 N171916 N171978	r c d t t gg e		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs
1256 1257 1258 1259 1260 1261 1262 1263 1264 1265	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A 4420 A 24220 A	N171518 N171521 N171526 N171526 N171607 N171646 N171655 N171774 N171779 N171799 N171916 N171978	r c d t t gg e		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs
1256 1257 1258 1259 1260 1261 1262 1263 1264 1265	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A 4420 A 24220 A	N171518 N171521 N171526 N171607 N171646 N171655 N171774 N171779 N171799 N171916 N171978	r c d t t gg e		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus]  ESTs
1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A 4420 A 24220 A	N171518 N171521 N171526 N171607 N171646 N171655 N171774 N171779 N171799 N171916 N171978	r c d t ygg e ij,kk jkk a,z		(Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus]  ESTs
1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A 4420 A 24220 A 22239 A 6645 A	N171518 N171521 N171526 N171526 N171607 N171646 N171655 N171774 N171799 N171916 N171978 N171998 N171998 N171998	r c d t gg e ij,kk a,z r		[Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus]  ESTs, Moderately similar to I48672 p8 MTCP-1 - mouse [M.musculus]  ESTs  ESTs  ESTs
1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A 4420 A 24220 A 22239 A 6645 A 1506 A 19012 A	N171518 N171521 N171526 N171526 N171607 N171646 N171655 N171774 N171779 N171799 N171916 N171978 N171998 N171998 N171998 N172056	r c d t gg e ij,kk j,kk a,z r		[Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus]  ESTs, Moderately similar to I48672 p8 MTCP-1 - mouse [M.musculus]  ESTs
1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267	13453 A 17220 A 11761 A 5292 A 6667 A 2795 A 11696 A 15449 A 4420 A 24220 A 22239 A 6645 A 1506 A 19012 A	N171518 N171521 N171526 N171526 N171607 N171646 N171655 N171774 N171779 N171799 N171978 N171998 N171998 N171998 N172051 N172056 N172097	r c d t gg e ij,kk j,kk a,z r g,kk		[Endoplasmic reticulum-associated amyloid beta- peptide binding protein) [R.norvegicus]  ESTs, Moderately similar to I48672 p8 MTCP-1 - mouse [M.musculus]  ESTs  ESTs  ESTs

ABLE	1;	GenBank A	<del>~ 1 * 2 * * 2</del>		Atty. Ref. 44921-5090-01-WO/2105485
בת ות	GI CO	D No.			Unigene Sequence Cluster Title
EQ.ID	GLGUI	UINO.	Model Code:	Known Gene Name	Unigene Sequence Cluster Title
	l				ESTs, Weakly similar to RTN1_RAT Reticulon 1
	1				(Neuroendocrine-specific protein) (S-rex)
1272		3 Al172183	c		[R.norvegicus]
1273	697	4 AI172263	d,r		ESTs ESTS
1274		3 Al172265	cc,dd		
1275		3 Al172271	r		ESTs
	200	074172271	<del> '</del>		ESTs
1276	214	0 Al172272	LL.		ESTs, Weakly similar to A53004 transcription
1277	0400	0 A1172272	hh		elongation factor S-II - rat [R.norvegicus]
		8 Al172281	g		ESTs
1278	128	7 Al172299	kk		ESTs
				HMm:interleukin 2 receptor,	ESTs, Highly similar to 149280 interleukin-2 recept
1279	427	8 AI172304	е	gamma chain	gamma chain progress and the first factor
1280	1170	2 Al172305	е		gamma chain precursor - mouse [M.musculus]
1281	1326	6 Al172326	j,k,ii		
1282	2339	0 Al172328	e	DNA binding	ESTs
1283		7 Al172352		RNA binding protein p45AUF1	RNA binding protein p45AUF1
1284		Al172332	hh,jj,kk		ESTs
1204	2420	A11/2423	a,h,l,o,hh		ESTs
4005					ESTs, Weakly similar to HCCA2 protein [Homo
1285	220	AI172472	cc,dd		sapiens] [H.sapiens]
					ESTs, Weakly similar to A54756 isocitrate
					debydrogonase (NADD.) (FO 4 4 4 40)
1286	1729 <sup>-</sup>	Al172491	gg		dehydrogenase (NADP+) (EC 1.1.1.42), cytosolic
1287	12043	Al172567	ii		rat [R.norvegicus]
1288	13070	Al172569	h,l		ESTs
1289		Al172598	ij,kk		EST
1290		AI172036	ЈЈ,КК		ESTs
1230	1117	A1175005	<u> r</u> _		ESTs
		1			
				1	ESTs, Moderately similar to COF1_RAT COFILIN
1291	7740	Al175011	r,hh		NON-MUSCLE ISOFORM [R.norvegicus]
- 1					ESTs, Moderately similar to WS3_HUMAN WS-3
1292	17679	Al175025	hh		PROTEIN [H.sapiens]
1293	8053	AI175033	p,q		ESTs
			j,k,p,q,ee,ff,jj,k		EOIS
1294	2331	Al175045	k		
1295		Al175100	h,l,kk,ll		ESTs
-		74170100	II,I,KK,II		ESTs
1296	10110	A1475004		Guanidinoacetate	
1290	19110	Al175281	hh	methyltransferase	Guanidinoacetate methyltransferase
400-					ESTs, Weakly similar to S08464 T-cell alloantigen
1297	21252	Al175328	n,o		RT6.1 - rat [R.norvegicus]
1298		AI175348	jj,kk		ESTs ESTs
1299	13460	AI175375	a,y,z,ee,ff,kk		ESTs
			171-1-01111111		
					ESTs, Weakly similar to RASH_RAT
1300	4445	Al175466	], [		TRANSFORMING PROTEIN P21/H-RAS-1 (C-H-
1301		Al175508	1110		RAS) [R.norvegicus]
1,001	10000	VI 11 0000	j,k		ESTs
1300	1050-	A1475554			ESTs, Highly similar to EF1B_MOUSE Elongation
1302	1050/	AI175551	h,i,w,x,kk		factor 1-beta (EF-1-beta) [M.musculus]
1303	9979	AI175594	ji		ESTs   Cotta) [Williamscalus]
					ESTs, Weakly similar to A53237 I(3)S12 protein -
			] [		If the / Drosophilo males and 1 //
1304	2261	Al175619	lii l		fruit fly (Drosophila melanogaster) (fragment)
1305		AI175777	j,k		[D.melanogaster]
$\overline{}$			lin.		ESTs
	1900/	AI175875	las by		Rattus norvegicus Sprague-Dawley lipid-binding
1306	13004	711/00/0	aa,bb		protein mRNA, complete cds
1306					Rattus norvegicus Sprague-Dawley lipid-binding
	4000-	414=====	1		
1306		AI175875	li		Drotein mRNA, complete cde
	21755	A1175875 A1175977 A1175990	li r		protein mRNA, complete cds ESTs

ABLE 1		(ConDo-1: 4	. 1		Atty. Ref. 44921-5090-01-WO/2105485
EQUD:	CI CO	GenBank Acc			的位置,15000000000000000000000000000000000000
era in.	GEGC IF	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1309	2245	AI175992			ESTs, Highly similar to beta-catenin-interacting
1310			<u>  r                                   </u>		[protein ICAT [Mus musculus] [M.musculus]
1310	2040	AI176004	f,g		ESIS
4244	0004				ESTs, Highly similar to PM5P_HUMAN Protein pM
1311 1312		Al176007	y,z		precursor [H.sapiens]
1312	12298	AI176055	aa,bb		ESTs
		1			ESTs, ESTs, Highly similar to S15892 pyruvate
				HMm:pyruvate dehydrogenase	dehydrogenase (lipoamide) (EC 1.2.4.1) beta chai
1313		Al176117	hh	(lipoamide) beta	rat [R.norvegicus]
1314		Al176121	f,g		ESTs
1315	6686	Al176130	d,jj,kk		ESTs
			T		
1316	17223	Al176140	lr .		ESTs, Highly similar to testis expressed gene 189
1317		Al176160	n,o		[Mus musculus] [M.musculus]
			1.,0	<del> </del>	ESTs
1318	6782	AI176170	е	EVEOS binding produit 4 (40) 5)	State of the state
			<del>                                     </del>	FK506-binding protein 1 (12kD) FBJ murine osteosarcoma viral	FK506-binding protein 1 (12kD)
1319	10182	Al176185	n a aa		The state of the s
1320	22765	Al176265	p,q,gg	(v-fos) oncogene homolog	homolog
.020	22700	A1170203	j,k,p,q,kk		ESTs
					ESTs, Highly similar to UAP1_HUMAN UDP-N-
				ſ	acetylhexosamine pyrophosphorylase (Antigen X)
- 1				1	(AGX) (Sperm-associated antigen 2) Includes: IID
1				1	N-acetylgalactosamine pyrophosphorylase (AGX-1
4004	40000				UDP-N-acetylglucosamine pyrophosphorylase
1321	12999	Al176276	h,l,p,q,y,z,gg		(AGX-2)] [H.sapiens]
					ESTs, Highly similar to B Chain B, Crystal Structure
					Of The D1d2 Sub-Complex From The Human Snm
1322	16438	Al176294	cc,dd		Core Domain [H.sapiens]
					ESTs, Weakly similar to CO1B_RAT Coronin 1B
1323	13339	Al176308	s,t		(Coronin 2) [R.norvegicus]
1324	13511	AI176331	l,m		ESTs [R. norvegicus]
			-		
ļ					ESTs, Weakly similar to YQT3_CAEEL
1325	13504	Al176354	gg		HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN
1326		Al176362	a,y,z,bb,kk,il		CHROMOSOME III [C.elegans]
	- 33.1		a, y, z, DD, KK, II		ESTs
1327	19006	Al176393	oo bb ll		Rattus norvegicus Sprague-Dawley lipid-binding
1021	13000	A1170000	aa,bb,ll		protein mRNA, complete cds
- 1	ľ				ESTs, Highly similar to S41115 probable
1328	17020	Al176422	i		flavoprotein-ubiquinone oxidoreductase (EC 1.6.5)
1329			11	·	- numan [H.sapiens]
1328	24314		hh		ESTs
4000	4545		h,l,j,k,y,z,ee,ff,		ESTs, Highly similar to SMRT2 metallothionein II -
1330	15191		kk		rat [R.norvegicus]
1331	24763	AI176488	jj,kk	nuclear factor I/B	nuclear factor I/B
10.55					ESTs, Highly similar to NIDO_RAT NIDOGEN
1332			f,g		(ENTACTIN) [R.norvegicus]
1333		AI176505	hh		ESTs [Kultorvegicus]
1334	15959	N176540	d,r		ESTs ·
I_					2010
			la la	HMm:heat shock protein, 86	ESTs Moderately similar to troop and a
1335	16518	N176546			ESTs, Moderately similar to HS9B_RAT Heat shock
			-,,-,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		protein HSP 90-beta (HSP 84) [R.norvegicus]
1336	5507	N176584	c		Rattus norvegicus insulin-like growth factor binding
			<del></del>		protein 5 mRNA, 3' UTR
	ı	1	j		ESTs, Weakly similar to tumor protein p53-binding
1337	3610	1176588	,		protein; topoisomerase I binding protein [Home
1338		//	<u>,k</u>		saplens] [H.sapiens]
1339			j		ESTs
1000		1176810	e,j,k,kk		ESTs
1340	6821 A	1470044 1			

ABLE		Gen Rank A	<b>0.</b>   6. 20 granta	A A A A A A A A A A A A A A A A A A A	Atty: Ref. 44921-5090-01-WO/2105485
FO ID	GI GC II	D No:	Maria de la Calabara	表表 1. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A Marketin of the Atlanta of the term
			4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Known Gene Name	Unigene Sequence Cluster Title
1341	1691	7 Al176951	h,l		ESTs
4040	1004			ribosomal protein, mitochondria	1,
1342	1031	0 Al176961	n,o	L12	ribosomal protein, mitochondrial, L12
					protein, mitochonunai, L12
				Cbp/p300-interacting	
		İ	p,q,r,bb,ee,ff,jj,	transactivator, with Glu/Asp-rich	Cbp/p300-interacting transactivator, with Glu/Asp
1343	1612	4 AI176963	kk	carboxy-terminal domain, 2	rich carboxy-terminal domain, 2
				terraina derriani, z	ESTs Moderately almited Times
1344		2 Al176995	c	i	ESTs, Moderately similar to T13963 formin relate
1345	1649	3 Al177049	d		protein, lymphocyte specific - mouse [M.musculu
1346	3969	AI177055			ESTs
1347	285	2 Al177059	c,g,kk		ESTs
1348		7 AI177099	hh		
			<del></del>		ESTs
			1		ESTs, Weakly similar to OAF_DROME Out at firs
1349	5943	AI177105	),k		protein (Contains: Out at first short protein)
	30-70		l),n		IID.melanogasteri
					ESTs, Weakly similar to S49158 complement
1350	12210	Al177119	Lie		protein C1q beta chain precursor - rat
1351		Al177119	kk		[R.norvegicus]
1352			c		ESTs
1332	/103	Al177256	h,i		ESTs
		İ			ESTs, Weakly similar to GMCR_MOUSE
- 1		ł			Granulocyte-macrophage colony-stimulating factor
4050	40-00				receptor alpha chain precursor (GM-CSF-R-alpha
1353		Al177280	w,x		(GMR) [M.musculus]
1354		Al177312	a		ESTs
1355		AI177357	r		2010
1356	14989	AI177366	f,g,l,m,kk	Integrin, beta 1	Integrin, beta 1
					ESTs Weakly similar to KLDC MOUSE Law
					ESTs, Weakly similar to KLR6_MOUSE Killer cell
1357	17826	Al177403	w,x		lectin-like receptor 6 (T-cell surface glycoprotein L
,					49F) (LY49-F antigen) [M.musculus]
- 1			1		ECTo Llighty observed to Toomer to the
1358	24129	Al177590	b		ESTs, Highly similar to T08750 hypothetical protein
1					DKFZp586E1519.1 - human (fragment) [H.sapiens
1359	17570	Al177683	n,o,hh		D-44
1360	9521	AI177706	b,u,v		Rattus norvegicus mRNA for hnRNP protein, partia
1361		Al177734	1		ESIS
			+		ESTs
. 1	ĺ			j	ESTs, Weakly similar to T20254 hypothetical
1362	6334	Al177765	<u> </u>		protein C55A6.1 - Caenorhabditis elegans
	3004		b		[C.elegans]
1	- 1		1		ESTs, Moderately similar to acid sphingomyelinas
1363	22222	AI177804	-		like phosphodiesterase 3a [Mus musculus]
,500	22002	11//004	aa,bb		[M.musculus]
1364	11704	1177040	1		ESTs, Highly similar to SAS_HUMAN Sarcoma
1004	11/91/	Al177843	aa,bb		amplified sequence (H.saniens)
				1	ESTs, Highly similar to CDK1 MOUSE Cyclin-
1	- 1		]	[0	dependent kinase 2-associated protein 1 (CDK2-
	- 1		1	1:	associated protein 1) (Putative oral cancer
400=	. اً	114		],	suppressor) (Deleted in oral cancer-1) (DOC-1)
1365		1177871	gg	li li	M.musculusi
1366	15315	N177911	h,i ca		calpactin I heavy chain
i	T				STs, Moderately similar to S23251 protein-tyrosin
į	j		1	li li	rinase /FC 2.7.1.110\ adv =======
1367	5929 A	1177962	hh i		rinase (EC 2.7.1.112) ark precursor - mouse
					M.musculus]
1	į			l.º	STs, Weakly similar to transforming growth factor
じじロ	2091 A	1177967	r,aa,bb	ļt	eta (TGF-beta) masking protein large subunit Rattus norvegicus] [R.norvegicus]

TABLE	1	GenBank Ad			Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GI GÖ IF	No.		· · · · · · · · · · · · · · · · · · ·	
ברת וחי	GEGGIL	7 NO	Model Code	Known Gene Name	Unigene Sequence Cluster Title
					ESTs, Highly similar to TGIF_MOUSE 5'-TG-3'
1369	19184	Al178025	p,q,kk	i	INTERACTING FACTOR (HOMEOBOX PROTEI
1370	17320	Al178069	kk		( TOII ) [IVI.IIIusculus]
1371		Al178214			ESTs
1372			hh		ESTs
13/2	23928	Al178222	ii		ESTs
					ESTs Moderately similar to Tables
1373	6059	Al178245	c	I	ESTs, Moderately similar to T13963 formin related
					protein, lymphocyte specific - mouse [M.musculus
		1		1	Lots, weakly similar to \$51973 hypothetical
1374	4073	Al178272	hh		protein YAL046c - yeast (Saccharomyces
1375		Al178277	d		[cerevisiae] [S.cerevisiae]
	0140	A1170217			ESTs
i			1		ESTs, Highly similar to SYFB_MOUSE
1					Phenylalanyl-tRNA synthetase beta chain
				HMm:phenylalanine-tRNA	(Phonylologica ADMA III
1376	6502	Al178283	lr .	synthetase-like	(Phenylalanine-tRNA ligase beta chain) (PheRS)
1377		Al178361	n,o	Officiase-like	[M.musculus]
1378		Al178384	hh		ESTs
1379		Al178394			ESTs
1380			С		ESTs
		AI178527	a,y,z		ESTs
1381		Al178688	s,t		ESTs
1382	14530	Al178738	b		ESTs
- 1					
1383	15091	Al178740	cc,dd	1	ESTs, Highly similar to A56418 transcription factor
1384		Al178746		<del> </del>	delta - mouse [M.musculus]
1385		Al178751	p,q,y,z		ESTs
1000	10000	A1170/31	_  ii	sialyltransferase 5	sialyltransferase 5
4000	40040			eukaryotic translation initiation	
1386	18848	Al178816	n,o	factor 4E	
					eukaryotic translation initiation factor 4E
- 1					ESTs, Weakly similar to T23419 hypothetical
1387	13592	AI178914	lii		protein K07F5.14 - Caenorhabditis elegans
					[C.elegans]
1388	23043	AI178968	l	1	ESTs, Weakly similar to S70642 ubiquitin ligase
1389	10007	AI178971	b	<u></u>	Nedd4 - rat (fragment) [R.norvegicus]
1303	10907/	411/09/1	C,V	Hemoglobin, alpha 1	Hemoglobin, alpha 1
	1				ESTs, Highly similar to B Chain B, Three-
				İ	Dimensional Charles Costs
1390	17358	\l179147	g		Dimensional Structure Of Human Electron Transfer
			9	Pattus populations	Flavoprotein To 2.1 A Resolution [H.sapiens]
ı			1	Rattus norvegicus	
8	1/1002	N179150	l	mitochondrial genome.	
1391			bb,cc,dd	9/22Length = 16,3	Rattus norvegicus CDK110 mRNA
		1179167	j,k,y,z		ESTs
1392		1179227	ii		ESTs
1393		1179260	kk		
1394		1179356	w,x	plysia ras-related homolog A2	ESTs
1395		1179366	ee,ff	prysia ras-relateu nomolog A2	plysia ras-related homolog A2
			30,11		ESTs
1396	12011 A	1170200	_		ESTs, Highly similar to open reading frame 12 [Mus
	IZVIIIA	1119300	С		musculus] [M.musculus]
420-	40		7		ESTs, Highly similar to RIKEN cDNA 0610040D20
1397	19783 A		f,g		IfMus musculus (M musculus)
1398	13029 A	1179391	e,t,kk		[Mus musculus] [M.musculus]
1399	15438 A			colleged type V alaba 0	ESTs
1400	15042 A			collagen type V, alpha 2	collagen type V, alpha 2
1401	13619 A		a,j,k		ESTs
	100 19 A	175404	j,k		ESTs
1400	40004		a,p,q,r,y,z,gg,k		
1402	16081 A	179610	k i	Heme oxygenase	Heme ovygonoso
				.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	Heme oxygenase
1403	3094 AI	179700	b,l,m		ESTs, Weakly similar to AGRT agrin - rat
1404			il		[R.norvegicus] ESTs
17071					

TABLE 1	1.18		12.	18 No.	Atty. Ref. 44921-5090-01-WO/2105485
050 0	0, 00, 10	GenBank Acc.		国际设计工作等 医红色 经额上的	7 102 1 0030-0 1-WO/2 103465
SEQ ID	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1					ESTs, Highly similar to HSPC038 protein [Homo
1405	18895	Al179916	b,l,m		sapiens] [H.sapiens]
1406		Al179971	С	Hemoglobin, alpha 1	Hemoglobin, alpha 1
1406	1687	Al179971	b,c,v	Hemoglobin, alpha 1	Hemoglobin, alpha 1
			1		ESTs, Weakly similar to CPI3_RAT CONTRAPSIN-
			1	1	LIKE PROTEASE INHIBITOR 3 PRECURSOR (CP
1					23) (SEDINE PROTES OF INJURITOR 4) (SE
1407	6455	Al179984	aa,bb		23) (SERINE PROTEASE INHIBITOR 1) (SPI-1) [R.norvegicus]
1408		Al179988	j,k,kk		ESTs ESTs
1409		AI180081	cc,dd	<del> </del>	
1111		74700007	100,00	<del> </del>	ESTs
1410	19828	Al180087	d		ESTs, Weakly similar to OZF_RAT Zinc finger
1411		A1180239	kk	<del></del>	protein OZF (POZF-1) [R.norvegicus]
1412		A1180259			ESTs
1412	3402	A1100252	e,r		ESTs
1 4440	47000	A1400004			ESTs, Moderately similar to JC4978 oxidative
1413		Al180281	b,l,m		stress protein A170 - mouse [M.musculus]
1414	3352	Al180334	b,u,v		ESTs
1					ESTs, Weakly similar to LYOX_RAT Protein-lysine
1415	8180	AI180353	hh		6-oxidase precursor (Lysyl oxidase) [R.norvegicus]
					ESTs, Weakly similar to T14106 probable GTPase-
1416	14337	Al180414	b,c,i,m		activating protein SPA-1 - rat [R.norvegicus]
1417	7117	Al227612	11		ESTs ESTS
1418		Al227639	lu .		ESTs
1419		Al227715	a,ee,ff	Retinoblastoma-related gene	
1420	23015	Al227724	l,s,t,li	- Totaloulastorila-related gene	Retinoblastoma-related gene
1421	2055	Al227751	111	<del> </del>	ESTs
			<del>"</del>		ESTs
1422	13672	AI227763	laa		ESTs, Highly similar to S26650 DNA-binding protein
1423	22012	Al227887	gg		5 - human [H.sapiens]
1423	40474	Al227887 Al227961	e,aa,bb	cell division cycle 42	cell division cycle 42
			c,ii		EST
1425		AI228147	<b>g</b> g		ESTs
1426		Al228284	j,k		ESTs
1427	12946	Al228291	a,ee,ff,kk,ll		ESTs
]					ESTs, Highly similar to craniofacial development
1428		AI228299	bb		protein 1 [Mus musculus] [M.musculus]
1429		Al228301	ee,ff,jj,kk		ESTs
1430			ee,ff		ESTs
1431			b,v		ESTs
14,22			cc,dd		ESTS
			1		
1433	1473	A1228548	aa		ESTs, Highly similar to S10A_RAT S-100 protein,
				<del></del>	alpha chain [R.norvegicus]
	j		; i		ESTs, Weakly similar to T16757 hypothetical
1434	16053	A1228596	2 D G V = #		protein R144.3 - Caenorhabditis elegans
1435		110000000	a,p,q,y,z,ee,ff		[C.elegans]
1436			99		ESTs
1430	132/0	AI228760	ι		ESTs
لديها	45000	11000000		stearoyl-Coenzyme A	Rat DNA polymerase alpha mRNA, 3' end, stearoyl-
1437	15078	AI228830	j,k	desaturase 2	Coenzyme A desaturase 2
ı	1				ESTs, Weakly similar to T26088 hypothetical
			į		protein W02B12.7 - Caenorhabditis elegans
1438	2210	AI228963	hh		[C.elegans]
				Synaptobrevin 1, Vesicle-	[ganoj
	1		ļ		Synaptobrevin 1, Vesicle-associated membrane
14ัวษา	10203	AF229196	w,x,cc,dd		
1440	13826	1229304	h,l,hh,jj,kk		protein (synaptobrevin 2)
144	12024		h,l		ESTs
1774			n,o		ESTs
			aa,bb		ESTs
1443	1864314				ESTs

TABLE	-	·IGenPart	·	Ž	Atty, Ref. 44921-5090-01-WO/2105485
SEO ID	GI GC II	GenBank Ac			化表面 第二人 化二甲基磺胺 医皮肤 医二氏病 医二氏病
3EG 1D	الغائج ال	אוס	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4444	4007	11000			Rattus norvegicus mRNA for class I beta-tubulin,
1444	1397	7 Al229707	r		complete cds
1445	1521	2 Al229753	p,q,t,y,z,ee,ff	ADP-ribosylation factor 2	ADP-ribosylation factor 2
					ESTs, Highly similar to 2202300B
					keratin:ISOTYPE=K19 [Rattus norvegicus]
1446		Al229785	cc,dd		[R.norvegicus]
1447		Al229843	kk		ESTs
1448		Al229854	hh		ESTs
1449	13886	Al230116	99		ESTs
				ectonucleoside triphosphate	EOIS
1450	23042	Al230130	s,t,ii	diphosphohydrolase 2	onlanual and de tall at a service
				Lipricoprioriyarolase 2	ectonucleoside triphosphate diphosphohydrolase
1451	7650	Al230142	w,x		ESTs, Weakly similar to KUCR_RAT Kupffer cell
1452		Al230156	b		receptor [R.norvegicus]
1453	18528	Al230284	c		ESTs
1454	2372	Al230373	j,k		ESTs
1455		Al230381			ESTs
1456		Al230430	p,q		ESTs
1457	6560	Al230440	ii 		ESTs
1458		A1230440 A1230460		NA POLICE III	ESTs
1459		A1230460 A1230479	C	MARCKS-like protein	MARCKS-like protein
1460			b		ESTs
1400	23998	Al230578	s,t,ii		ESTs
1461	20404	A1020504	ļ.,		ESTs, Weakly similar to TES1_RAT TESTIN 1/2
1401	22484	Al230591			PRECURSOR (CMB-22/CMB-23) [R.norvegicus]
4400					ESTs, Moderately similar to RL34_RAT 60S
1462	9412	Al230691	f,g		RIBOSOMAL PROTEIN L34 [R.norvegicus]
1463		Al230716	a,II		ESTs [R. Horvegicus]
1464		Al230743	hh	actin-related protein 3	actin-related protein 3
1465	9171	AI230747	b		ESTs
					ESTs, Highly similar to BI3_MOUSE Brain protein
1466	22387	AI230753	f,g		13 [M.musculus]
- 1	- 1				io (minusculus)
1					ESTs, Moderately similar to cargo selection protein
1			1		(mannose 6 phosphate receptor binding pr; cargo
					selection protoin (manage Cale and a selection p
1467	24270	AI230758	n,o		selection protein (mannose 6 phosphate receptor
	ļ				binding protein) [Homo sapiens] [H.sapiens] ESTs, Moderately similar to cyclin-dependent
- }					kinage inhibitor 2: CDI/2
					kinase inhibitor 3; CDK2-associated dual specificity
			1	HHs:cyclin-dependent kinase	phophatase; cyclin-dependent kinase interacting
			]	inhibitor 3 (CDK2-associated	protein 2; kinase-associated phosphatase; cyclin-
1468	14430	1230798	r	dual specificity phosphatase)	dependent kinase interactor 1 [Homo sapiens]
1469		1230826	n,o	ouen specificity priosphatase)	[[H.sapiens]
1470		1230830	ii,o		ESTs
<del></del>	. 320/	0000	<del> "  </del>		ESTs
1471	8036	1230884			ESTs, Highly similar to HMBA-inducible [Homo
1472		1230915	100		[sapiens] [H.sapiens]
1473		1230915	gg		ESTs
1474	11802 4	1230939	aa,bb		ESTs
1475	16087 A	1234044	W,X		ESTs
1476	10007 A	1234000	cc,dd		ESTs
		1231038	s,t		ESTs
1477	13934 A	1231044	W,X		ESTs
1478	17903 A	1231083	t		ESTs
1479	24072 A	1231093	9		ESTs
4405				•	ESTs, Highly similar to R3RT3A ribosomal protein
1480	20845 A	1231140	w,x		L23a cytosolic (validated)
l					L23a, cytosolic [validated] - rat [R.norvegicus] ESTs, Highly similar to S611_HUMAN Protein
					transport protoin Social all-based with the
1481	21816 A	231217	11		transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1) [R.norvegicus]
					NOCOUL BIDDIS-11 IK NONANICHE!

TABLE		GenBank Ac	3.1	a been and been	Atty. Ref. 44921-5090-01-WO/2105485
SEOIU.	ici co	Celipank Ad	4. 1 4. 1 4. 1 4. 1	Para Property of	3、整理的 在2000年度1000年度1000年度1000年度1000年度1000年度
گات طائات	GLGC	D No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
				Cystatin C (cysteine proteinas	On going ocqueilige Gluster Title
1482	243	27 Al231292	00	inhibitor	
	<del>                                     </del>	1/11/2012/02	99	inhibitor)	Cystatin C (cysteine proteinase inhibitor)
4.400	000			prolyl 4-hydroxylase alpha	
1483		04 Al231310	ee,ff	subunit	prolyl 4-hydroxylase alpha subunit
1484	1396	6 Al231421	d,t		ESTs ESTs
1485	1557	2 Al231472	f,g	procollagen, type I, alpha 1	
			1119	proconagen, type i, alpha i	procollagen, type I, alpha 1
1486	800	4 Al231532	1_		ESTs, Highly similar to Z183_HUMAN Zinc finger
1100	- 000	4 AIZS 1532	Г		protein 183 [H.sapiens]
440=			1		ESTs, Highly similar to S14538 transition protein
1487	1309	2 Al231547	jj,kk		mouse M museulus
					mouse [M.musculus]
1488	1927	1 AI231566	s,t	1	ESTs, Highly similar to MAX_RAT MAX protein
1489	242	2 AI231615	3,1		[[R.norvegicus]
1490	0004	2 A 23 0 3	r		ESTs
		2 Al231724	C		ESTs
1491		2 Al231778	lii		ESTs
1492	641	2 Al231787	а		
		T	<del> </del>	<del> </del>	ESTs
- [		1		1	ESTs, Highly similar to BAG3_MOUSE BAG-fami
Ī		İ			molecular chaperone regulator-3 (BCL-2 binding
الممار		.1	1	1	athanogene-3) /BAC 3) /Bal 3 to 3
_ 1493	<u>1517</u>	1 Al231792	ee,ff		athanogene-3) (BAG-3) (Bcl-2-binding protein Bis)
			1		[M.musculus]
1494	233	Al231798	hh	1	ESTs, Highly similar to T-complex expressed gen
	200	7/1201730	[111]		Z   IVIUS MUSCUlus   IM. musculus
4405					ESTs, Moderately similar to I68673 gene X123
1495	2316	Al231799	y,z	1	profoin human (france to 10 1000/3 gene X123
- 1					protein - human (fragment) [H.sapiens]
- 1		ļ		1	ESTs, Weakly similar to A55190 transitional
1496	7036	AI231801		1	endoplasmic reticulum ATPase (EC 3.6.1)
1497			n,o,cc,dd		[validated] - rat [R.norvegicus]
1497	12435	Al231810	j,k,jj,kk,ll		ESTs ESTs
					ECTs Weekly state   North
1498	13116	Al231812	c		ESTs, Weakly similar to Y55B1AL.2.p
			·		[Caenorhabditis elegans] [C.elegans]
- 1					ESTS, Highly similar to mitochondrial carrier
1499	24400	41004000			homolog 1; mitochondrial carrier homolog 1 isoform
		Al231822	h,l		b [Mus musculus] [M.musculus]
1500		Al231827	а		ESTs [Wild Indisculds]
1501	15173	Al231846	d		
1502		Al231992	hh		ESTs
1503		Al232014			EST
1303	3434	MIZ32014	y,z,ee,ff		ESTs
1504	19094	Al232021	g		ESTs, Highly similar to SUI1_MOUSE Protein
1505			cc,dd		translation factor SUI1 homolog [M.musculus]
1506		111			ESTS
	17020	11/20/2 TU4	d,gg		ESTs
ı		ſ		low density lipoprotein receptor-	
			İ	related protein associated	low density linearatein
1507	409	AI232268	r l	protein 1	low density lipoprotein receptor-related protein
				Proteill F	associated protein 1
					ESTs, Weakly similar to JC4914 anti-sigma cross-
1500	000-	110000	. 1	I	reacting protein homolog I beta precursor - human
1508	2085	AI232270	hh		[H.sapiens]
	T				CCTo Moderately 2
	j				ESTs, Moderately similar to B53434 cell surface
1509	14031	AI232295	<u> </u>		glycoprotein gp49B form 2 precursor - mouse
	1 1001/	11202230	<u> </u>		[M.musculus]
4546			1	purinergic receptor P2X, ligand-	
1510	4716	N232313			Difference recently DOV II
	T				purinergic receptor P2X, ligand-gated ion channel 4
1511	14034	N232321 r	1,0		ESTS, Highly similar to CGI-150 protein [Homo
1512	11872	10000			sapiens] [H.sapiens]
	45040	10000	k,p,q,y,z		ESTs
1513	15246	1232332	c,dd		ESTs
1514	6509 A	1232361			
1515	4891		h		ESTs
1516	3143 4	1232408			ESTs

TABLE 1		· :	2		Atty. Ref. 44921-5090-01-WO/2105485
		GenBank Acc.		· (1) 10 (1) (1) (1) (1) (1) (1)	The second secon
	GLGC ID		Model Code	Known Gene Name	Unigene Sequence Cluster Title
1517	11157	Al232494	W,X		ESTs
					ESTs, Weakly similar to S24C_HUMAN Protein
			1		transport protein Sec24C (SEC24-related protein (
1518	13645	Al232694	hh		[[H.sapiens]
					ESTs, Weakly similar to E.coli YCAC like
1519	7285	Al232731	<b>g</b> g		[Caenorhabditis elegans] [C.elegans]
					ESTs, Highly similar to CG51_HUMAN Protein CG
1520	3100	Al232741	hh		I51 [H.sapiens]
					ESTs, Weakly similar to T27038 hypothetical
					protein Y49E10.2 - Caenorhabditis elegans
1521		A1232948	hh		[C.elegans]
1522		AI232982	ee,ff		ESTs
1523	4855	AI233024	jj,kk		ESTs
					ESTs, Weakly similar to HE47_RAT Probable ATF
1524		Al233147	y,z	1	dependent RNA helicase p47 [R.norvegicus]
1525	11561	Al233182	b		ESTs PT [1. Horvegicus]
l					ESTs, Weakly similar to YQO9_CAEEL
			1	1	Hypothetical 141.2 kDa protein EEED8.9 in
1526	21948	Al233191	hh	1	chromosome II [C.elegans]
					omotiosomo n [o.c.ogano]
					ESTs, Highly similar to RS18_HUMAN 40S
1527	15107	Al233220	h,I		ribosomal protein S18 (KE-3) (KE3) [R.norvegicus]
i					ESTs, Highly similar to cytokine receptor-like factor
1			ł		1; cytokine receptor like molecule 3 [Mus musculus
1528	5228	Al233311	h,l,n,o		[M.musculus]
					ESTs, Weakly similar to ribosomal protein S23
1529		Al233316	hh		[Rattus norvegicus] [R.norvegicus]
1530	4475	AI233374	n,o		ESTs
1531	14095	AI233468	jj,kk		ESTs
1532	4670		w,x		ESTs
1533		AI233743	hh		ESTs
1534			hh		ESTs
1535	15085	Al233829	cc,dd,hh	P11 protein	P11 protein
				- Francisco	ESTs, Weakly similar to PAB1_MOUSE
					Polyadenylate-binding protein 1 (Poly(A)-binding
1536	15685	Al233870	hh		protein 1) (PABP 1) (PABP1) [M.musculus]
1537		Al233965	r		ESTs (FASE 1) (FASE 1) [M.Musculus]
1538			hh		ESTs
1539	6532	Al234105	j,k,p,q		ESTs
1540			a,ee,ff,jj,kk		ESTs
1541		Al234251	hh		ESTs
1542		A1234283	n,o,hh		ESTs
1543		AI234326	cc,dd		EST
1544		AI234496	11		ESTs
1545		Al234664	cc,dd		ESTs
1546	23964	AI234748	a,kk		ESTs
1547				DEXRAS1 (Dexras1)	DEXRAS1 (Dexras1)
1548			jj,kk		ESTs
			****	growth and transformation-	
1549	18444	AI234915	ii	dependent protein	growth and transformation-dependent protein
					ESTs, Weakly similar to ELV4_RAT ELAV-like
			ļ		protein 4 (Parangonicotic constant and the
1550	13293	AI235032	hh		protein 4 (Paraneoplastic encephalomyelitis antiger
1551			d		HuD) (Hu-antigen D) [R.norvegicus]
1552			jj,kk		ESTs .
				tissue inhibitor of	15018
1553	15004	A1235224		metalioproteinase 1	tionus inhibitor of matella and
1554			a,y,z	motoroproteinase t	tissue inhibitor of metalloproteinase 1
			-,,,,-		ESTs

Ally, Ref. 44921-5090-01-WOZ105485   Ally, Ref. 44921-5090-01-WOZ105485   Ally, Ref. 44921-5090-01-WOZ105485   Model, Code   Known Gene Name   Unique Sequence Cluster Type	
HMm/low density lipoprotein   ESTs, Highly similar to S25111 alpha-2-mouse   HMm/low density lipoprotein   ESTs, Highly similar to S25111 alpha-2-mouse   Mm/low density lipoprotein   1   ESTs, Weakly similar to MiC2-HJMANT-c   surface glycoprotein (22-HJMANT-c   surface glycoprotein (22-HJMANT-c   surface glycoprotein (22-HJMANT-c   surface glycoprotein (22-HJMANT-c   surface glycoprotein (22-HJMANT-c   surface glycoprotein (22-HJMANT-c   surface glycoprotein (22-HJMANT-c   surface glycoprotein (13-HJMANT-c   surface glycoprotein (13-HJMANT-c   surface glycoprotein (13-HJMANT-c   surface glycoprotein (13-HJMANT-c   surface glycoprotein (13-HJMANT-c   surface glycoprotein (13-HJMANT-c   surface glycoprotein (13-HJMANT-c   surface glycoprot	<del>·                                    </del>
High   High	
1565	
1555   14722   Al235284   99	
1556   1472   Al235284   99	•
Strate gycoprolein E2 precursor (E2 antigol (CD99) (MIC2 protein) (12E7)   H.saplens	
1557	-cell
1557	igen)
1559   14094   Al235377	•
1559   8440   Al235611   b   ZAP 36/annexin IV   ZAP 36/annexin	
1559   8440   Al235611   b   ZAP 36/annexin IV   ZAP 36/annexin	ei
1560   3650   Al235738	ensl
1561	
1561	rea
1561   14642   Al235874   h,	
1561   14642   Al235874   h, l	Aicrofib.
1562   2687   Al235877   S.t   STS, Highly similar to 2019405A upstream regulator element-binding protein [Rattus norvegicus] [R.norvegicus] [R.norvegicus] [R.norvegicus] [R.norvegicus] [R.norvegicus] [R.norvegicus] [R.norvegicus] [R.norvegicus] [R.norvegicus] [STS, Highly similar to NIDO_RAT NIDOGE (ENTACTIN) [R.norvegicus] [STS, Highly similar to NIDO_RAT NIDOGE (ENTACTIN) [R.norvegicus] [STS (ENTACTIN) [R.norvegicus] [STS (ENTACTIN) [R.norvegicus] [STS (ENTACTIN) [R.norvegicus] [STS (ENTACTIN) [R.norvegicus] [STS (ENTACTIN) [R.norvegicus] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [D.melanogaster] [STS (ES	
ESTs, Highly similar to 2019405A upstream regulator element-binding protein [Rattus norvegicus] [R.norvegicus	(MAG
1562   2687 Al235877   s.t	
1563   4770 Al235915   d,il   ESTS     1564   22717 Al235948   g   ESTS, Highly similar to NIDO_RAT NIDOGE     1565   14776 Al235950   w,x,jj,kk   ESTS     1566   14861 Al236045   c   ESTS     1567   14869 Al236049   aa,bb   aa,bb   (D.melanogaster)     1568   23230 Al236146   t   ESTS     1569   14594 Al236152   b,d,u,v   ESTS     1570   18513 Al236152   b,d,u,v   ESTS     1571   14884 Al236212   ii   ESTS     1572   5007 Al236229   s,t,aa,bb   ESTS     1573   22212 Al236294   kk   the table of the table of the table of the table of the table of table	n
1563	
1564   22717   Al235948   g	
Internation   Internation	
Internation   Internation	EN
1566	
1567	
1567	
1567	,
1568   23230   Al236146   t	ir)
1569   14594   Al236152   b,d,u,v   ESTs     1571   14884   Al236212   II   ESTs     1572   5507   Al23629   s,t,aa,bb   ESTs     1573   22212   Al236294   kk   ESTs   ESTs   ESTs     1574   18610   Al236307   I,m   ESTs     1575   15051   Al236332   j,k,p,q,y,z,ee,ff   ESTs, Highly similar to IF6_MOUSE Eukaryot translation initiation factor 6 (eIF-6) (B4 integrated interactor) (CAB) (p27(BBP)) [M.musculus]     1576   4911   Al236405   cc,dd   ESTs, Highly similar to S43429 diamine N-acetyltransferase (EC 2.3.1.57) - mouse     1577   15075   Al236473   p,q   ESTs, Highly similar to RiKEN cDNA 170002     1578   14901   Al236405   cc,dd   ESTs, Highly similar to RiKEN cDNA 170002     1579   9546   Al236520   n,o   ESTs     1580   17950   Al236500   kk   ESTs     1580   17950   Al236601   p,q,ee,ff   ESTs     1581   18259   Al236601   p,q,ee,ff   ESTs     1582   11445   Al236613   r   ESTs     1584   22443   Al236613   r   ESTs     1585   12098   Al237075   t   HMs:hepatitis B virus x   HHs:hepatitis B virus x     1578   Highly similar to hepatitis B virus x   HHs:hepatitis B virus x     1579   1570	17
1570	
1570	
1571	
1572   5.007   Al236229   s,t,aa,bb   ESTs	111-B A-
1573   22212   Al236294   kk   ESTs   ESTs, Highly similar to IF6_MOUSE Eukaryo translation initiation factor 6 (eIF-6) (B4 integriting interactor) (CAB) (p27(BBP)) [M.musculus]   ESTs   ESTs, Highly similar to S43429 diamine N-acetyltransferase (EC 2.3.1.57) - mouse (M.musculus)   ESTs, Highly similar to S43429 diamine N-acetyltransferase (EC 2.3.1.57) - mouse (M.musculus)   ESTs, Highly similar to RIKEN cDNA 170002 (Mus musculus)   ESTs, Highly similar to RIKEN cDNA 170002 (Mus musculus)   ESTs	
ESTs, Highly similar to IF6_MOUSE Eukaryot translation initiation factor 6 (eIF-6) (B4 integrinteractor) (CAB) (p27(BBP)) [M.musculus]	
1573   22212   Al236294	
1574	/otic
18610 Al236307   I,m	grin
1575	
1575	
1575	
1576	
1576	
1577   15075   Al236473   P.Q   ESTs     1578   14901   Al236481   ii   ESTs     1579   9546   Al236520   n,o   ESTs     1580   17950   Al236590   kk   ESTs     1581   18259   Al236601   P.Q.ee,ff   ESTs     1582   11445   Al236613   r   ESTs     1583   22939   Al236669   Y.Z.jj,kk   RAD54 like (S. cerevisiae)   Foreign 4) [M.musculus]     1584   22443   Al236761   ee,ff   ESTs     1585   11404   Al237002   hh   spermidine synthase   Spermidine synthase     1586   12098   Al237075   t   ESTs     1490   Al236520   n,o   ESTs     1581   ESTs   ESTs     1582   ESTs   ESTs     1583   ESTs     1584   22443   Al236761   ee,ff   ESTs     1585   12098   Al237075   t   ESTs     1586   12098   Al237075   t   ESTs     1587   ESTs     1588   ESTs   ESTs     1589   ESTs     1589   ESTs     1580   E	)29H06
1578	-201 100
1576	
1580   17950 Al236590   kk   ESTs     1581   18259 Al236601   p,q,ee,ff   ESTs     1582   11445 Al236613   r   ESTs     1583   22939 Al236669   y,z,jj,kk   RAD54 like (S. cerevisiae)   Forein 4) [M.musculus]     1584   22443 Al236761   ee,ff   ESTs     1585   1:404 Al237002   hh   spermidine synthase   Spermidine synthase     1586   12098 Al237075   t   ESTs     1483   ESTs   ESTs     1584   ESTs   ESTs     1585   1:404 Al237002   hh   spermidine synthase   Spermidine synthase     1586   1:404 Al237075   t   ESTs     1587   ESTs     1588   ESTs     1589   1:404 Al237075   t   ESTs     1589   1:404 Al237075   t   ESTs     1589   1:404 Al237075   t   ESTs     1589   1:404 Al237075   t   ESTs     1589   1:404 Al237075   t   ESTs     1580   1:	
1580 17950 Al236900 kk ESTs 1581 18259 Al236601 p,q,ee,ff ESTs 1582 11445 Al236613 r ESTs  1583 22939 Al236669 y,z,jj,kk Subunit of DNA polymerase zeta polymerase zeta catalytic subunit (Selzure relaprotein 4) [M.musculus] 1584 22443 Al236761 ee,ff ESTs 1585 1:404 Al237002 hh spermidine synthase spermidine synthase spermidine synthase 1586 12098 Al237075 t ESTs  HHs:hepatitis B virus x  HHs:hepatitis B virus x  HHs:hepatitis B virus x  B virus x-interacting protein; HBx-interacting protein; he	
1582 11445 Al236613 r ESTs  1583 22939 Al236669 y,z,jj,kk Subunit of DNA polymerase zeta protein 4) [M.musculus]  1584 22443 Al236761 ee,ff ESTs  1585 11404 Al237002 hh spermidine synthase spermidine synthase interacting protein; HBx-interacting protein; he wire x-interacting pr	
1582 11445 Al236613 r  HMm:REV3-like, catalytic subunit of DNA polymerase zeta polymerase zeta catalytic subunit (Seizure relapsoration 4) [M.musculus]  1584 22443 Al236761 ee,ff 1585 11404 Al237002 hh spermidine synthase spermidine synthase interacting protein; HBx-interacting protein; HBx-interacting protein; he he spermidine synthase interacting protein; HBx-interacting protein; he he spermidine synthase interacting protein; HBx-interacting protein; he synthase interacting protein; he sy	
HMm:REV3-like, catalytic subunit of DNA polymerase zeta protein 4) [M.musculus]  1584 22443 Al236761 ee,ff ESTs  1586 12098 Al237075 t ESTs  HMm:REV3-like, catalytic subunit of DNA polymerase zeta protein 4) [M.musculus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  HHs:hepatitis B virus x  HHs:hepatitis B virus x  B virus x-interacting protein; HBx-interacting protein; hep-  B virus x-interacting protein; MBx-interacting protein; hep-	
Subunit of DNA polymerase zeta   polymerase zeta catalytic subunit (Selzure relation	
Subunit of DNA polymerase zeta   polymerase zeta catalytic subunit (Selzure relation	
1583 22939 Al236669 y,z,jj,kk Subunit of DNA polymerase zeta polymerase zeta catalytic subunit (Seizure relation of DNA polymerase zeta polymerase zeta catalytic subunit (Seizure relation of DNA polymerase zeta polymerase zeta catalytic subunit (Seizure relation of DNA polyme	<b>\</b>
1584 22443 Al236761 ee,ff ESTs 1585 12098 Al237075 t ESTs  HHs:hepatitis B virus x  B virus x-interacting protein; HBx-interacting protein; hBx-in	elated
1586 12098 Al237075 t ESTs  Spermidine synthase spermidine synthase spermidine synthase ESTs  ESTs  ESTs  ESTs  ESTs  HHs:hepatitis B virus x  Interacting protein; HBx-interacting protein; hepatitis B virus x-interacting protein; hepatitis B	
i 12098 Al237075 t Spermidine synthase Spermidine synthase Spermidine synthase SSTs  ESTs  ESTs, Highly similar to hepatitis B virus x- interacting protein; HBx-interacting protein; hepatitis B virus x- interacting protein; HBx-interacting protein; hepatitis B virus x- interacting	
ESTs  ESTs, Highly similar to hepatitis B virus x- interacting protein; HBx-interacting protein; hepatitis B virus x interacting protein (9 6 6 7). When the state of the stat	
ESTs, Highly similar to hepatitis B virus x- interacting protein; HBx-interacting protein; help virus x-interacting protein (9 6 6 7) (No. 1)	
interacting protein; HBx-interacting protein; hell HHs:hepatitis B virus x	
I I I I S. I E PALLIS B VITUS X B VITUS X-interacting protein (0 6kD) (U	oncitt.
	epauus
	apiens]

	1	GenBank Ac			Atty. Ref.:44921-5090-01-WO/2105485
SEO ID	GL GC ID	No.	c. 14 14 14 14 14 14 14 14 14 14 14 14 14		A 2506 (2000-01-WO/2100485
OEQ ID	الم المالية	INO.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1588	3368	Al237331	l <sub>c</sub>		ESTS, Weakly similar to YCE3 HUMAN
1589		Al237535		L DO : I	Hypothetical protein CGI-143 IH capional
1590		Al237581	a,j,k,p,q,y,z	LPS-induced TNF-alpha factor	JLPS-Induced INF-alpha factor
1000	20200	A1237381	u,v		ESTs
1591	44000	4100			ESTs, Moderately similar to JC1241 beta-interfero
1091	11208	AI237586	kk		induced protoin and ID and IZ41 beta-interfero
4=0=					induced protein - rat [R.norvegicus]
1592	11375	Al237594	u,v	j	ESTs, Weakly similar to G01614 zinc finger protei
					127 - human [H.sapiens]
1593	18854	Al237636	f,g,l,m	[	ESTs, Weakly similar to CNE6_MOUSE Copine V
1594	3615	Al237645	t t	transferrin receptor	(Neuronal-copine) (N-copine) (M musculus)
1595	8759	Al237646	p,q,ee,ff	Transferrin receptor	transferm receptor
1596	14720	Al237648	99		ESTs
1597	14840	Al237698	kk		ESTs
1598	14842	Al237724	U,V		ESTs
	11012	71201124	u,v		ESTs
1599	0501	VIE30040			ESTs, Moderately similar to chromosome 20 open
1000	9301	AI638949	c,f,g,v		reading frame 116 [Homo sapiens] [H.sapiens]
1600	10040	A10000==	1.		ESTs, Highly similar to fox-1 homolog (C. elegans
	10340	AI638955	hh		[Mus musculus] [M.musculus]
1601		Al639001	r		ESTs [M.musculus]
1602	17214	A1639008	b,h,l		ESTs
1603	23781	A1639012	a,h,l,n,o		ESTs, Weakly similar to hypothetical protein
					MGC2601 [Homo saplens] [H.saplens]
1604	17108	Al639017	la l		ESTs, Weakly similar to T17453 ERG-associated
1605	4035	Al639023	cc,dd		protein ESET - mouse [M.musculus]
1606	15450	1639035	cc,dd		ESTs
			00,00		ESTs
	1		]		ESTs, Highly similar to Nedd4 WW binding# protein
1607	· 10071	แลงดูกรณ	004	İ	4; Nead4 WW-binding protein 4 (Mus musculus)
1608		1639060	a,q,y,z,ee,ff,ll		[M.musculus]
1609	25883 4	1639076	h,l,w,x		ESTs
1610		1639093	1.		
1611	22555 ^	1639103	hh		ESTs
1612			n,o		ESTs
1613	12400 A	1039107	n,o		ESTs
1614	13882 A	1639120	b		ESTs
	25895 A	1639128	jj,kk		ESTs
4045	25X4QIA	1639136	n,o		
1615					
1615 1616			11		FSTe
1616	5065 A	1639139	]		ESTs Highly circlinate at the
1616 1617	5065 A	1639139 1639151	9g		ESTs, Highly similar to pinin [Mus musculus]
1616 1617 1618	5065 A 18482 A 20073 A	1639139 1639151 1639152	99		
1616 1617 1618 1619	5065 A 18482 A 20073 A 15379 A	1639139 1639151 1639152 639162	gg b,c,u,v		ESTs, Highly similar to pinin [Mus musculus] [M.musculus]
1616 1617 1618 1619 1620	5065 A 18482 A 20073 A 15379 A 25907 A	1639139 1639151 1639152 639162 639167	99		ESTs, Highly similar to pinin [Mus musculus] [M.musculus] ESTs
1616 1617 1618 1619	5065 A 18482 A 20073 A 15379 A 25907 A	639139 639151 639152 639162 639167	gg b,c,u,v a,jj,kk,!! d		ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs
1616 1617 1618 1619 1620	5065 A 18482 A 20073 A 15379 A 25907 A 5159 A	1639139 1639151 1639152 1639162 1639167 1639185	gg b,c,u,v a,jj,kk,ll d c,u,v		ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622	5065 A 18482 Al 20073 Al 15379 Al 25907 Al 5159 Al 19795 Al	1639139 1639151 1639152 639162 639167 639185 639197	gg b,c,u,v a,jj,kk,ll d c,u,v		ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623	5065 A 18482 Al 20073 Al 15379 Al 25907 Al 5159 Al 19795 Al 19749 Al	1639139 1639151 1639152 639162 639167 639185 639197 639203	gg b,c,u,v a,jj,kk,ll d c,u,v u,v s,t		ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623 1624	5065 A 18482 Al 20073 Al 15379 Al 25907 Al 5159 Al 19795 Al 19749 Al 25918 Al	1639139 1639151 1639152 639162 639167 639185 639197 639203 639204	99 b,c,u,v a,jj,kk,ll d c,u,v u,v s,t		ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625	5065 A 18482 Al 20073 Al 15379 Al 25907 Al 5159 Al 19795 Al 19749 Al 25918 Al 20021 Al	1639139 1639151 1639152 639162 639167 639185 639197 639203 639204 639214	9g b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh		ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626	5065 A  18482 AI  20073 AI  15379 AI  25907 AI  5159 AI  19749 AI  25918 AI  20021 AI  20614 AI	1639139 1639151 1639152 1639162 1639167 1639185 1639197 1639203 1639204 1639214 1639246	9g b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh l,m	E E	ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627	5065 A  18482 AI  20073 AI  15379 AI  25907 AI  19795 AI  19749 AI  25918 AII  20021 AII  20614 AII  19962 AII	1639139 1639151 1639152 639162 639167 639185 639197 639203 639204 639214 639246 639248	9g b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh l,m h,l,j,k aa	E E	ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627	5065 A  18482 AI  20073 AI  15379 AI  25907 AI  5159 AI  19749 AI  25918 AI  20021 AI  20614 AI	1639139 1639151 1639152 639162 639167 639185 639197 639203 639204 639214 639246 639248	9g b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh l,m	E E	ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628	5065 A  18482 AI  20073 AI  15379 AI  25907 AI  19795 AI  19749 AI  25918 AI  20021 AI  20614 AI  19962 AI  17083 AI	1639139 1639151 1639152 639162 639167 639185 639197 639203 639204 639214 639214 639246 639248 639248	gg b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh l,m h,l,j,k aa e,gg	E E	ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628	5065 A  18482 AI  20073 AI  15379 AI  25907 AI  5159 AI  19749 AI  25918 AI  20021 AI  20614 AI  19962 AI  17083 AI  17215 AI  6	1639139 1639151 1639152 1639162 1639167 1639185 1639197 1639203 1639204 1639214 1639246 1639248 1639255	9g b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh l,m h,l,j,k aa	E E	ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628	5065 A  18482 AI  20073 AI  15379 AI  25907 AI  19795 AI  19749 AI  25918 AII  20021 AII  20614 AII  17083 AII  17215 AII  16016 AII	1639139 1639151 1639152 1639162 1639167 1639185 1639197 1639203 1639204 1639214 1639246 1639248 1639255 1639268	gg b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh l,m h,l,j,k aa e,gg	E E E	ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTS  ESTs  ESTS  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  E
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631	5065 A  18482 AI  20073 AI  15379 AI  25907 AI  19795 AI  19749 AI  25918 AII  20021 AII  20614 AII  17083 AII  17215 AII  17215 AII  20461 AII  20461 AII	1639139 1639151 1639152 1639162 1639167 1639185 1639203 1639204 1639204 1639214 1639246 1639248 1639248 1639255 1639268 1639308 1639350	gg b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh l,m h,l,j,k aa e,gg	E E E	ESTs, Highly similar to pinin [Mus musculus]  [M.musculus]  ESTs  ESTS
1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632	5065 A  18482 AI  20073 AI  15379 AI  25907 AI  19795 AI  19749 AI  25918 AII  20021 AII  20614 AII  17083 AII  17215 AII  16016 AII	639139	gg b,c,u,v a,jj,kk,ll d c,u,v u,v s,t hh l,m h,l,j,k aa e,gg	E E E	ESTs, Highly similar to pinin [Mus musculus] [M.musculus]  ESTs  ESTS  ESTs  ESTS  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  E

TABLE		GenBank Ac	, , , , , , , , , , , , , , , , , , ,	* * * * * * * * * * * * * * * * * * *	Atty. Ref. 44921-5090-01-WO/2105485
المانات	lei co	Olympank Yo	91亿经验公路	Known Gene Name	Unigene Sequence Cluster Title
o⊏d:in	Gree	D No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
					ESTs, Highly similar to RT06_MOUSE
1634	1915	2 Al639387	cc,dd		Mitochondrial 28S ribosomal protein S6 (MRP-S6
1635	2064	7 Al639402	20,00		[[M.musculus]
1636					ESTs
		4 Al639410	cc,dd		ESTs
1637	1009	7 Al639425	k,kk		ESTs
1638		7 Al639452	е		1013
1639	2003	2 Al639466	n,o		FOT
1640	2276	3 Al639474	e,gg	<del>                                     </del>	EST
				Libbergham of many land	ESTs
1641	2008	2 A1639488	د ا	HMm:transformed mouse 3T3	The state of the s
1642		8 Al639501		cell double minute 2	(fragments) [R.norvegicus]
1042	599	0 A1039501	11		ESTs
		1			ESTs, Weakly similar to T13607 hypothetical
				1	protein 97P4 2 fruit for / December 1
1643	2005	6 Al639504	w,x,ii	1	protein 87B1.3 - fruit fly (Drosophila melanogaster
1644	1986	4 Al639510	d		[D.melanogaster]
			<del>- </del>		ESTs
		1			EST, Weakly similar to SPCA_HUMAN Spectrin
1045	0000	11000000			alpha chain, erythrocyte (Erythroid alpha-spectrin)
1645	2008	Al639523	s,t,hh		[H.sapiens]
I				3'(2'),5'-bisphosphate	[i wodpieno]
1646	23219	AJ000347	n,o	nucleotidase	21/01) 51 51 1 1 1 1
				solute carrier family 5 (inositol	3'(2'),5'-bisphosphate nucleotidase
1647	25235	AJ001290	b.l.m	solute carrier family 5 (mosito)	
1648		AJ001929		transporters), member 3	
- 10 10	7002	73001323	f,aa	reticulocalbin	reticulocalbin
4040	00.40-	İ		Endothelial nitric oxide synthas	e
1649	20127	AJ011116	j,k,n,o	3	Endothelial nitric oxide synthase 3
					ECTo Liebber in the Control Synthase 3
1650	2401	AJ011607	u		ESTs, Highly similar to C46642 DNA primase (EC
			<u> </u>		2.7.7) 54K chain - mouse [M.musculus]
1651	20510	C06598	an hh		ESTs, Weakly similar to FK506 binding protein 2
	20010	000000	aa,bb		(13 kDa) [Rattus norvegicus] [R.norvegicus]
- 1			i		g = -j (orrogiodoj
				dodecenoyl-Coenzyme A delta	Rat mRNA for delta3, delta2-enoyl-CoA isomerase,
			ì	isomerase (3,2 trans-enoyl-	dodecencyl-Coenzymo A dolta increase,
1652	18686	D00729	g,hh	Coenyme A isomerase)	dodecenoyl-Coenzyme A delta isomerase (3,2 trans
!				dihydrolipoamide	enoyl-Coenyme A isomerase)
1653	5049	D10655	aw cc dd li kk	acetyltransferase	
	- 1110	2.0000	g,w,cc,dd,jj,kk		dihydrolipoamide acetyltransferase
1653	ENEN	DANCEE		dihydrolipoamide	
1000	5050	D10655	f,g,cc,dd	acetyltransferase	dihydrolipoamide acetyltransferase
ĺ				solute carrier family 25	200th and and a
	1			(mitochondrial adenine	
				nucleotide translocator) manta-	dealute and for the second
1654	19053	D12770	aa,bb	4	solute carrier family 25 (mitochondrial adenine
				7	IDUCIENTIAL transforator) momba- 4
		İ		Solute carrier family 25, member	
i				5 (adenine nucleotid	Solute carrier family 25, member 5 (adenine
				translocator 2, fibroblast isoform	nucleotid translocator 2, fibroblast isoform (ATP-
1655	18018	D12771	f,g	(ATP-ADP carrier protein))	ADP carrier protein))
1656	25257		s,t	protoniji	noi carrier protein))
1656			a,d		
1657	25041	214014		Cuelly D4	ESTs
		- 17017		Cyclin D1	Cyclin D1
1650	4700	205000	. 1	Retinoblastoma 1 (including	
1658	17264		<u>d</u> (	osteosarcoma)	Retinoblastoma 1 (including osteosarcoma)
1659	16610			cold shock domain protein A	cold shock domain nestein A
1 <del>6€</del> 0¦	25276	028966	S	Protein A	cold shock domain protein A
1661	25278	200=04		RAS n21 protein autic to 0	
			73	RAS p21 protein activator 2	
į			ļ,	proteasome (prosome,	ESTs, Highly similar to S60038 multicatalytic
	1		i r	nacropain) subunit, alpha type	and an add to the same of the
40 <u>00</u>	3029 E	20004	nh 7	inderopainty subutiff, alpha type	endopeptidase complex (EC 3.4.99.46) alpha chain

TABLE	Ţ	GenBank Acc	· · · · · · · · · · · · · · · · · · ·	2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GLGCI	D No.		开始 4年,第755年 美国的	· · · · · · · · · · · · · · · · · · ·
	OLGO,	DINO.	Model Code		Unigene Sequence Cluster Title
				proteasome (prosome,	
				macropain) 26S subunit,	protessomo /processomo
1663	188	4 D50695	s,t	ATPase, 4	proteasome (prosome, macropain) 26S subunit, ATPase, 4
				Solute carrier family 1 A1 (brai	Alrase, 4
1664	2114	7 D63772	j,k,p	glutamate transporter)	i i i i i i i i i i i i i i i i i i i
1665		6 D83538		glutalitate transporter)	(transporter)
1666		6 D84485	u,v	phosphatidylinositol 4-kinase	phosphatidylinositol 4-kinase
	2000	01004400	u,v		
					ESTs, Highly similar to JC5621 epidermal growth
4007	2070				factor-like protein, T16 precursor - rat
1667	22/6	2 D89730	bb		[R.norvegicus]
				fatty acid Coenzyme A ligase,	[[tanotvegicus]
1668	2098	4 D90109	lu	long chain 2	f-11
1669	2580	1 E12286	w,x	long chair z	fatty acid Coenzyme A ligase, long chain 2
		1	10,14		
1670	20456	H31144	j,k		ESTs, Moderately similar to 1914275A non-recept
1671		H31456			Tyr kinase [Homo sapiens] [H.sapiens]
1672			cc,dd		ESTs ESTS
		H31625	d		ESTs
1673	13083	H31665	ļt		ESTs
1674	19278	H31802	ii.kk	1	EST, Moderately similar to S12207 hypothetical
1675	4362	H31842	l,m		protein (B2 element) - mouse [M.musculus]
1676		H31982	b		ESTs
1677	6980	H33001			ESTs
1678		H33101	e,y,z,jj,kk		ESTs
			r		ESTs
1679		H33219	e,hh		ESTs
1680		H33426	a,h,jj,kk,ll		ESTs
1681		H33472	С		EST
1682	4407	H33528	h,I,p,q,y,z		
1683	4418	H33656	C		ESTs
1684	16714	H33660	d		ESTs
		1100000	<u>u</u>		ESTs
				1	ESTs, Highly similar to IF39_HUMAN Eukaryotic
1005	45074	1104400		i .	translation initiation factor 3 subunit 9 (eIF-3 eta)
1685	153/4	H34186	j,k		(elF3 p116) (elF3 p110) [H.sapiens]
1					(en o prio) (en o prio) [n.sapiens]
1686	17159	J00797	w,x,aa,bb,hh,ll	aloha-tubulin	alaha Autu II
			7-7-7-1-1-1	Rattus norvegicus	alpha-tubulin
	ì			mitochondial	
9	16130	J01435	bb	mitochondrial genome.	
<del></del>	-10100	001433	סט	9/22Length = 16,3	unknown Glu-Pro dipeptide repeat protein
- 1	1			Rattus norvegicus	1 1 === t-part protoni
اہ	05046	10440=		mitochondrial genome.	
9	25319	J01435	bb	9/22Length = 16,3	
	1			Rattus nor regious	
				mitochondrial genome.	
9	25050	J01435	bb	9/22Length = 16,3	
				Pattus populariana	
	- 1	ł	İ	Rattus norvegicus	
10	25054	104436	.,	mitochondrial genome.	
- 19	25051	N 1430	ob	9/22Length = 16,3	
400-	4000	10.000			Rat brain-specific identifier sequence RNA, clone
1687	16260	U1878 (	J,V		p1b224
				Branched chain alpha-ketoacid	P.0007
			1	J-11	Dennah ad at 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1688	17285 J	02827		_1 1	Branched chain alpha-ketoacid dehydrogenase
1689	17136 J	· · · · · · · · · · · · · · · · · · ·		dipila	subunit E1 alpha
1690	20549 K	(0.455.4			Tropoelastin
.550	20043	KU1701	<u>'</u>	Oxytocin/neurophysin	Oxytocin/neurophysin
4604	44000		· 10	outyrophilin-like 2 (MHC class II f	The second of the second secon
1691	14968 K	(02815 c	<u>.                                    </u>		hutvronhilin liko 2 (MUC alasa u sasastu n
i	. 1			PR-ET2 encoded	butyrophilin-like 2 (MHC class II associated)
1692	_23486 K				-D FTO
					DK-F I Z PROCHED prochevelopmental protein
1693	381 L	00124 lh	,l,m		PR-ET2 encoded oncodevelopmental protein Elastase 2, pancreatic

TABLE		GenBank /	Accid Section 200		VD 0.05 30 4 44
SEQ ID	GLGC I	D No.	Model Code	Known Gene Name	Unigerie Sequence Cluster Title
				Structure specific recognition	Joingene Sequence Cluster Title
1694	1750	08 L08814	ä	protein 1	Chryster and 10
1695	2535	4 L13025	g	protein i	Structure specific recognition protein 1
1696		9 L13202	n,o	forkhead box D3	
1697		1 L17077	е	TOTALICAG BOX DO	
1698	696	3 L18889	е	calnexin	
					Raffus populations and a series
1699	2452	0 L20869	e		Rattus norvegicus pancreatitis associated protein (PAPIII0) mRNA, complete cds
				POU domain, class 2,	(1 At mo) mixtua, complete cas
1700	2581	6 L23863	n,o	transcription factor 3	POU domain class 2 transactivities (
					POU domain, class 2, transcription factor 3 ESTs, Highly similar to A53047 6-
4-0.4					phosphofructokinase (EC 2.7.1.11) - rat
1701		8 L25387	w	phosphofructokinase, platelet	[R.norvegicus]
1701	2537	7 L25387	hh	phosphofructokinase, platelet	[ and togloud]
4700	4000				ESTs, Moderately similar to I54552 hypothetical
1702	1368	2 L38482	е	HHs:cell division cycle 34	serine proteinase - rat [R.norvegicus]
4700	4405			cytochrome c oxidase, subunit	rat [ranot vegicus]
1703 1704		5 L48209	hh	VIIIa	cytochrome c oxidase, subunit VIIIa
1704		6 M13011	l,m,ll		, and a state of our anit white
1705		M13100	р		
1705		M13100	hh		
1705		M13100	f,g		
1706		M13100	hh		ESTs
1707		M13101	t		
1707	1400	M14050	e	Heat shock 70kD protein 5	ESTs, Heat shock 70kD protein 5
1708	2074	1444070	1.	Cytochrome P450, subfamily	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
1700	20714	M14972	s,t	IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
1709	10055	M15562			Rat (diabetic BB) MHC class II alpha chain RT1.D
1709	19200	W 10062			(u)
1709	10256	M15562	1.		Rat (diabetic BB) MHC class II alpha chain RT1.D
1710		M18529	C		alpha (u)
1711		M21354	99		
	10421	1012 1334	f,g	procollagen, type III, alpha 1	procollagen, type III, alpha 1
		İ	-	Phonekinstratas t	ESTs, Highly similar to A32296 ubiquinol-
			1 1	HHs:ubiquinol-cytochrome c	cytochrome-c reductase (EC 1.10.2.2) Rieske iron-
1712	15049	M24542	aa,bb	reductase, Rieske Iron-sulfur	sultur protein precursor - rat (fragment)
1713		M27207		polypeptide 1	[R.norvegicus]
1714		M32757	l,m	procollagen, type I, alpha 1	procollagen, type I, alpha 1
			13:11		
1715	15580	M33648	y,z		Rat mitochondrial 3-hydroxy-3-methylglutaryi-CoA
			<del>-1''-</del>		synthase mRNA, complete cds
1716	17211	M34331	cc,dd		Pottus services Balla s
			<del>    -   -                              </del>		Rattus norvegicus mRNA for ribosomal protein L35
1716	26030	M34331	g		Pattus nonverious This is
				Rattus norvegicus	Rattus norvegicus mRNA for ribosomal protein L35
				nitochondrial genome.	
11	25439	M35826	bb 9	/22Length = 16,3	
				<u> </u>	Rat mRNA for MHC class II antigen RT1.B-1 beta-
	l				chain, Rattus norvegicus MHC class II antigen
1717		M36151	С		RT1.B beta chain mRNA, partial cds
1718		M36410	ee,ff,gg s	epiapterin reductase	Sepiapterin reductase
1719	17145	M38566		erine protease inhibitor	Serine protease inhibitor
4705					Rat general mitochondrial matrix processing
1720		M57728	c		protease (MPP) mRNA, 3' end
1721	24844	M58040	u,v tr	ansferrin receptor	transferrin receptor
İ	1				
1722	0405-		c	a channel, voltage-dependent,	Ca channel, voltage-dependent, L type, alpha 1c
1 / ///	24662H	M59786		أيا الماسية	subunit

TABLE 1	e e	GenBank Ac	oci i i i i i i	and the second	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID		D No.	Model Code	Known Gene Name	(1) 基础处理 (1) 10 10 10 10 10 10 10 10 10 10 10 10 10
1723		7 M60666			Unigene Sequence Cluster Title
1724		0 M62992	aa	Tropomyosin 1 (alpha)	Tropomyosin 1 (alpha)
1725		3 M64780	l,m		
1725		4 M64780	r,jj,kk	Agrin	Agrin
1725	10/4	41004780	<u> </u>	Agrin	Agrin
1		1		ATP-binding cassette, sub-	
- 1				family B (MDR/TAP), member	1
1700	570			(P-glycoprotein/multidrug	ATP-binding cassette, sub-family B (MDR/TAP),
1726	5/3	3 M81855	d	resistance 1)	member 1 (P-glycoprotein/multidrug resistance 1
		1		dimerization cofactor of	, systematical distribution (
4707			i	hepatocyte nuclear factor-1-	
1727		2 M83740	l,m	alpha	
1728	376	2 M86341	s,t	ADP-ribosylarginine hydrolase	ADP-ribosylarginine hydrolase
				Fibroblast growth factor receptor	or ESTs, Highly similar to JC1450 fibroblast growth
1729		M91599	cc,dd	4	factor receptor 4 - rat [R.norvegicus]
1730	25470	M95791	e,aa,bb		lactor receptor 4 - rat [rt.norvegicus]
				ATPase, Ca++ transporting,	
1731	<u>179</u> 9	M96626	cc,dd,gg	plasma membrane 3	ATPaga Call transporting
			T	Rattus norvegicus acetyl-CoA	ATPase, Ca++ transporting, plasma membrane 3
- 1			1	acyltransferase, 3-oxo acyl-	
			1	CoAthiolase A (Acaa), mRNA.	Applied Co.A. and the
1732	23698	NM_012489	li	11/22Length = 1619	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA
			<del> </del>	Rattus norvegicus Aldehyde	thiolase A 1, peroxisomal
- 1		j		reductase 1 (low Km aldose	
1				reductase) (5.8 kb Pstl	
				frament	
1				fragment, probably the	
1733	15514	NM_012498	i	runctional gene) (Aldr1), mRNA.	Aldehyde reductase 1 (low Km aldose reductase)
-1700	10011	14141_012496	_ ii	11122Lengui - 1339	(5.8 kb Pstl fragment, probably the functional general
1				Rattus norvegicus ATPase,	<u> </u>
1				Na+K+ transporting, alpha	i e
1734	500	NN 040505	l	2(Atp1a2), mRNA. 11/22Length	
1734	583	NM_012505 .	h,l	= 519	ATPase, Na+K+ transporting, alpha 2 polypeptide
1					
				Rattus norvegicus Brain derived	d
4705	47.15			neurothrophic factor	
1735	1/45	NM_012513	p,q,ll	(Bdnf),mRNA. $4/22$ Length = 185	Brain derived neurothrophic factor
1				Rattus norvegicus Calmodulin	
				III (Calm3), mRNA. 11/2Length	
1736	20518	NM_012518	n,o,r	= 691	Calmodulin III
ŀ		-		Rattus norvegicus	
1	l		]	Ca++/calmodulin-dependent	
	j			protein kinase 2delta subunit	
				/O 100	Cattles modulin dance don't all the
1737	25365	NM_012519	u,v,ii	= 5637	Ca++/calmodulin-dependent protein kinase II, delta subunit
				Rattus norvegicus	Sandill .
1	!			Ca++/calmodulin-dependent	
!	i		, 1	protein kinase 2delta subunit	
	ľ		1 1	/ <del>-</del>	lo- 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1737	2735	NM_012519	$ _{r}$	C00~	Ca++/calmodulin-dependent protein kinase II, delta
		012010		Rattus norvegicus	subunit
	l		[ [	Ca++/calmodulin-dependent	
				protein kinase 2delta subunit	
1737	2726	VM_012519	[,,   <sup>(</sup>	(Camk2d), mRNA. 11/22Length	Ca++/calmodulin-dependent protein kinase II, delta
1/3/	4/30	AINI_012519		= 503/	subunit
ı				Rattus norvegicus Catalase	
- 1		NA 040500	[ j(	Cat), mRNA. 11/22Length =	
1720	40711		lil 12	2495	<b>-</b>
1738	15741	VIVI_U1252U			Catalase
1738	15741	NVI_U1252U		Rattus norvegicus creatine	Catalase
1738					Catalase

TABLE	1 1111	GenBank Ac	<del> </del>		Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC II	No.	Model Code	Known Gene Name	
			1,	The second of the second control of the seco	Unigene Sequence Cluster Title
		İ		Rattus norvegicus creatine	
1739	446	BNM_012529	10	kinase, brain (Ckb), mRNA.	
	1	- 11M_012023	9	11/22Length = 1146	Creatine kinase, brain
	ł	1		Rattus norvegicus	
		1		Catecholamine-O-	
	ļ	1		methyltransferase	
1740	44446			(Comt),mRNA. 11/2Length =	
1740	11118	NM_012531	f,g	1531	Catecholamine-O-methyltransferase
		ł		Rattus norvegicus	
	1			Catecholamine-O-	
		ł		methyltransferase	
4-1-				(Comt),mRNA. 11/2Length =	
1740	11116	NM_012531	f,g	1531	Catachalanta a
					Catecholamine-O-methyltransferase
				Rattus norvegicus	
			i	Ceruloplasmin (ferroxidase)	1
<u>1741</u>	16520	NM_012532	С	(Cn) mPNA 44/201	
			<del> </del>	(Cp), mRNA. 11/22Length = 37	Ceruloplasmin (ferroxidase)
				Rattus norvegicus Crystallin,	
1742	20357	NM_012534	cc,dd	alpha polypeptide A (Cryaa),	
		1111_012004	100,00	mRNA. 3/22Length = 156	Crystallin, alpha polypeptide A
				Rattus norvegicus cytochrome	
1743	20704	NM_012541	on hh	P45, 1a2 (Cyp1a2),	Cytochrome P450, subfamily I (aromatic compound
	20104	14W_012541	aa,bb	mRNA.11/22Length = 1542	inducible), member A2 (Q42, form d)
	1			Rattus norvegicus D site	/ (u /=, lonn u)
-				albumin promoter binding	1
1744	4700	NIL 040540	L	protein (Dbp), mRNA.	
-1744	1/02	NM_012543	f	11/22Length = 1671	D site albumin promoter binding protein
			j	Rattus norvegicus D site	- end disental promoter billuling protein
				albumin promoter binding	
				protein (Dbp), mRNA.	1
1744	1763	NM_012543	hh	11/22Length = 1671	Doite albumin
i	i			Rattus norvegicus angiotensin	D site albumin promoter binding protein
				1 converting enzyme 1 (Ace),	Angiotonola Lasaus II
1745	· 225 N	M_012544	aa,bb	mRNA. 11/22Length = 4142	Angiotensin I-converting enzyme (Dipeptidyl
- !	-			Rattus norvegicus Early growth	carboxypeptidase 1)
			a,h,l,p,q,y,z,ee	response 1 (Egr1), mRNA.	
1746	23868 N	IM_012551	,ff	11/22Length = 3112	F- 1
T				Rattus norvegicus Early growth	Early growth response 1
- 1				response 1 (Egr1), mRNA.	
1746	?3869N	M_012551	a,h,I,p,q,y,z	44/001 11 1	
			-1.00640114	Raffus nonvasions C-1	Early growth response 1
		Į.	ſ	Rattus norvegicus Early growth	
1746	23871N	M_012551	ויבעם	response 1 (Egr1), mRNA.	
		012001	p,q,y,z,ii	11/22Length = 3112	Early growth response 1
ĺ	I		1	Rattus norvegicus Early growth I	
1746	23872 1	M_012551	!'	response 1 (Egr1), mRNA.	
	20012  11	w_U12001	o,q,y,z	11/22Length = 3112	Early growth response 1
İ	.			Rattus norvegicus Fibrinogen.	S.
1747	احرم	4 045===		gamma polypeptide (Fgg)	
1747	64/7 N	V_012559 z	<u> </u>	nRNA. 11/2Length = 1358	Fibrinogen, gamma polymentida
j	ł	T		Rattus norvegicus Fibrinogen,	Fibrinogen, gamma polypeptide
			lo	jamma polypeptide (Fgg),	
1747	6478 NA	<u>И_012559</u> у	z r	-DAIA 44401	
-		/	· ''	Rattus norvegicus Głucokinase	Fibrinogen, gamma polypeptide
- 1	1		l,	Gok) mPNA 44 Pol - "	
1/40	งไม่เกีย	i_012565	mno :0	Gck), mRNA. 11/22Length =	
$\neg   \neg$		_5.2000  1,		326	Blucokinase
İ	1	1	.	Tallus norvegicus Gap junction	
	1	j	ĮP.	rotein, alpha 1, 43 kD(connexin	J
		1	14	3) (Gja1), mRNA. 11/2Length =	
-42	483 214	_012567 s	. 1'	768	ı

TABLE		: GenBank A	CC.   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC I	∷ GenBank A D No.	Model Code		1 27 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1-1			Inijodei Code	The state of the s	Unigene Sequence Cluster Title
	l			Rattus norvegicus Histone H1	-
1750	1000	S N. 040576		(H1f), mRNA. 11/2Length =	j
1750	1002	5 NM_012578	p,q	1779	Histone H1-0
				Rattus norvegicus Histone H1	-
				(H1f), mRNA. 11/2Length =	
1750	1602	6 NM_012578	p,q,s,t,ee,ff	1779	Histone H1-0
	ļ			Rattus norvegicus Heme	Tristone H1-0
			ĺ	oxygenase (Hmox1), mRNA.	
1751	1608	0 NM_012580	p,q,y,z,kk	1/22Length = 87	
				Rattus norvegicus Homeo box	Heme oxygenase
				A2 (Hove) mBNA 4000	
1752	170	BNM_012581	lii	A2 (Hoxa2), mRNA. 1/22Lengtl	
		21111_012301	- 11	= 1576	homeobox A2
}		1	[	Rattus norvegicus Homeo box	
1752	1700	NIM 040504	1,	A2 (Hoxa2), mRNA. 1/22Lengt/	h
1752	170	NM_012581	l,m	= 1576	homeobox A2
İ		1		Rattus norvegicus 5-	
		1	1	hydroxytryptamine (serotonin)	
4			1	receptor 1A (Htr1a), mRNA	1
1753	20313	NM_012585	b,u,v	11/22Length = 1269	5-Hydroxydryntamino (oceatanta)
1				Rattus norvegicus insulin-like	5-Hydroxytryptamine (serotonin) receptor 1A
,		[		growth factor binding protein3	
- 1			ĺ	(lgfbp3), mRNA. 11/22Length =	
1754	15098	NM_012588	bb	2352	
				Rattus norvegicus Interleukin 6	Insulin-like growth factor-binding protein (IGF-BP3
1		ĺ		(interferent hete 3) (III)	
1755	24716	NM_012589	j,k,p,q	(interferon, beta 2) (II6), mRNA.	
		1111_012000	איאייון	11/22Length = 146	Interleukin 6 (interferon, beta 2)
				D-11	
		Ì		Rattus norvegicus Isovaleryl	
1756	4450	NIM GAGGOO		Coenzyme A dehydrogenase	
1730	4400	NM_012592	C	(Ivd), mRNA. 11/22Length = 214	Isovaleryl Coenzyme A dehydrogenase
				I will a lioi acdicno Faciale	- The state of the
4757	-40-			dehydrogenease B (Ldhb),	ł
1757	/125	NM_012595	aa,bb	mRNA.11/2Length = 1217	Lactate dehydrogenease B
				Rattus norvegicus Lipoprotein	ESTs, Highly similar to JH0790 lipoprotein lipase
	ľ			lipase (Lpl), mRNA.	VEC 3.1.1.34) propure and the
1758	18386	NM_012598	w,x	11/22Length = 3617	(EC 3.1.1.34) precursor - rat [R.norvegicus],
l l	T			Rattus norvegicus Lipoprotein	Lipoprotein lipase
				lipase (Lpl), mRNA.	
1758	18387	NM_012598	w,x	44400) 11	
			† · · · · ·	Rattus norvegicus v-myc avian	Lipoprotein lipase
- 1	- 1			myelocytomatosis viral	
J			1	1	•
1759	2628	VM_012603	lanau-	oncogene hornolog (Myc),	Avian myelocytomatosis viral (v-myc) oncogene
		012003	a,p,q,y,z		homolog
İ				Rattus norvegicus v-myc avian	
	- 1			myelocytomatosis viral	
1750	2000	114 040000	a,j,k,p,q,y,z,ee	oncogene homolog (Myc),	Avian myelocytomatosis viral (v-myc) oncogene
1759	2029 1	IM_012603	,ff,kk	mRNA. 11/22Length = 2168	homolog
- 1	j		i	Rattus norvegicus	3
			1 1	Neurofibromatosis type 1 (Nf1),	
1760	25450 N	IM_012609	n,o	mRNA. 11/2Length = 9132	
				Rattus norvegicus Nerve	
		1		growth factor receptor, fast	
- 1	1	ł	į l	(Nofe) mpNA 44/01	
		M_012610		(Ngfr),mRNA. 11/2Length =	
1761	1298 N		<u>u</u>	3259	Nerve growth factor receptor, fast
1761	1298 N	012010			
1761	1298 N	012010	1	Lyaring Holdedichs Melde	
1761	1298 N	012010		growth factor receptor, fast	
761				Lyaring Holdedichs Melde	

		. GenBank Ac			Atty. Ref. 44921-5090-01-WO/2105485
EQ ID	GLGC I	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
				Rattus norvegicus natriuretic	The sequence cluster. Title
	1			peptide receptor 1 (Npr1),	
1762	638	NM_012613	aa,bb	mRNA.11/22Length = 468	Nintelland 12 an
				Rattus norvegicus	Natriuretic peptide receptor A/Guanylate cyclase
		ŀ		Neuropeptide Y (Npy), mRNA.	
1763	24508	NM_012614	c	11/22Length = 539	
				Rattus norvegicus S1 calcium	Neuropeptide Y
			ļ	binding protein A4	
				(S1a4),mRNA. 1/22Length =	
1764	20589	NM_012618	h,l,n,o,w,x	487	C400 1: 1: 1: 1:
				Rattus norvegicus serine (or	S100 calcium-binding protein A4
1				cysteine) proteinase	
				inhibitor,member 1 (Pai1),	serine (or cysteine) proteinase inhibitor, clade E
1765	15540	NM_012620	a,kk	mRNA. 11/22Length = 353	(nexin, plasminogen activator inhibitor type 1),
				Rattus norvegicus Protein	member 1
Ī				kinase C, type I (gamma type)	
	1			(Prkcg), mRNA. 11/2Length =	
1766	25133	NM_012628	99	3113	
			33	Rattus norvegicus protein	
- 1			1	tyrosine phosphatase, non-	
			1	recentor type 4 /Dis-41	
1767	1841	NM_012637	d,jj,kk	receptor type 1 (Ptpn1), mRNA. 1/22Length = 4127	
		012007	[U,JJ,KK	Pattus popusions and di	protein tyrosine phosphatase, non-receptor type 1
1	İ			Rattus norvegicus protein	
İ	1			tyrosine phosphatase, non-	
1767	1844	NM_012637	nava	receptor type 1 (Ptpn1), mRNA.	I was a superposition of the s
-		1111_012007	p,q,y,z	1/22Length = 4127	ltvne 1
j	ľ			Ratius norvegicus RI1 class Ib	ESTs, Weakly similar to A60716 somatotropin
1768	14924	NM_012645	cc,dd	lacue (171 IVMS)' WEMY'	Intron-related protein RDE.25 - rat (fragment)
		1111_012010	CC,GG	11/22Length = 154	[R.norvegicus], RT1 class lb gene
	-			Rattus norvegicus syndecan 4	
1769	94231	VM_012649	j,k,y,z	(Sdc4), mRNA. 11/22Length = 2462	
		012040	J,N,Y,Z		Ryudocan/syndecan 4
	ŀ			Rattus norvegicus Secreted	
	1			acidic cystein-rich glycoprotein	
1770	16217	VM_012656	c,aa,bb	(osteonectin) (Sparc), mRNA.	Secreted acidic cystein-rich glycoprotein
	- 102.77	012000	0,88,00	11/2Length = 225	(osteonectin)
				Rattus norvegicus Secreted	
1			1	acidic cystein-rich glycoprotein	
1770	16218	M_012656	n,o	(osteonectin) (Sparc), mRNA.	Secreted acidic cystein-rich glycoprotein
			1.,,0	11/2Length = 225	(osteonectin)
	l		]	Rattus norvegicus Secreted	
!			į į	acidic cystein-rich glycoprotein	
1770	16219 N	IM_012656	r aa	(osteonectin) (Sparc), mRNA.	Secreted acidic cystein-rich glycoprotein
<del>-  </del> -			r,gg	11/2Length = 225	(osteonectin)
	1			Rattus norvegicus Secreted	
				acidic cystein-rich glycoprotein	
1770	16220 N	M_012656	h,l,aa,bb	(osteonectin) (Sparc), mRNA.	Secreted acidic cystein-rich glycoprotein
<del></del>		0 12000	וויויוםמיטח	11/2Length = 225	(osteonectin)
i			1	Rattus norvegicus Secreted	
1	j	i		acidic cystein-rich glycoprotein	
1770	16221 N	M_012656	d !	osteonectin) (Sparc), mRNA.	Secreted acidic cystein-rich glycoprotein
		012000		11/2Length = 225	(osteonectin)
ļ			j	Rattus norvegicus steroid	
$Tr_{1}$	A LINEY AR	M_012661	00 dd	sulfatase (Sts), mRNA.	
	~100/ NI	W_U12001	cc,dd 1	1/22Length = 2472	Steroid sulfatase
	1	- 1		Rattus norvegicus vesicle-	
t	į	i	Į.	ssociated membrane protein 2	
772	16107	M_012663	, (C	Vamp2), mRNA. 1/22Length =	Vesicle-associated membrane protein
	1012/108	viuiznna li	,k 2	71	(synaptobrevin 2)

ABLE 1	1:	GenBank Acc	<b>3</b> [1] [1] (1] (1] (2]	21 V - 27 - 1 - 20 - 22 - 2	Atty. Ref. 44921-5090-01-WO/2105485
EO IÓ	GLGC IC	No.	Model Code		The state of the s
	0.00 1.	71.00.	INIOGEL COGE:	Known Gene Name	Unigene Sequence Cluster Title
	•		1	Rattus norvegicus troponin T2	
4770	2405			(Tnnt2), mRNA. 11/22Length =	
1773	2485	NM_012676	aa,bb	196	Troponin T, cardiac
				Rattus norvegicus Tropomycin	7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
				4 (Tpm4), mRNA. 11/22Length	
1774	1514	NM_012678	bb	= 9	Tropomyosin 4
				Rattus norvegicus Dystrophin	Tropolityosiii 4
i		•		(Dmd), mRNA. 11/22Length =	
1775	425	NM_012698	hh	124	Ductrookin
				Rattus norvegicus	Dystrophin
1				prostaglandin E receptor 3 (	
				cubturo ED3VDt2	
1776	501	NM_012704	lii	subtype EP3)(Ptger3), mRNA.	
		11111_012104		1/22Length = 1253	Rat kidney prostaglandin EP3 receptor
l			1	Rattus norvegicus	
- 1				prostaglandin E receptor 3 (	
4770	500			subtype EP3)(Ptger3), mRNA.	
1776	503	NM_012704	n,o	1/22Length = 1253	Rat kidney prostaglandin EP3 receptor
]		i			produgicinal Li o receptor
1				Rattus norvegicus proteosome	
Ī				(prosome, macropain) subunit,	
- 1				beta type 9 (large multifunctiona	,[
				protease 2) (Psmb9), mRNA.	
1777	4003	NM_012708	le	11/22Length = 88	
			<del> </del>	Rattus norvegicus	Low molecular mass polypeptide 2
i				adrename dell's (4.1.)	
1778	322	NM_012715	d ==	adrenomedullin (Adm), mRNA.	
1778 322	MM_012/15	d,gg	11/22Length = 1395	Adrenomedullin	
- 1				Rattus norvegicus Solute	
			İ	carrier 16 (monocarboxylic acid	
1				transporter), member 1	
				(Slc16a1), mRNA. 11/2Length =	Solute carrier 16 (monocarboxylic acid transporter
1779	20888	NM_012716	c,e	332	member 1
				Rattus norvegicus Solute	inchiper 1
	1		(	carrier 16 (monocarboxylic acid	
				transporter), member 1	
				(Sic16o1) mDNA 44/01	
1779	20889	NM_012716	e,aa,bb	332	Solute carrier 16 (monocarboxylic acid transporter)
****	20000	1414_012710	le,aa,bb	JJZ	member 1
				Rattus norvegicus Calcitonin	
i	1		ł i	receptor-like receptor	
1700	4000	NN 04074-	][	(Calcri),mRNA. 11/22Length =	
1780	1632	NM_012717	u,v	295	Calcitonin receptor-like receptor
				Rattus norvegicus lipase A,	- Inter-
				lysosoma! acid (Lipa),	
1781	<u>255</u> 63	NM_012732	f,g	mRNA.1/22Length = 3144	Cholesterol esterase (pancreatic)
				Rattus norvegicus lipase A,	onoresteror esterase (pancreatic)
				lysosomal acid (Lipa),	
1781	16613	NM_012732			Obstacland 1
			9	Rattus norvegicus retinol-	Cholesterol esterase (pancreatic)
ļ	i		[ [		
1782	23806	VM_012733		binding protein 1 (Rbp1),	
.,,,,,	200001	*IVI_U 12/ 33	j,k	mRNA.11/22Length = 695	Retinol-binding protein 1
}				Rattus norvegicus Hexokinase	
4700	0500			2 (Hk2), mRNA. 11/22Length =	
1783	25264	NM_012735	y,z,gg	3635	
	-			Rattus norvegicus Giycerof-3-	
			ĺ	phosophate dehydrogenase	
	1		12	(Mitochonddal) (Gnay works )	Chrosel 2 shapes + 1 1 1 1 =
1784	25650	IM_012736	a la	11/2Length = 24	Glycerol-3-phosophate dehydrogenase 2
		4 121 00			(mitochondrial)
				Rattus norvegicus Pyruvate	
1785	1470	IM_012744		carboxylase (Pc), mRNA. 1/2Length = 3945	

	1	GenBank /	Acc:	Property of the second	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	Grec II	No.	Model Co		
					Unigene Sequence Cluster Title
	1			Rattus norvegicus signal	
	1		ļ	transducer and activator of	
1786	34:	NM_01274	7 n,o	transcription 3 (Stat3), mRN	VA. ∤
			, 11,0	11/22Length = 2924	Signal transducer and activator of transcription
		İ	- 1	Raitus norvegicus Nucleolii	n or transcription.
1787	8829	NM_012749	j,k,hh,kk	(Nci), mRNA. 11/22Length =	
			אַרוווויער	2142	Nucleolin
				Rattus norvegicus Glucose	
		1		transporter 4, insuline-	
1788	3600	NM_012751	а	responsive (Glut4), mRNA.	solute carrier family 2 (facilitated glucose
				11/22Length = 256	transporter), member 4
1				Rattus norvegicus Glucose	
				transporter 4, insuline-	
1788	3601	NM_012751		responsive (Glut4), mRNA.	solute carrier family 2 (facilitated glucose
		012/01		11/22Length = 256	
				Rattus norvegicus Fyn proto	-
1789	13731	NM_012755	l <sub>r</sub>	oncogene (Fyn), mRNA.	
		012700	<del> '</del>	9/22Length = 1844	Fyn proto-oncogene
- 1	1		1	Rattus norvegicus insulin-like	
1790	15174	NM_012756	_	growth factor 2 receptor (lgf2)	r).
		1111_012750	m	mRNA. 11/22Length = 881	Insulin-like growth factor 2 receptor
l	1			Rattus norvegicus caspase 1	
1791	180661	VM_012762	aa,bb	(Casp1), mRNA. 11/22Length	) =
	- 100001	111_012102	aa,00	129	Interleukin 1beta converting enzyme
				Rattus norvegicus caspase 1	
1791	18068	M_012762	10	(Casp1), mRNA. 11/22Length	=
	70000	111_012702	e	129	Interleukin 1beta converting enzyme
			1	Rattus norvegicus Cyclin D3	
1792	17257 N	M_012766	o so bb so 6	(Ccnd3), mRNA. 11/22Length	=
	1120111		e,aa,bb,ee,f		Cyclin D3
ł	ŀ		1	Rattus norvegicus Cyclin D3	
1792	17261 N	M_012766	l m	(Ccnd3), mRNA. 11/22Length	=
		012700	l,m	1843	Cyclin D3
	1			Rattus norvegicus aquaporin 1	
1793	5758 N	M_012778	223	(Aqp1), mRNA. 11/22Length =	Aquaporin 1 (aquaporin channel forming integral
	0700 111	W_012176	p,q,s,t	2623	
	1		1	Rattus norvegicus aquaporin 5	
1794	104 NI	M_012779	1	(Aqp5), mRNA. 11/22Length =	
		014113	ļii	1426	Aquaporin 5
1			1	Rattus norvegicus Cytochrom	C
			1	oxidase subunit VIII-H	
1795	449 NIA	1_012786	hh	(heart/muscle) (Cox8h), mRNA.	
<del>-  </del> -		_012700	1111	111/22Length = 33	Cytochana
- 1	- 1			Rattus norvegicus Cytochrom o	(nearymuscle)
1				oxidase subunit VIII-H	J
795	450 NM	_012786	f h.h	(heart/muscle) (Cox8h), mRNA.	
	10011414	_012/00	f,hh	11/22Length = 33	Cytochrome c oxidase subunit VIII-H (heart/muscle)
- 1	- 1			Della	(near/muscle)
1				Rattus norvegicus Drosophila	
-	I			discs-large tumor	
				suppressorhomologue (synapse	
796	1952 NM	012700		(associated protein) (Dlg1).	Drosophila discs-large tumor suppressor
7	.002 1414]	V12/00	99	mRNA. 11/2Length = 3256	homologue (synapse associated protein)
į	1			Rattus norvegicus Dual	To hope associated protein)
1	İ	1		Specificity Yak1-related kinase	ļ
797 2	4113 NM_	042704		(Dyrk),mRNA. 11/22Lenath =	dual-specificity tyrosine-(Y)-phosphorylation
	7 LLSHVIV)	.012791 Je		284	

3.20	1	GenBa	nk Acc		12.4 (4.1 (4.1 (4.1 (4.1 (4.1 (4.1 (4.1 (4	Atty. Ref. 44921-5090-01-WO/2105485
SEQ.ID	GLGC	IDINO	iik Acc.	Model Code		All the state of t
-2504		.5 1.10.	3,70%	Model Code		Unigene Seguence Cluster Title
	ł				Rattus norvegicus Dual	
	ł	1		}	Specificity Yak1-related kinase	9
1797	104	35			(Dyrk),mRNA. 11/22Length =	ESTs, dual-specificity tyrosine-(Y)-phosphorylation
1/9/	181	35 NM_01	2791	e,gg,li	284	regulated kinase 1a
					Rattus norvegicus	- Santos Isriado 70
	1			1	Guanidinoacetate	
	l	j			methyltransferase	
					(Gamt),mRNA. 11/22Length =	
1798	169	7 NM_012	2793	b,u,v,jj,kk	924	Guanidinogantata
					Rattus norvegicus glutathione	Guanidinoacetate methyltransferase
	1			]	transferase, theta 2 (Gstt2),	٠ .
1799	96	1 NM_012	796	g	mRNA. 9/22Length = 1258	ability of the second
					111 UV C 0/22Lengur - 1236	glutathlone S-transferase, theta 2
		1			Rattus norvegicus Inhibitor of	
		ĺ			DNA hinding 4 halfala a	
				ĺ	DNA binding 1, helix-loop-helix	
1800	1024	8 NM_012	707	h 11a - 4 - 111	protein (splice variation) (ld1),	Inhibitor of DNA binding 1, helix-loop-helix protein
-1000	1024	O INIVI_UIZ	191	b,j,k,s,t,u,jj,kk	mRNA. 1/22Length = 1124	((splice variation)
					Rattus norvegicus Smoothene	d
1801	2004	0 104 040			(Smoh), mRNA. 1/22Length =	
1001	2024	6 NM_012	807	l,m,s	2382	Smoothened
					Rattus norvegicus alpha-	
1		1			methylacyl-CoA racemase	
					(Amacr), mRNA. 11/22Length =	
1802	1503	2 NM_0128	316	j,k,jj,kk	154	alpha-methylacyl-CoA racemase
					Rattus norvegicus Annexin III	alpha-filetrylacyi-CoA racemase
1			- 1		(Lipocortin III) (Anx3),	
1803	2135	NM_0128	323	ii	mRNA.11/22Length = 1454	Anneste 40
				***************************************	mada i i i i i z z z z z z z z z z z z z z	Annexin A3
					Rattus norvegicus Cystatin beta	
1804	2853	NM_0128	38	n,o	(Coth) mphia 44(0)	
				110	(Cstb), mRNA. 11/2Length = 59 Rattus norvegicus Epithelial	Cystatin beta
					mambrana malifi 4 (5)	
1805	338	NM_0128	43		membrane protein 1 (Emp1),	
		1441_0120	<del>7</del> 5		mRNA.11/22Length = 981	Epithelial membrane protein 1
[			1		Rattus norvegicus Epoxide	
ı			- 1		hydrolase 1 (microsomal	
1806	17511	NIA 0400	1		xenobiotic hydrolase) (Ephx1),	Epoxide hydrolase 1 (microsomal xenobiotic
1000	1/541	NM_0128	44	,d	mRNA. 1/22Length = 1242	hydrolase)
			- 1		Rattus norvegicus Growth	
1			- 1	ſ	hormone - releasing receptor	
40.5					(Ghrhr), mRNA. 11/2Length =	
1807	1249	NM_0128	50 Ju	,v	1629	Growth hormono, releasing and
					Rattus norvegicus Lysosomal	Growth hormone - releasing receptor
1					associated membrane protein 1	
1				l.		1
1808	18770	NM_01285	57 h		44/01	Lysosomal associated membrane protein 1 (120
					Rattus norvegicus Matrix Gla	kDa)
- 1	ł			i.	orotoin (Man) - Dila	
1809	13151	NM_01286	2	,o,ii	protein (Mgp), mRNA.	
		0120C	<del>~  ''</del>		11/22Length = 521	Matrix Gla protein
ļ	}			l.	Rattus norvegicus nuclear	
	J			15	ranscription factor-Y gamma	
1810	4220	NIM 0400-			Nfyc),mRNA. 11/22Length =	
1810	4338	NM_01286	6 u,		23	CCAAT binding factor of CBF-C/NFY-C
	1			T	rattus norvegicus	
الممه	0.40:-			lo		tumor necrosis factor receptor superfamily, member
1811	24617	VM_01287	0 ii	i1	1/22Length = 2432	11b (osteoprotegerin)
]	1		T		Rattus norvegicus Ribosomal	. 15 (ostgobrorgatiti)
				0	rotein L39 (Rpl39), mRNA.	
1812	20945	M_01287	5 cc	,dd 1		Ribosomal protein L39

116	1 2	GenBank Acc	े हैं। <u>जन्म स्टब्स्टर</u>		Atty, Ref. 44921-5090-01-WO/2105485
ĘO ID	igi go ir	No.			· 通過影響的 化自然表示 化激素 化二氯甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基
حري با	OLOC IL	ZINO.	Model Code	the second secon	Unigene Sequence Cluster Title
	1	,		Rattus norvegicus Ribosomal	
1813	4720		1	protein S29 (Rps29), mRNA.	
1013	1/300	NM_012876	g,hh	11/22Length = 318	Ribosomal protein S29
	)	ł		Rattus norvegicus Ribosomal	
1813	17206	NN4 040070	1.	protein S29 (Rps29), mRNA.	
1013	17300	NM_012876	_ f	11/22Length = 318	Ribosomal protein S29
				Rattus norvegicus secreted	
1814	22054	NN4 040004		phosphoprotein 1 (Spp1),	
1014	23031	NM_012881	h,l,n,o,w,x	mRNA.11/22Length = 1457	Sialoprotein (osteopontin)
				Rattus norvegicus	
		1		Thymopoletin (lamina	
				associated polypeptide2)	
1815	16074	NIM 040007	1	(Tmpo), mRNA. 11/2Length =	
1013	100/1	NM_012887	y,ii	358	Thymopoletin (lamina associated polypeptide 2)
				Rattus norvegicus Adenosin	, , , , , , , , , , , , , , , , , , ,
1816	16700	NM 010005	l	kinase (Adk), mRNA.	
1010	10/08	NM_012895	u,v	11/22Length = 1123	Adenosin kinase
l			İ	Rattus norvegicus Acid nuclear	
- 1				phosphoprotein 32 (leucine rich	)
1817	197	NIM 040000	L	(Anp32), mRNA. 11/2Length =	
1017	107	NM_012903	r	117	Acid nuclear phosphoprotein 32 (leucine rich)
1				Rattus norvegicus Annexin 1	
1818	7100	NIM 040004		(p35) (Lipocortin 1) (Anx1),	
1010	/ 190	NM_012904	a,ll	mRNA.11/22Length = 142	Annexin 1 (p35) (Lipocortin 1)
- 1				Rattus norvegicus Aortic	
			1	preferentially expressed gene 1	
1819	1934	NM_012905	٠	(Apeg1), mRNA. 11/22Length =	
1010	1054	14141_012905	d	138	Aortic preferentially expressed gene 1
1				Rattus norvegicus Arrestin,	
1820	16581	NM_012911		beta 2 (Arrb2), mRNA.	
1020	10001	1401_012911	gg	11/22Length = 1758	Arrestin, beta 2
i				Rattus norvegicus Activating	
				transcription factor 3	
1821	24431	VM_012912	22222	(Atf3),mRNA. 11/22Length =	
100	2.7011	1012312	a,p,q,y,z,ee,ff	1893	Activating transcription factor 3
	[	:		Rattus norvegicus ATPase,	
	1			Ca++ transporting,	
1822	24783	NM_012914	kk	ubiquitous(Atp2a3), mRNA.	
.	200	1111_012014	INN	11/22Length = 4472	ATPase, Ca++ transporting, ubiquitous
1	j			Rattus norvegicus ATPase inhibitor (rat mitochondrial	
				IF1protein) (Atpi), mRNA.	
1823	6108	M_012915	С	4.401	ATD. I I I I I I I I I I I I I I I I I I I
$\neg \uparrow$				Rattus norvegicus Calcium	ATPase Inhibitor (rat mitochondrial IF1 protein)
	}			channel subunit alpha 2	
	J			delta(dihydropyridine - sensitive	
	. [				
824	1765 N	IM_012919		4/001 11 004	calcium channel, voltage-dependent, alpha2/delta
		_=		Rattus norvegicus Cyclin G1	subunit 1
1	-	1	],	(Cong1), mRNA. 11/22Length =	
825	20757 N	M_012923		0400	Stralin C4
				Rattus norvegicus Cell surface	Cyclin G1
	1			glycoprotein CD44	
	-	1		hyaluronatebinding protein)	
i	i	i	11	A 144 —	Coll purfoce above and at 1 and a second
826	1625 N	M_012924	gg (2	(00	Cell surface glycoprotein CD44 (hyaluronate bindir
			29		protein)

ABLE	1.7	GenBank Acc	\$ 14.00 10.00		Atty, Ref. 44921-5090-01-WO/2105485
EQ ID	GLGC	D No.		Known Gene Name	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	OLCO!	2 140.	Intodei Code		Unigene Sequence Cluster Title
	l	1		Rattus norvegicus Carnitine	
		1		palmitoyltransferase 2	
				(Cpt2),mRNA. 11/22Length =	
1827	197	7 NM_012930	a,w,x,cc,dd	2296	Carnitine palmitoyltransferase 2
				Rattus norvegicus v-crk-	Oarmane pairintoyta ansierase 2
	]			associated tyrosine kinase	
	ļ			substrate (Cdass) - DAIA	
1828	1860	4 NM_012931	111.00	substrate (Crkas), mRNA.	
7020	1003	7 1VIVI_012931	j,k,gg	11/22Length = 3335	v-crk-associated tyrosine kinase substrate
		ŀ		Rattus norvegicus v-crk-	
		1		associated tyrosine kinase	
4000				substrate (Crkas), mRNA.	
1828	1869	5 NM_012931	j,k,y,z	11/22Length = 3335	v-crk-associated tyrosine kinase substrate
				Rattus norvegicus Crystallin,	Crystallin, alpha polypeptide 2, ESTs, ESTs,
				alpha polypeptide 2 (Cryab),	Modely similar to Taccory
1829	1372	3 NM_012935	aa,bb	mRNA. 11/21Length = 528	Weakly similar to T46637 transcription factor 1,
		1	,	Rattus norvegicus crystallin,	neural - rat [R.norvegicus]
ľ		1	]	hota B2 (C-15-10)	
1830	10	NM_012937	_	beta B2 (Crybb2), mRNA.	
.500	70	14101_01293/	n	11/22Length = 735	R.norvegicus CRYBB2 gene (crystallin, beta B2)
ļ			1		
		1	1	Rattus norvegicus Cytochrome	
40-1			1_	P45 1b1 (Cyp1b1), mRNA.	
1831	190	NM_012940	j,k	11/2Length = 4964	Cytochrome P450 1b1
ı				Rattus norvegicus Cytochrom	Oylocationie P450 101
			1	P45 Lanosterol 14 alpha-	
1			1	demothylese (Cyr.E4)	}
1832	20928	NM_012941	l,m	demethylase (Cyp51), mRNA.	
		1111_012041	1,111	11/22Length = 226	Cytochrom P450 Lanosterol 14 alpha-demethylas
- 1				Rattus norvegicus Diphtheria	
			]	toxin receptor (heparin binding	1
j				epidermal growth factor - like	
4000				growth factor) (Dtr), mRNA.	Diphtheria toxin receptor (heparin binding
1833	223	NM_012945	a,p,q,ee,ff	11/2Length = 155	epidermal growth factor - like growth factor)
				Rattus norvegicus Heat shock 1	personnal growth factor - like growth factor)
			] .	kD protein 1 (chaperonin 1)	
				(Hspe1), mRNA. 11/2Length =	
1834	5033	NM_012966	s,t	(113961), IIIKNA. 11/2Lengin =	
		5,2000	-,-		Heat shock 10 kD protein 1 (chaperonin 10)
- 1				Rattus norvegicus Heat shock 1	
1				kD protein 1 (chaperonin 1)	
1024	E004	NINA CACCOCC		(Hspe1), mRNA. 11/2Length =	
1834	5034	NM_012966	ee,ff	68	Heat shock 10 kD protein 1 (chaperonin 10)
				Rattus norvegicus Intercellular	Total Total Total
			ļ.	adhesion molecule 1 (lcam1),	
1835	2555	NM_012967	a,y,z,kk	mRNA. 11/2Length = 262	Intercellular adhanian mast
				Rattus norvegicus Laminin	Intercellular adhesion molecule 1
			[,	chain heta 2 /l ambox mara	
1836	22434	NM_012974	lm [	chain beta 2 (Lamb2), mRNA.	
		012014	l,m ·	11/2Length = 5581	Laminin chain beta 2
		ļ		Rattus norvegicus Laminin	
1026	20406	NA 04007:	ļ	chain beta 2 (Lamb2), mRNA.	•
1836	22435	NM_012974	C	11/2Length = 5581	Laminin chain beta 2
	- 1			Rattus norvegicus Lectin,	- Conditi Bold 2
1		ĺ		galactose binding, soluble	
	- 1			(Galectin-5) (Lgals5), mRNA.	
1837	956	NM_012976			1 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	300			1/2Length = 872	Lectin, galactose binding, soluble 9 (Galectin-9)
1	- 1		'	verras ucivedicas raciu,	
!	1		[9	alactose binding, soluble	
			18	(Galectin-y) (Lgalsy), mkna.	
1838	، ایدیم	NM_012977 i		1/2Length = 1545	

ABLE 1	•	GenBank Acc	N	1 · · · A	Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GI GO IF	No.:			4 1 17 A 17 A 17 A 17 A 17 A 17 A 17 A 1
ا جاري	GLGGIL	NO.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
				Rattus norvegicus Lectin,	The second secon
		1		galactose binding, soluble	
	ľ		1	9(Galectin-9) (Lgals9), mRNA	
1838	958	NM_012977	kk	11/2Length = 1545	
			<del> </del>	Rattus norvegicus Msh	Lectin, galactose binding, soluble 9 (Galectin-9)
ı				(Dragabile)	
			ł	(Drosophila) homeo box	
1839	574	NINA 040000		homolog (Msx2),mRNA.	
1003	- 37	NM_012982	cc,dd	11/22Length = 42	Msh (Drosophila) homeo box homolog
1			l	Rattus norvegicus Nuclear	, y women box nomolog
1040	70.4			Factor IA (Nfia), mRNA.	
1840	/64	NM_012988	ee,ff	11/2Length = 3368	Nuclear Factor IA
				Rattus norvegicus	Tradical Factor IA
- 1		1		Nucleoplasmin-related protein	
- 1				(Nuclearprotein B23 (Npm1),	
1841	17394	NM_012992	hh,kk	mRNA. 11/2Length = 1232	<b>1</b> , , , , , , , , , , , , , , , , , , ,
			1	Rattus norvegicus Protein	Nucleoplasmin-related protein (Nuclear protein B2
-			1	disulfide isomerses (Dec)	
			1	disulfide isomerase (Prolyl4-	
1				hydroxylase, beta polypeptide)	
1842	10202	NM_012998		(P4hb), mRNA. 11/2Length =	Protein disulfide isomerase (Prolyl 4-hydroxylase
1042	19090	NW_012998	h,I	246	beta polypeptide)
				Rattus norvegicus Subtilisin -	
40.40				like endoprotease (Pace4).	
1843	24263	NM_012999	f	mRNA. 1/21Length = 4153	Subtilisin - like endoprotease
				Rattus norvegicus Subtilisin -	Subulisin - like endoprolease
1			1	like endoprotease (Pace4),	
1843	24264	NM_012999	g	mRNA. 1/21Length = 4153	0.130
			19	Rattus norvegicus	Subtilisin - like endoprotease
- 1	1		1		
- 1				phosphatidylethanolamine N-	
1844	2/718	NM_013003	ļ <u>.</u>	methyltransferase(Pemt),	
	247 10	VIVI_013003	<u>                                    </u>	mRNA. 11/22Length = 893	Phosphatidylethanolamine N-methyltransferase
!					,
- 1	1			Rattus norvegicus Protein	
	i			kinase, AMP-activated, gamma	
40.45				1non-catalytic subunit (Prkga1).	
1845	1467	NM_013010	ii	mRNA. 11/22Length = 1328	Protein kinase, AMP-activated, gamma
ı				Rattus norvegicus Tyrosine 3-	Totelli kinase, Alvir-activated, gamma
i	1	ĺ		monooxygenase/tryptophan 5-	
				monooxygenase activation	
1	1			protein, zeta polypeptide	
!	- 1		i	(Vishaz) mDNA 44/001	
1846	25279 N	IM_013011	n.,	(Ywhaz), mRNA. 11/22Length =	Tyrosine 3-monooxygenase/tryptophan 5-
		0 10011	p,q	1687	monooxygenase activation protein, zeta polypeptid
1				Rattus norvegicus Tyrosine 3-	120,000
		1		monooxygenase/tryptophan 5-	
ĺ		i		moncoxygenase activation	
	- 1	ł	1	protein, zeta polypeptide	
4046			Į,	(Ywhaz), mRNA. 11/22Length =	Tyrosine 3-monooxygenase/tryptophan 5-
1846	3404 N	M_013011	p,q	1687	monogygenase activeties
i				Rattus norvegicus Prosaposin	monooxygenase activation protein, zeta polypeptide
:	- 1		la la	sulfated	
1	1	j		glycoprotein,sphingolipid	
- 1		1	ļ.	and the second second	
1847	23545IN	M_013013	,m ,i	nydrolase activator) (Psap),	Prosaposin (sulfated glycoprotein, sphingolipid
		0 100 10	,,,, l	iiriva, i i/2Length = 2175	hydrolase activator)
- 1			1.	ratius norvegicus Persephin	
1848	70170141	14 042044	J(	Pspn), mRNA. 11/22Length =	
1040	201/8 N	M_013014 v	V <sub>1</sub> X 4	171	Persephin
İ	ł		T	Rattus norvegicus Ras-related	
:	i	i	s	mall GTP binding protein 3A	
. 1			la	Rab3a), mRNA. 11/2Length =	
349	20229 N	И_013018 k	k là	140	Ras-related small GTP binding protein 3A

TABLE 1		e .			Atty. Ref. 44921-5090-01-WO/2105485
		GenBank Acc.		[1] (1) 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	( ) 製 ( ) 製
SEQ ID	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title:
				Rattus norvegicus RhoA -	and the state of t
1	ĺ			binding serine/threosine kinase	
			1	alpha (ROK - alpha) (Rock2),	RhoA - binding serine/threosine kinase alpha (ROK -
1850	1338	NM_013022	r	mRNA. 11/2Length = 447	alpha)
				Rattus norvegicus	
				Selenoprotein W muscle 1	
				(Sepw1), mRNA. 7/21Length =	
1851	17894	NM_013027	gg	664	Selenoprotein W muscle 1
1				Rattus norvegicus Solute	
•				carrier family 34 (sodium	
i i				phosphate), member 1	
4050	4=4=4			(Slc34a1), mRNA. 11/22Length	R.norvegicus ASI mRNA for mammalian equivalent
1852	1/1/4	NM_013030	l,m	= 244	of bacterial large ribosomal subunit protein L22
1				Rattus norvegicus Solute	
1				carrier family 34 (sodium	
				phosphate), member 1	
1050	40076	NINA 040000		(Slc34a1), mRNA. 11/22Length	Solute carrier family 17 (sodium/hydrogen
1852	100/6	NM_013030	cc,dd	= 244	exchanger), member 2
				Rattus norvegicus ATP-binding	
			1	cassette, sub-family C	
				(CFTR/MRP), member 9	
1853	722	NM_013040	: L	(Abcc9), mRNA. 4/22Length =	ATP-binding cassette, sub-family C (CFTR/MRP),
1000	755	14141_013040	j,k	6628	member 9
1 1				Rattus norvegicus Transforming	
1 1				growth factor beta stimulated	
1 1				glowin lactor beta stimulated	
1854	17401	NM_013043	2 n a 7 ee ff bb	clone 22 (Tgfb1i4), mRNA. 11/2Length = 1666	
		1411_010040	a,p,q,z,ce,11,kk	Rattus norvegicus Tryrotropin	Transforming growth factor beta stimulated clone 22
				releasing hormone (Trh),	
1855	11113	NM_013046	l,k,p,q,u,v,gg	mRNA. 11/22Length = 768	Thurstronin releasing house
			11.1514101199	Rattus norvegicus Tryrotropin	Thyrotropin releasing hormone
		-		releasing hormone (Trh),	
1855	11114	NM_013046	k,n,o,y,z,kk	mRNA. 11/22Length = 768	Thyrotropin releasing hormone
			7.7077	Rattus norvegicus Coagulation	Triyronopiii releasing normone
				factor III (thromboplastin,	
				tissuefactor) (F3), mRNA.	
1856	24874	NM_013057	r	11/2Length = 1683	Coagulation factor III (thromboplastin, tissue factor)
					(unonibopiasun, ussue lactor)
				Rattus norvegicus Inhibitor of	
[				DNA binding 3, dominant	
				negative helix-loop-helix protein	Inhibitor of DNA binding 3, dominant negative helix-
1857	15253	NM_013058	n,o,s,t	(Id3), mRNA. 11/22Length = 568	loop-helix protein
	,			Rattus norvegicus alkaline	
		ļ		phosphatase, tissue-	
]				nonspecific(Alpl), mRNA.	
1858	14997	NM_013059	e,ee,ff	11/22Length = 2415	Tissue-nonspecific ALP alkaline phosphatase
				Rattus norvegicus Protein	
1				phosphatase 1, catalytic	
4050	2420~	NIA 048005	,	subunit,beta isoform (Ppp1cb),	Protein phosphatase 1, catalytic subunit, beta
1859	2128/	NM_013065	l,m	mRNA. 11/22Length = 276	isoform
			ı	Rattus norvegicus CD74	
			l l	antigen (invariant palaypeptide	1
	- 1	İ	į.	of majorhistocompatibility class	
1860	16024	VIM 013000			CD74 antigen (invariant polypeptide of major
1000	10824	VM_013069	c,cc,dd	mRNA, 11/2Length = 115	histocompatibility class II antigen-associated)

1. 1.		GenBank <sup>®</sup>	Acc:	3 20 46 - 1 12 7 14 15 15 15 15 15 15 15 15 15 15 15 15 15	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	ID No.	Acc. Model Code	Known Gene Name	1.1.1.11.11.11.11.11.11.11.11.11.11.11.
					Unigene Sequence Cluster Title
	1	ł		Rattus norvegicus CD74	
	i			antigen (invariant polpypeptic	de
			ĺ	of majorhistocompatibility cla	ss
4000	400			II antigen-associated) (Cd74)	, CD74 antigen (invariant polpypeptide of major
1860	169	25 NM_01306	9 c,n,o	mRNA. 11/2Length = 115	
				Rattus norvegicus CD74	histocompatibility class II antigen-associated)
		1		antigen (invariant polpypeptid	
		1		of majorhistocompatibility class	
				If antigen-associated) (Cd74),	
1860	169	26 NM_01306	9 c	manugeri-assuciated) (Cd/4),	
			<u> </u>	mRNA. 11/2Length = 115	histocompatibility class II antigen-associated)
- 1				Rattus norvegicus CD74	
İ				antigen (invariant polpypeptid	e
			1	of majorhistocompatibility class	s .
4000				Il antigen-associated) (Cd74),	
1860	2567	6 NM_013069	9  c,m	mRNA. 11/2Length = 115	
1				Rattus norvegicus Protein-L-	
- 1			1	isoaspartate (D-aspartate) O-	
- 1		j		methyltransferase (Pcmt1),	
1861	1718	1 NM_013073	100	metrytransferase (Pcmt1),	Protein-L-isoaspartate (D-aspartate) O-
		77414_010070	gg	mRNA. 11/22Length = 1658	methyltransferase
j			İ	Rattus norvegicus Protein-L-	
- 1				isoaspartate (D-aspartate) O-	
1861	0400	0.11.		methyltransferase (Pcmt1),	Protein-L-isoaspartate (D-aspartate) O-
1001	2183	0 NM_013073	aa,bb	mRNA. 11/22Length = 1658	methyltransferase
ł		į		Rattus norvegicus Ornithine	- Instry to carolic a de
				carbamoyltransferase (Otc),	
1862	<u> 1328:</u>	3 NM_013078	b	mRNA. 11/2Length = 1519	0-14-1-
				Rattus norvegicus syndecan 2	Ornithine carbamoyltransferase
- 1		1		(Sdc2), mRNA. 11/22Length =	
1863	1529	NM_013082	hh	(2153	
		10.0002			Ryudocan/syndecan 2
- 1				Rattus norvegicus Acyl-	
				Coenzyme A	
İ				dehydrogenase,short-branched	•
1001	00040			chain (Acadsb), mRNA,	Acyl-Coenzyme A dehydrogenase, short-branched
1864	20242	NM_013084	gg	11/2Length = 1322	Ichain
				Rattus norvegicus Urinary	Mail
				plasminogen activator,	
- 1				urokinase(Plau), mRNA.	
1865	20878	NM_013085	Ь	11/2Length = 1454	1,12
					Urinary plasminogen activator, urokinase
	İ			Pattus noncentario Comm	
			alka - · · -	Rattus norvegicus CAMP	
1866	257	NIM 042000	a,j,k,p,q,y,z,ee	responsive element modulator	
1000	337	NM_013086	,ff	(Crem),mRNA. 11/2Length = 67	CAMP responsive element modulator
				Rattus norvegicus CD81	
J	í			antigen (target of	
	- 1		1	antiproliferativeantibody 1)	
	- 1		1	(Cd81), mRNA. 11/2Length =	
1867	8899	NM_013087		133	0004 11 11
			<del>                                     </del>		CD81 antigen (target of antiproliferative antibody 1)
	ľ			Pattue populations T	
	- 1		1	Rattus norvegicus Tumor	
1868	1521	NM_013091		necrosis factor receptor (Tnfr1),	Tumor necrosis factor receptor superfamily,
	1021	4141 019091	a,s,t,ee,ff,jj,kk	mRNA. 11/22Length = 213	member 1a
				Rattus norvegicus Hemoglobin.	
lecc	400	10.4.4		alpha 1 (Hba1), mRNA.	
1869	1684	VM_013096	b,c,v	11/2Length = 556	Hemoglobin clabs 4
ĺ				Rattus norvegicus Hemoglobin,	Hemoglobin, alpha 1
	- 1			alpha 1 (Hba1), mRNA.	
869	1685	IM_013096	b,c,v 1	4/01 11	
					Hemoglobin, alpha 1

TABLE		GenBank Ac	C. 17:403.000	·	Atty: Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC I	No.	Model Cod		The state of the s
	1 200 2 2	1	Model Cod	Transfer to the state of the st	Unigene Sequence Cluster Title
	1	1		Rattus norvegicus Hemoglobi	in,
1869	1688	NM_013096		alpha 1 (Hba1), mRNA.	
	1000	7/11//_013030	С	11/2Length = 556	Hemoglobin, alpha 1
		1		Rattus norvegicus Hemoglobii	n,
1869	1689	NM_013096	b,c,v	alpha 1 (Hba1), mRNA.	
	1.000	14141_013030	D,C,V	11/2Length = 556	Hemoglobin, alpha 1
		l		Rattus norvegicus Hemoglobir	n,
1869	26150	NM_013096	c,v	alpha 1 (Hba1), mRNA.	
		1.111_010000	C,V	11/2Length = 556	
			ŀ	Rattus norvegicus Guanine	
				nucleotide binding, protein,	
		,		alpha inhibiting polypeptide 3	
1870	19949	NM_013106	l,m	(Gnai3), mRNA. 11/2Length =	Guanine nucleotide binding, protein, alpha inhibitin
		7.11010100	11,111	Pattus populations ATP	polypeptide 3
1			1	Rattus norvegicus ATPase	
l		1	1	Na+/K+ transporting beta	
1871	23709	NM_013113	f,g	1polypeptide (Atp1b1), mRNA.	
			1,9	11/2Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
	1			Rattus norvegicus ATPase	
				Na+/K+ transporting beta	
1871	23710	NM_013113	hh	1polypeptide (Atp1b1), mRNA. 11/2Length = 2528	
			<del>                                     </del>	Rattus norvegicus Selectin,	ATPase Na+/K+ transporting beta 1 polypeptide
				platelet (Selp), mRNA.	
1872	38	NM_013114	aa,bb	11/22Length = 3185	
				7 1722 Lengur - 3103	Selectin, platelet
- 1	1		1	Rattus norvegicus	
	1		1	Prostaglandin F receptor (Ptgfr),	
1873	7854	NM_013115	h,l	mRNA. 11/22Length = 3	
			.,,	Rattus norvegicus CD38	Prostaglandin F receptor
ı			)	antigen (ADP-ribosyl cyclase /	
ŀ	1			cyclicADP-ribose hydrolase)	
				(Cd38), mRNA. 11/2Length =	0000 11 11-
1874	2005 N	IM_013127	e,bb	2248	CD38 antigen (ADP-ribosyl cyclase / cyclic ADP-
				Rattus norvegicus	ribose hydrolase)
				Carboxypeptidase E (Cpe),	
1875	21840 N	M_013128	w,ll		0-1
			<del></del>	Rattus norvegicus Annexin V	Carboxypeptidase E
				(Anx5), mRNA. 11/22Length =	
1876	16649 N	M_013132	c,gg	14447	Annovin V
				Rattus norvegicus Meprin 1	Annexin V
				alpha (Mep1a), mRNA.	
1877	5837 N	M_013143	cc,dd	144 (00)	Meprin 1 alpha
				Rattus norvegicus 5-	мерии гариа
		Į.		hydroxytryptamine (serotonin)	}
40-0				receptor 5A (Htr5a), mRNA.	
1878	786 Ni	VI_013148	1,0	144/001 1) 4==-	5-hvdrovytryptamino (coret-e-t-)
- 1		T			5-hydroxytryptamine (serotonin) receptor 5A
l				Rattus norvegicus Plasminogen	
4070				activator, tissue (Plat),	
1879	46 NA	/_013151 p	,q	mRNA.11/22Length = 2445	Plasminogen activator, tissue
- 1				Rattus norvegicus	deminiogen delivator, ussue
1		ŀ		CCAAT/enhancerbinding.	Į.
1000	040		k,p,q,y,z,gg,k	protein (C/EBP) delta (Cebpd),	• 1
1880	21682 NN	1_013154 k		mRNA. 11/2Length = 12	CCAAT/enhancerhinding seeded (0)
				Rattus norvegicus	CCAAT/enhancerbinding, protein (C/EBP) delta
- 1	- 1	1		CCAAT/enhancerbinding,	
1000			1	protein (C/EBP) delta (Cehnd)	
1880 2	21683 NM	_013154 e	j,k,p,q,y,z.kk	CNA 44101	CAAT/enhancerbinding, protein (C/EBP) delta
				···	was rengancementing protois (CIEDD) J-k-

10,000		GenBank Ac	2.11. (54. 3.5.	(a) (b) (b) (c) (c) (c) (c) (c) (c) (c) (c) (c) (c	Atty. Ref. 44921-5090-01-WO/2105485
EQ ID	GLGC I	No.	Model Code	Known Gene Name	Hariaga Cogus
			1,110,000, 49,90		Unigene Sequence Cluster Title
		j		Rattus norvegicus Very low	
		ļ	1	density lipoprotein receptor	
1881	24067	NIM 040455	1	(Vidir), mRNA. 11/22Length =	
1001	24007	NM_013155	kk	2952	Very low density lipoprotein receptor
				Rattus norvegicus Cathepsin L	- y - p-p-retent receptor
			1	(Ctsl), mRNA. 11/22Length =	
1882	3430	NM_013156	c,l,m,t,kk	1386	Cathepsin L
1				Rattus norvegicus Cathepsin L	Oddiop3ii1 E
ĺ				(Ctsl), mRNA. 11/22Length =	
1882	3431	NM_013156	c,kk	1386	0.11
			- OJAK	Rattus norvegicus Cathepsin L	Cathepsin L
				(Ctal) - DNA 44 199	
1882	25567	NM_013156	116.4.14	(Ctsl), mRNA. 11/22Length =	
1002	20001	141AI_0 19 190	j,k,t,kk	1386	
				Rattus norvegicus Insulin	
4000	404-	418.4	1	degrading enzyme (Ide), mRNA	
1883	1310	NM_013159		11/22Length = 4276	Insulin degrading enzyme
				Rattus norvegicus Max	
			1	interacting protein 1 (Mxi1),	ESTs Moderately similar to 149/4 DATA
1884	3465	NM_013160	h,l	mRNA.11/2Length = 922	ESTs, Moderately similar to MXI1_RAT MAX
			T:	Rattus norvegicus Pancreatic	interacting protein 1 (MXI1 protein) [R.norvegicus
				lipase (Pnlip), mRNA.	
1885	200	NM_013161	b,l,m	144/201 a- W. 4400	
		010101	0,1,111	11/22Length = 1492	Pancreatic lipase
- 1			1	5 "	
- 1				Rattus norvegicus solute carrier	r[
4000	2040		1	family 11 member 2 (Sic11a2),	Solute carrier family 11 member 2 (natural
1886	2012	NM_013173	r	mRNA. 1/22Length = 449	resistance-associated macrophage protein 2)
l			1		instance associated macropriage protein 2)
Ţ	ļ			Rattus norvegicus transforming	1
				growth factor, beta 3 (Tgfb3),	
1887	21722	NM_013174	jj,kk	mRNA. 11/22Length = 2633	Town of the state
			1111111	11122Lengu = 2033	Transforming growth factor, beta 3
!	1		l	Pattus pagracions to a f	
i	1		İ	Rattus norvegicus transforming	
1887	21723	NM_013174		growth factor, beta 3 (Tgfb3),	
1007	21/201	VIVI_013174	p,q	mRNA. 11/22Length = 2633	Transforming growth factor, beta 3
I I				Rattus norvegicus Hypocretin	
- 1	[			(orexin) neuropeptide	
400-				precursor(Hcrt), mRNA.	
1888	22306	NM_013179	aa,bb	11/2Length = 585	Hypocretin (orexin) neuropeptide precursor
				Rattus norvegicus Protein	
. 1	- 1	1		kinase, cAMP dependent,	
	- 1			regulatory, type 1 (Prkar1a),	
1889	1314/	IM_013181	f		D 11.1
	1		·	mRNA. 11/2Length = 1433	Protein kinase, cAMP dependent, regulatory, type
-	. ]	İ		i	
				Rattus norvegicus Hemopoletic	
	1250	N 04040=		cell tyrosine kinase (Hck),	
1900	1258	M_013185	hh	mRNA. 11/2Length = 1911	Hemopoletic cell tyrosine kinase
1890				Rattus norvegicus	J. Sound Initiado
1890				Phospholipase C, gamma 1	
1890				, , , , , , , , , , , , , , , , ,	
				(Plcq1), mRNA, 11/221 ength - 1	
1890	1714 N	M_013187	a,kk	(Plcg1), mRNA. 11/22Length = 516	Phoopheliness C
	1714 N	M_013187	a,kk	516	Phospholipase C, gamma 1
	1714 N	M_013187		516 Rattus norvegicus Myosin,	Phospholipase C, gamma 1
	1714 N	M_013187		516 Rattus norvegicus Myosin, heavy polypeptide 9, non-	Phospholipase C, gamma 1
1891				516 Rattus norvegicus Myosin, heavy polypeptide 9, non- muscle(Myh9), mRNA.	Phospholipase C, gamma 1
				516 Rattus norvegicus Myosin, heavy polypeptide 9, non- muscle(Myh9), mRNA. 11/22Length = 66	
1891			99	516 Rattus norvegicus Myosin, heavy polypeptide 9, non- muscle(Myh9), mRNA. 11/22Length = 66 Rattus norvegicus Interleukin 2	Phospholipase C, gamma 1  Myosin, heavy polypeptide 9, non-muscle
1891	1970 N		99	516 Rattus norvegicus Myosin, heavy polypeptide 9, non- muscle(Myh9), mRNA. 11/22Length = 66	

TABLE 1		GenBank Acc.	in the second second		Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GI GC ID	No.	Model Code	(   1   1   1   1   1   1   1   1   1	
OLG ID	i orda'in	NO	lylodei Code	Known Gene Name	Unigene Sequence Cluster Title
		į		Rattus norvegicus	
				Aminolevulinate synthase 2,	
1894	16//8	NM_013197	h	deita (Alas2), mRNA.	
1004	10440	NW_013197	b,c,v	11/2Length = 1899	Aminolevulinate synthase 2, delta
				Rattus norvegicus Dynamin 2	
1895	1693	NM_013199	00	(Dnm2), mRNA. 11/22Length = 3463	<b>D</b>
	1000	1410_010100	99	Rattus norvegicus Carnitine	Dynamin 2
			1	palmitoyltransferase 1, muscle	
				(Cpt1b), mRNA. 11/22Length =	Combine relieffeet
1896	20855	NM_013200	a,w,x,hh	2826	Carnitine palmitoyltransferase 1 beta, muscle
			uju pigrii.	Rattus norvegicus Camitine	isoform
				palmitoyltransferase 1, muscle	
				(Cpt1b), mRNA. 11/22Length =	Carpitino polmita disposione a 4 h d
1896	20856	NM_013200	a,w,x,aa,hh,ll	2826	Carnitine palmitoyltransferase 1 beta, muscle isoform
				Rattus norvegicus aflatoxin B1	13010111
			İ	aldehyde reductase (Afar),	
1897	20864	NM_013215	b,I,m	mRNA.11/22Length = 1272	aflatoxin B1 aldehyde reductase
					diadoxiii b1 alderiyde reddciase
i				Rattus norvegicus Ras homolog	
				enriched in brain (Rheb),	1
1898	23362	NM_013216	е	mRNA.11/2Length = 188	Ras homolog enriched in brain
				Rattus norvegicus afadin (AF-	The memoring of microca in brain
1899	20728	NM_013217	cc,dd,ee,ff	6), mRNA. 11/2Length = 5957	afadin
				Rattus norvegicus afadin (AF-	
1899	20729	NM_013217	jj,kk	6), mRNA. 11/2Length = 5957	afadin
4000				Rattus norvegicus afadin (AF-	
1899	20731	NM_013217	99	6), mRNA. 11/2Length = 5957	afadin
1900	20722	NIM 040047	,	Rattus norvegicus afadin (AF-	
1899	20/32	NM_013217	b,u,v	6), mRNA. 11/2Length = 5957	afadin
				Rattus norvegicus ankyrin-like	
1900	18313	NM_013220	la lik	repeat protein (Alrp),	
1300	10313	14141_013220	a,kk	mRNA.11/22Length = 1749	cardiac ankyrin repeat protein
	ļ			Rattus norvegicus HMG-box	
1901	1495	NM_013221	v 7 00 bb	containing protein 1 (Hbp1),	
- 7001	1,100	1414_010221	y,z,aa,bb	mRNA.11/22Length = 2642	HMG-box containing protein 1
1	ĺ			Rattus norvegicus growth	
1902	1396	NM_013222	d	factor, erv1 -like (Gfer), mRNA.11/22Length = 1226	Annual Control of the control of the
		0 ! ULLL	<del>-</del>	Rattus norvegicus ribosomal	augmenter of liver regeneration
				protein S26 (Rps26), mRNA.	
1903	815	NM_013224	g,h,l,w,x	11/22Length = 435	ribosomal protein S26
			J	Rattus norvegicus ribosomal	moosomai protein 826
				protein L32 (Rpl32), mRNA.	
1904	18305	NM_013226		11/22Length = 465	
				Rattus norvegicus adenylate	
1	1			cyclase activating polypeptide 1	
	j			(Adcyap1), mRNA. 11/22Length	
1905	17972	VM_016989		= 2681	adenylate cyclase activating polypeptide 1
				Rattus norvegicus adrenergic,	y of others don't during polypepulue 1
	l			alpha 1B, receptor	
4000				(Adra1b),mRNA. 11/22Length =	
1906	64 1	VM_016991	jj,kk	218	Adrenergic, alpha 1B-, receptor
				Rattus norvegicus arginine	Out of the test of
400-	04555		į	vasopressiii (איף), הותוא.	
1907	24868	NM_016992	n,o	11/22Length = 62	Arginine vasopressin (Diabetes Insipidus)
i				Rattus norvegicus arginine	
1907	04000	11.040555	<u> </u>	vasopressin (Avp), mRNA.	
14H7I	24869IN	NM_016992	n,o	141001 11 00	Arginine vasopressin (Diabetes insipidus)

TABLE		GenBank A~			Atty. Ref: 44921-5090-01-WO/2105485
SEO ID	GLGC	GenBank Acc		1. 其是 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	
	OLCO II	<b>3</b> [NO	Model Code	The state of the s	Unigene Sequence Cluster Title
				Rattus norvegicus	distance and the second
	1	1		Carboxypeptidase A1	
4000				(pancreatic) (Cpa1),mRNA.	
1908	2435	4 NM_016998	c	11/2Length = 131	Carbonamontidos a A 4 4
				Rattus norvegicus Cytochrom	Carboxypeptidase A1 (pancreatic)
	1	l		P45, subfamily IVB,	
	1	,		polypeptide1 (Cyp4b1), mRNA	
1909	20921	NM_016999	s,t	1/22Length = 192	
			19,1	Rattus norvegicus	Cytochrome P450, subfamily IVB, polypeptide 1
				Glycoroldobydo 2 -b - b	
			1	Glyceraldehyde-3-phosphate	
1910	8417	NM_017008	aa	dehydrogenase(Gapd), mRNA	
			aa	11/22Length = 1233	Glyceraldehyde-3-phosphate dehydrogenase
		1		Rattus norvegicus Glutamate	
į				receptor, ionotropic, N-methyl I	D-
1911	24676	NM_017010	laa bb	aspartate 1 (Grin1), mRNA.	Glutamate receptor, ionotropic, N-methyl D-
	27010	VIVI_017010	aa,bb	3/21Length = 4213	lachartato 1
				Rattus norvegicus Glutathione	
			[	S-transferase, mu type 2 (Yb2)	
1912	. 24042	NIM OATOLA		(Gstm2), mRNA. 11/2Length =	
1912	21013	NM_017014	b	155	Glutathione-S-transferase, mu type 2 (Yb2)
- 1				Rattus norvegicus	Transfer o transferase, fild type 2 (YD2)
4040	47045	*** * * * * * * * * * * * * * * * * * *		Glucuronidase, beta (Gusb),	
1913	1/815	NM_017015	w,x	mRNA. 11/22Length = 2472	Glucuronidase, beta
- }	1			Rattus norvegicus Interleukin 6	Oldodronidase, pela
4044				receptor (II6r), mRNA.	
1914	6598	NM_017020	j,k	11/22Length = 4614	Interleukin 6 receptor
- 1	- 1			Rattus norvegicus Lactate	Interleukin o receptor
				dehydrogenase A (Ldha),	
1915	17807	VM_017025	h,i	mRNA. 11/22Length = 169	I make to the control of the control
1				Rattus norvegicus	Lactate dehydrogenase A
- 1	İ			Phosphodiesterase 4B, cAMP-	
i	1	ļ	:	specific (dunce (Drosophila)-	
1	1		İ	homolog phosphodiesterase E4)	j
- 1			10	(Pde4b), mRNA. 4/22Length =	
1916	14247	M_017031 F	1,1	3133	Phosphodiesterase 4B, cAMP-specific (dunce
				Rattus norvegicus peripheral	(Drosophila)-homolog phosphodiesterase E4)
			l <sub>r</sub>	nyelin protein 22 (Pmp22),	1
1917	_ 4500 N	IM_017037  ii	i li	nRNA. 11/22Length = 1816	<u></u>
				Rattus norvegicus Protein	Peripheral myelin protein
J				hosphatase 2 (formerly	
-	1		15	A),catalytic subunit, alpha	
			2		
1918	3203 N	M_017039 c		soform (Ppp2ca), mRNA.	Protein phosphatase 2 (formerly 2A), catalytic
				112ELGHYHT - 104	subunit, alpha isoform
		1	1.	Rattus norvegicus Protein	
	1	1	lb.	hosphatase 2 (formerly	
		1	2	A),catalytic subunit, beta	
1919	24597 NI	М_017040 b.	is	oform (Ppp2cb), mRNA.	Protein phosphatase 2 (formerly 2A), catalytic
	00/ [14]	017040 D,	l,m,u,v 1	7/22CCHUUI - 1043	subunit, beta isoform
١.	!	1	1 6	vallus norvegicus Solute	1
Ì	1	1	C6	arrier family 4, member 2,	,
1		]	aı	nionexchange protein 2	
820	24207	1.047040	(S	Slc4a2), mRNA. 11/2Length =	Solute carrier family 4, member 2, anion exchange
220	-409/N	/_017048 u,	v,ii  45	57	Protein 2
ł			R	attus norvegicus Solute	TOTO IN A
,		Î	ica	rrier family 4, memper 3.	
ļ		1	1		
!		1	an	Nonexchange protein 3	
! : : :	24695 NN		an I(S	lonexchange protein 3 lc4a3), mRNA. 11/2Length = 15	Solute carrier family 4, member 3, anion exchange

TABLE?		GenBank Acc	(F)	TRIPLE STATE OF	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC'i	No.	Model Code	the contract of the contract o	A Marie Contract of the Contra
			, INIOGEI COGE	12 11 15 16 16 16 16 16 16 16 16 16 16 16 16 16	Unigene Sequence Cluster Title
		1		Rattus norvegicus Superoxide	
1922	2007	E NIM 047050	1	dismutase 1, soluble (Sod1),	
1322	2007	5 NM_017050	hh	mRNA.12/21Length = 65	Superoxide dismutase 1, soluble
			1	Rattus norvegicus Superoxide	The state of the s
4000				dismutase 1, soluble (Sod1),	
1922	20870	6 NM_017050	r	mRNA.12/21Length = 65	Superoxide dismutase 1, soluble
				Rattus norvegicus Sorbitol	
			1	dehydrogenase (Sord), mRNA.	
1923	1876	NM_017052	w,x	11/22Length = 1358	Sorbitol dehydrogenase
	•			Rattus norvegicus bcl2-	Corbitor derrydrogenase
- 1				associated X protein (Bax),	
1924	910	NM_017059	ld	mRNA. 11/22Length = 579	RelC enceptate to the
				Rattus norvegicus bcl2-	Bcl2-associated X protein
- 1				associated X protein (Bax),	
1924	911	NM_017059	d	mRNA. 11/22Length = 579	
				Rattus norvegicus bcl2-	Bcl2-associated X protein
				readus not vegicus boiz-	
1924	912	NM_017059	d,I,m	associated X protein (Bax),	
- 1021	012	14141_077000	U <sub>1</sub> 1111	mRNA. 11/22Length = 579	Bcl2-associated X protein
				Rattus norvegicus Hras-	
1925	10540	NIM 017000	L.	revertant gene 17 (Hrev17),	
1320	13043	NM_017060	h,l	mRNA. 1/22Length = 966	ESTs
			ļ	Rattus norvegicus lysyl oxidase	
4000	4040			(Lox), mRNA. 11/22Length =	
1926	1942	NM_017061	f,11	4557	Lysyl oxidase
				Rattus norvegicus lysyl oxidase	
				(Lox), mRNA. 11/22Length =	
1926	1943	NM_017061	s,t	4557	Lysyl oxidase
1				Rattus norvegicus Importin beta	L) b) i oxidase
	1,0			(Impnb), mRNA. 11/2Length =	1
1927	1427	NM_017063	hh	2991	Importin beta
				Rattus norvegicus Lysosomal-	Importin beta
1	ł			associated membrane protein 2	
1				(Lamp2), mRNA. 11/2Length =	
1928	6653	NM_017068	d	1548	llygger of a second of the sec
				Rattus norvegicus Lysosomal-	Lysosomal-associated membrane protein 2
	1			associated membrane protein 2	
- 1	}			(Lamp2) will a 14/01	
1928	6654	NM_017068	b,v	(Lamp2), mRNA. 11/2Length =	
-		····_017000	U,V		Lysosomal-associated membrane protein 2
[	- 1	1		Rattus norvegicus Glutamine	
- 1		1		synthetase (glutamate-	
1929	11152	NM_017073	ما داداد	ammonialigase) (Glul), mRNA.	
1020	11102	VIVI_U 1/U/3	c,s,t,kk	11/2Lengt = 2793	Glutamine synthetase (glutamate-ammonia ligase)
		t		Rattus norvegicus Glutamine	10 Ingusto
		I		synthetase (glutamate-	
1020	11450	NA 047075		ammonialigase) (Glul), mRNA.	
1929	111031	IM_017073	y,kk	11/2Length = 2793	Glutamine synthetase (glutamate-ammonia ligase)
- 1	- 1			I varios norvedicas Acetyl-Co A 1	(3.3 carridio caratronia figase)
	ĺ			acetyltransferase 1,	
400-				mitochondrial (Acat1), mRNA.	
1930	18956 N	IM_017075 a	aa_	11/2Length = 1715	Acetyl-Co A acetyltransferase 1, mitochondrial
				Rattus norvegicus Acetyl-Co A	1, millochondrial
				acetyltransferase 1,	
		i		mitochondrial (Acatt), mRNA.	
1930	18957 N	M_017075 r	,s,t,ll		Acad Co. A
			1-10111	ratus norvegicus rumoi-	Acetyl-Co A acetyltransferase 1, mitochondrial
	- 1			associated alvont-t	
!				associated glycoprotein pE4	
1931	023 11	M_017076 a	,p,q,y,z,ee,ff	(Tage4), mRNA. 11/2Length =	
12011				2171	fumor-associated glycoprotein pE4

TABLE 1	. (5. )	GenBank Ac	<u> </u>	11. (1.0)	Atty, Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC I	) No	Model Code	Known Gene Name	计操纵模 人名德马德 连续统 医乳压性炎
77 7 17 1	19501		iviodei code	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Unigene Sequence Cluster Title
				Rattus norvegicus CD1D antigen (Cd1d), mRNA.	
1932	152	3 NM_017079	h,l,n,o,w,x	11/2Length = 1835	CD4D onlines
			1.1,1.1,0,1.1,2.	Rattus norvegicus biglycan	CD1D antigen
				(Bgn), mRNA. 11/22Length =	Small proteoglycan I (biglycan), bone (BSPG1)
1933	22552	2 NM_017087	n,o_	2446	(bone/cartilage protectycan 1 precursor)
				Rattus norvegicus GDP-	(total anago proteorycan i precursor)
4004				dissociation inhibitor 1 (Gdi1),	·
1934	1383	3 NM_017088		mRNA.11/2Length = 139	GDP-dissociation inhibitor 1
				Rattus norvegicus Bruton	
		1		agammaglobulinemia tyrosine	
1935	2366	NM_017092		kinase (Tyro3), mRNA.	
1000	20000	01709Z	u,v	12/2Length = 3726	Bruton agammaglobulinemia tyrosine kinase
				Rattus norvegicus growth	
1936	10886	NM_017094	ii	hormone receptor (Ghr), mRNA 11/22Length = 295	
			- "	Rattus norvegicus growth	Growth hormone receptor
				hormone receptor (Ghr), mRNA	
1936	10887	NM_017094	ii.kk	11/22Length = 295	Growth hormone receptor
				Rattus norvegicus growth	Growth normone receptor
				hormone receptor (Ghr), mRNA.	
1936	10888	NM_017094	e,r,hh	11/22Length = 295	Growth hormone receptor
ĺ			]	Rattus norvegicus Cathepsin C	
4007	0450			(dipeptidyl peptidase I)	
1937	2150	NM_017097	a,li	(Ctsc),mRNA. 11/2Length = 185	Cathepsin C (dipeptidyl peptidase I)
İ			ļ	Rattus norvegicus potassium	
- 1				inwardly-rectifying channel,	
1938	15517	NM_017099		subfamily J, member 8 (Kcnj8),	Inwardly rectifying potassium channel gene,
.000	10017	1414_017033	С	mRNA. 11/22Length = 158 Rattus norvegicus	subfamily J-8 (ATP sensitive)
				Peptidylprolyl isomerase A	
				(cyclophilin A)(Ppia), mRNA.	
1939	4391	NM_017101	s,t	11/22Length = 743	Pentidularalul icomorgae A (austantilla A)
			1	Rattus norvegicus potassium	Peptidylprolyl isomerase A (cyclophilin A)
1				voltage-gated channel,	
				subfamily H (eag-related),	
				member 3 (Kcnh3), mRNA.	potassium voltage-gated channel, subfamily H (ea
1940	15776	NM_017108	u,v	11/22Length = 3715	related), member 3
				Rattus norvegicus granulin	
1941	20745	NINA 047440		(Grn), mRNA. 11/22Length =	
1541	20/40	NM_017113	f,g	2113	granulin
	J			Rattus norvegicus granulin	
1941	20746	NM_017113	j,cc,dd,gg	(Gm), mRNA. 11/22Length = 2113	
		17 110	jiwiadigg	Rattus norvegicus hippocalcin	granulin
	ļ		_	(Hpca), mRNA. 11/22Length =	
1942	1375	NM_017122	n,o	laroa - I	hippocalcia
				Rattus norvegicus CD63	hippocalcin
				antigen (Cd63), mRNA.	
1943	1435	NM_017125	kk	442001 11 00	Cd63 antigen
	T			Rattus norvegicus ferredoxin 1	unugon
40.				(Fdx1), mRNA. 11/22Length =	
1944	21662	VM_017126	a,ee,ff	838	ferredoxin 1
	- 1			Rattus norvegicus ferredoxin 1	
1344	04000	N. 047455		(Fdx1), mRNA. 11/22Length =	
1.4	Z1663[N	VM_017126	.ff	838	ferredoxin 1

TABLE		GenBank Ac	<del> </del>		Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GLCC	No.	College Control	HANGEL BURN	2 - 100405
	JOEGO II	3 110.	Model Code	The state of the s	Ünigene Sequence Cluster Title
	1			Rattus norvegicus	The second secon
4045	0450		1	neuraminidase 2 (Neu2),	
1945	2452	2 NM_017130	U,V	mRNA. 11/22Length = 166	neuraminidase 2
	l		ľ	Rattus norvegicus	
4040		1		calsequestrin 2 (Casq2), mRN	A.
1946	16	7 NM_017131	b,e,u,v,il	11/22Length = 1681	calsequestrin 2
				Rattus norvegicus reticulocalb	in
4047				2 (Rcn2), mRNA. 11/22Length	=
1947	2091	NM_017132	d	219	reticulocalbin 2
		1		Rattus norvegicus squalene	Total God Bill 2
4040				epoxidase (Sqle), mRNA.	
1948	1668	NM_017136	li	11/22Length = 2199	squalene epoxidase
				Rattus norvegicus laminin	Squalerie epoxidase
				receptor 1 (67kD, ribosomal	
				protein SA) (Lamr1), mRNA.	
1949	24885	NM_017138	h,i,w,x	11/22Length = 118	lominia was a tanad
I				Rattus norvegicus laminin	laminin receptor 1
				receptor 1 (67kD, ribosomal	
			1	protein SA) (Lamr1), mRNA.	
1949	24886	NM_017138	h,l,w,x	11/22Length = 118	land.
				Rattus norvegicus dopamine	laminin receptor 1
				receptor D3 (Drd3), mRNA.	
1950	492	NM_017140	l,m,n,aa	11/22Length = 1481	
T			1	Rattus norvegicus DNA	dopamine receptor 3
			İ	polymerase beta (Polb), mRNA.	
1951	24106	NM_017141	s,t,bb	11/22Length = 3298	
			10,000	Rattus norvegicus DNA	DNA polymerase beta
			1	Polymorana beta (Dalla) - Pana	
1951	24107	NM_017141	n	polymerase beta (Polb), mRNA. 11/22Length = 3298	
			<del>"</del>	Rattus norvegicus cofilin 1	DNA polymerase beta
- 1			ŀ	(Cff4) mBNA 44/00 - 4	
1952	15364	NM_017147	lii	(Cfl1), mRNA. 11/22Length = 139	
				Rattus norvegicus cofilin 1	cofilin 1, non-muscle
	J			(Cfl1) mBNA 44504 1	
1952	15365	NM_017147	aa,bb,ll	(Cfl1), mRNA. 11/22Length = 139	
			aa,bb,ii		cofilin 1, non-muscle
-	- 1			Rattus norvegicus cysteine rich	
1953	13392	NM_017148	_	protein 1 (Csrp1), mRNA.	
1000	10002	110_017 140	е	1/22Length = 143	cysteine rich protein 1
1	ļ			Rattus norvegicus	
1				mesenchyme homeo box 2	•
1954	17287	M_017149	::	(Meox2), mRNA. 11/22Length =	
	172071		ii	2244	mesenchyme homeobox 2
	1			Rattus norvegicus ribosomal	
1955	16053	IM_017151	~	protein S15 (Rps15), mRNA.	
	10000	IIVI_U1/101	g	11/22Length = 487	ribosomal protein S15
- 1		1		Rattus norvegicus ribosomal	
1955	16054	IM 047454		protein S15 (Rps15), mRNA.	
1300	1050411	IM_017151	99	11/22Length = 487	ribosomal protein S15
1	1	j		Rattus norvegicus ribosomal	
1055	16055	M 04747		protein S15 (Rps15), mRNA.	
1955	10905 N	M_017151 I	,m,s,t	11/22Length = 487	ibosomal protein S15
- 1	1			Rattus norvegicus xanthine	Proton City
1050	040		i,e,j,k,n,o,y,z,	dehydrogenase (Xdh), mRNA.	
1956	21975 N	M_017154	k	11/22Length = 4198	anthine dehydrogenase
1		1		Rattus norvegicus ribosomal	and deliverogenase
- 1				protein S6 (Rps6), mRNA.	
1957	17104 N		,1	11/22Length = 81	

TABLE 1	[k]   4.				Atty. Ref. 44921-5090-01-WO/2105485
050.10	2, 22, 5	GenBank Acc		100 10 10 10 10 10 10 10 10 10 10 10 10	1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
SEO.ID	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
				Rattus norvegicus ribosomal	
1957	17105	NIM 047400		protein S6 (Rps6), mRNA.	
1907	17 105	NM_017160	h,l	11/22Length = 81	ribosomal protein S6
		1		Rattus norvegicus ribosomal protein S6 (Rps6), mRNA.	
1957	17106	NM_017160	חיס	11/22Length = 81	ribenessal variable on
		71111_017100	11,0	Rattus norvegicus glutathione	ribosomal protein S6
İ				peroxidase 4 (Gpx4),	
1958	17686	NM_017165	hh	mRNA.11/22Length = 872	glutathione peroxidase 4
1				Rattus norvegicus stathmin 1	garastiono potoxidado 4
4050	00700	J		(Stmn1), mRNA. 11/22Length =	Leukemia-associated cytosolic phosphoprotein
1959	20702	NM_017166	j,k,y,z	154	stathmin
				Rattus norvegicus zinc finger	
				protein 36, C3H type-like 1	
1960	20919	NM_017172	а	(Zfp36l1), mRNA. 5/22Length = 2741	
		077 772		Rattus norvegicus serine (or	zinc finger protein 36, C3H type-like 1
] [		ł		cysteine) proteinaseinhibitor,	
				clade H, member 1 (Serpinh1),	serine proteinase inhibitor, clade H (heat shock
1961	17301	NM_017173	c,f,g,j,k,y,z	mRNA. 11/22Length = 263	protein 47), member 1
				Rattus norvegicus	, , , , , , , , , , , , , , , , , , ,
]				phospholipase A2, group 5	
1962	0270	NINA 047474		(Pla2g5), mRNA.11/22Length =	
1902	93/6	NM_017174	jj,kk	183	phospholipase A2, group V
1				Rattus norvegicus T-celi death associated gene (Tdag),	
1963	19031	NM_017180	p,q	mRNA.11/22Length = 1353	T call death access to
		011 100	1919	IIII GVA. 1 1122Lerigiii ~ 1999	T-cell death associated gene
1 1				Rattus norveglcus H2A histone	,
				family, member Y (H2afy),	
1964	1488	NM_017182	h	mRNA. 1/22Length = 157	H2A histone family, member Y
1 :				Rattus norvegicus UNC-119	
				homolog (C. elegans)	
1965	5676	NM_017188	00 ff	(Uncl19),mRNA. 11/22Length =	
1000	0070	1410_017 100	ee,ff	1264   Rattus norvegicus signal	UNC-119 homolog (C. elegans)
			Ī	sequence receptor 4 (Ssr4),	
1966	9124	NM_017199	h,i,hh	mRNA.11/22Length = 757	signal sequence receptor, delta
				Rattus norvegicus S-	oignai sequence receptor, della
'	ļ			adenosylhomocysteine	
أحمما				hydrolase (Ahcy),mRNA.	
1967	20779	NM_017201	b,l,m	11/22Length = 229	S-adenosylhomocysteine hydrolase
	I			Rattus norvegicus cytochrome	
1968	14694	NM_017202	aa	c oxidase, subunit 4a (Cox4a), mRNA. 11/22Length = 696	
1000	1 7004	0 1/202	uu	Rattus norvegicus solute carrier	cytochrome c oxidase, subunit IVa
	.			family 6, member 6	
	- 1			(Sic6a6),mRNA. 11/22Length =	1
1969	24859	NM_017206	h,l	2489	Solute carrier 6 ,member 6 (taurine transporter)
	İ			Rattus norvegicus microtubule-	The state of the s
[ 1	İ	,		associated protein tau	[
1970	43030	NM 047040	11 Jele	(Mapt),mRNA. 11/22Length =	i
1970	10330	NM_017212	jj,kk	524 Rattus norvegicus microtubule-	microtubule-associated protein tau
, !   !				associated protein tau	
				(Mapt),mRNA. 11/22Length =	İ
أمحره	12940	NM_017212	а	- I	microtubule-associated protein tau
-					microrangie-associated biofeill (gn

TABLE 1			W. 7 7	£ .	Atty. Ref. 44921-5090-01-WO/2105485
SEQ!ID	GLGC ID	GenBank Acc.	Madal Cadal		
ŞEQ.ID	GEGCID	INO.	Iviodei Codei,	Known Gene Name	Unigene Sequence Cluster Title
]			1	Pathus nonregious 6	
				Rattus norvegicus 6-pyruvoyl- tetrahydropterin synthase (Pts),	1
1971	1527	NM_017220	ee,ff	mRNA. 11/22Length = 1176	6 pyriyoyi totrohydrontosta
		011220	00,11	711 172 Length - 1170	6-pyruvoyl-tetrahydropterin synthase
				Rattus norvegicus 6-pyruvoyl-	
				tetrahydropterin synthase (Pts),	
1971	20632	NM_017220	aa,bb	mRNA. 11/22Length = 1176	ESTs
l i					
			İ	Rattus norvegicus 6-pyruvoyl-	
1971	10028	NM_017220	l,m	tetrahydropterin synthase (Pts),	
107,	10020	14141_017 220	1,111	mRNA. 11/22Length = 1176	ESTs
i l				Rattus norvegicus solute carrier	
				family 1, member 2 (Slc1a2),	
1972	11989	NM_017222	hh	mRNA. 11/22Length = 4269	ESTs
				Rattus norvegicus solute carrier	1
4070	40007	NIN		family 1, member 2 (Slc1a2),	
1972	18967	NM_017222	r	mRNA. 11/22Length = 4269	ESTs
				Rattus norvegicus solute carrier	
				family 22 (organic anion transporter), member 6	
				(Slc22a6), mRNA. 1/22Length =	solute corrier family 20 (
1973	1510	NM_017224	u	2227	solute carrier family 22 (organic anion transporter), member 6
			··	Rattus norvegicus peptidyl	inchiber o
				arginine deiminase, type 2	ESTs, Highly similar to RS18_HUMAN 40S
				(Pdi2),mRNA. 11/22Length =	ribosomal protein S18 (KE-3) (KE3) [R.norvegicus],
1974	15108	NM_017226	u,v	457	peptidyl arginine deiminase, type II
		ł		Rattus norvegicus peptidyl	
				arginine deiminase, type 2	·
1974	18148	NM_017226		(Pdi2),mRNA. 11/22Length = 457	manufadad annibut a si bir si
		7111_017220	,0	Rattus norvegicus	peptidyl arginine deiminase, type II
	Ī			phosphatidylinositol transfer	
				protein (Pitpn), mRNA.	
1975	24598	NM_017231		11/22Length = 1638	phosphatidylinositol transfer protein
				Rattus norvegicus	
	1	l		prostaglandin-endoperoxide	
1976	20102	NM_017232		synthase 2 (Ptgs2), mRNA.	
1970	20193	14141_U 17 232		11/22Length = 444 Rattus norvegicus	prostaglandin-endoperoxide synthase 2
	1	ļ		phosphatidylethanolamine	
			ŀ	binding protein (Pbp), mRNA.	
1977	15598	NM_017236	ii	11/22Length = 175	phosphatidylethanolamine binding protein
				Rattus norvegicus myosin	
		ŀ	į	heavy chain, polypeptide 6	
1070	4400	NIM 047000			myosin heavy chain, polypeptide 6, cardiac muscle,
1978	1498	NM_017239		Pattus population musela	alpha
		l		Rattus norvegicus myosin heavy chain, polypeptide 6	
		ŀ			myosin hoosy shain nalimantida C acadea
1978	1497	NM_017239			myosin heavy chain, polypeptide 6, cardiac muscle, alpha
				Rattus norvegicus myosin	шрни
	ĺ		į	neavy criain, polypepude 7	
4070	00 105			(Myh7),mRNA. 11/22Length =	
1979	20482	VM_017240 c	o,g k	5925	myosin heavy chain, cardiac muscle, fetal
19/9	20482	VM_U1/24U	7,g   18	0925	myosin heavy chain, cardiac muscle, fetal

	14.	GenBank A	CC;	14 · 图 8 · 8 · 30 · 30 · 30 · 4 · 5	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID:	GLGC I	D No.	Model Code	e Known Gene Name	
<u> </u>		5 (19/4) 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	in ligitude Code		Unigene Sequence Cluster Title
	l	1		Rattus norvegicus myosin	
	l	1		heavy chain, polypeptide 7	
				(Myh7),mRNA. 11/22Length =	_
1979	2048	3 NM_017240	) la	5925	1
				Rattus norvegicus myosin	myosin heavy chain, cardiac muscle, fetal
		1		ratius norvegicus myosin	
			ľ	heavy chain, polypeptide 7	
4070			1	(Myh7),mRNA. 11/22Length =	:
1979	2048	4 NM_017240	е	5925	
1				Rattus norvegicus myosin	myosin heavy chain, cardiac muscle, fetal
1		1		heavy chain, polypeptide 7	
- 1			ĺ	(Muh7) - DNA 44 (COL	
1979	379	0 NM_017240		(Myh7),mRNA. 11/22Length =	
.070	370	011111-017240	c,g	5925	EST
				Rattus norvegicus eukaryotic	
i				translation elongation factor	
1				2(Eef2), mRNA. 11/22Length =	_
1980	1756	NM_017245	l,m	2626	
		017240	1911		eukaryotic translation elongation factor 2
- 1		1	1	Rattus norvegicus eukaryotic	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
į		1	1	translation elongation factor	
				2(Eef2), mRNA. 11/22Length =	_
1980	17563	NM_017245	h,i	2626	
				Rattus norvegicus	eukaryotic translation elongation factor 2
- 1		ı	ľ		
j		1		heterogeneous nuclear	
1004	47504	1114 04-04-		ribonucleoprotein A1(Hnrpa1),	
1981	1/501	NM_017248	l,m	mRNA. 11/22Length = 1696	heterogeneous nuclear ribonucleoprotein A1
				Rattus norvegicus	inclored nuclear inconucleoprotein A1
			Ì	heterogeneous nuclear	
				ribonuoloopeatain A4/11	
1981	17502	NM_017248	J	ribonucleoprotein A1(Hnrpa1),	
	11002	14141_017240	l,m	mRNA. 11/22Length = 1696	heterogeneous nuclear ribonucleoprotein A1
			ł	Rattus norvegicus POU	- The street coop roton (A)
l			Į	domain, class 3, transcription	
				factor 4(Pou3f4), mRNA.	
1982	16601	NM_017252	s,t	11/22Length = 125	DOLL I I I I I I I I I I I I I I I I I I
				Rattus norvegicus purinergic	POU domain, class 3, transcription factor 4
			1	reaction POV Continue raise	
- 1			1	receptor P2Y, G-protein coupled	d
4000	4400			2 (P2ry2), mRNA. 11/22Length	
1983	1496	NM_017255	aa,bb	= 211	purinergic receptor P2Y, G-protein coupled 2
i	1			Rattus norvegicus B-cell	parmergio receptor P21, G-protein coupled 2
	I			translocation gene 1 (Btg1),	
1984	19	NM_017258	ln a	mDNA 44/00 " (big I),	
		<u>-</u>	p,q	mRNA.11/22Length = 1464	B-cell translocation gene 1, anti-proliferative
1	İ		1	Rattus norvegicus B-cell	, ,
1005	4.5.5.			translocation gene 2 (Btg2),	1
1985	15300	NM_017259	p,q,kk	mRNA.11/22Length = 2519	Early induced gone B or the set of
i	T			Rattus norvegicus B-cell	Early induced gene, B-cell translocation gene 2
ı				Itranslocation gene 2 (Disc)	
1985	15301	NM_017259	iknaves	translocation gene 2 (Btg2),	
	.0001		j,k,p,q,y,z,gg	mRNA.11/22Length = 2519	Early induced gene, B-cell translocation gene 2
l				Rattus norvegicus B-cell	genez
			1	translocation gene 2 (Btg2).	
985	15299	NM_017259	y,z	mRNA.11/22Length = 2519	Early induced some D. III.
ı				Rattus norvegicus arachidonate	Early induced gene, B-cell translocation gene 2
•	I			5-lipovigonoso activisti	
	- 1			5-lipoxygenase activating	
1986	7500	IAA 047000		protein (Alox5ap), mRNA.	
300	1093	IM_017260	W,X	11/22Length = 54	Arachidonate 5-lipoxygenase activating protein
i				Rattus norvegicus arachidonate	protein
i				5-lipoxygenase activating	
i	i		:	protein (Alox5ap), mRNA.	
986	7594 A	M_017260	w,x,ii	44/001	
	· • • • • • • • • • • • • • • • • • • •	IIVI. U I / ZOU	W. X II	1111111 Opelb - E1	Arachidonate 5-lipoxygenase activating protein

TABLE	13	GenBank Ac	\$ 15 . \$5.5 \$ . 1	N. Parasa	Atty. Ref. 44921-5090-01-WO/2105485
SEO ID.	GLGC I	) No			Company of the contract of the
OCG, ID.	OLOC IL	SUMO.	Model Code	Known Gene Name	Unigene Seguence Chistor Titlo
	Ĭ	i		Rattus norvegicus 3-hydroxy	3-
	1	1		methylglutaryl-Coenzyme	
	1		ļ	Asynthase 1 (Hmgcs1), mRN/	Δ
1987	20600	NM_017268	- jii	11/22Length = 3275	
				Rattus norvegicus 3-hydroxy-	3-hydroxy-3-methylglutaryl-Coenzyme A synthase
		1	1	methylglutaryl-Coenzyme	-
		ĺ	1	Asynthase 1 (Hmgcs1), mRNA	
1987	20601	NM_017268	r	11/22Length = 3275	
				Rattus norvegicus aldehyde	3-hydroxy-3-methylglutaryl-Coenzyme A synthase
	1	l		dehydrogenase family 1,	
		1		subfamily A4 (Alaba - 4)	
1988	20913	NM_017272	n,o	subfamily A4 (Aldh1a4), mRNA	
		1111_017272	11,0	11/22Length = 224	aldehyde dehydrogenase family 1, subfamily A4
			j	Rattus norvegicus glycerol-3-	, occiding / t
				phosphate	
				acyltransferase, mitochondrial	
1989	00004			(Gpam), mRNA. 11/22Length =	:
1909	20281	NM_017274	99	2646	I
ĺ	l			Rattus norvegicus adaptor	glycerol-3-phosphate acyltransferase, mitochondria
ĺ			1	protein complex AP-1, beta 1	
,,,,				subunit (Ap1b1), mRNA.	
1990	17959	NM_017277	s,t	11/22Length = 3679	Adaptor protein accept with a
		-		Rattus norvegicus proteasome	Adaptor protein complex AP-1, beta 1 subunit
				(prosome, macropain) subunit,	
				alpha type 1 (Psma1), mRNA.	Protocomo (vers
1991	15142	NM_017278	l,m	11/22Length = 1174	proteasome (prosome, macropain) subunit, alpha
			1	Rattus norvegicus proteasome	Itype 1
- 1				(prosome magnetic) and	
			1	(prosome, macropain) subunit,	
1992	15538	VM_017283	-	alpha type 6 (Psma6), mRNA.	proteasome (prosome, macropain) subunit, alpha
	.00001	017200	<del> </del>	11/22Length = 932	type 6
- 1	-		]	Rattus norvegicus sodium	
	- 1		j j	channel, voltage-gated, type 1,	
1993	20570	IM 047000	1	beta polypeptide (Scn1b).	sodium channel, voltage-gated, type I, beta
1000	200/9	M_017288	aa,bb	mRNA. 11/22Length = 149	polypeptide
			1	Rattus norvegicus ATPase.	,,-
			[1	Ca++ transporting, cardiac	
400.1				muscle, slow twitch 2 (Atp2a2),	ATPase Catt tropposting and
1994	_12347 N	M_017290	11	mRNA. 11/22Length = 5648	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
	]_			Rattus norvegicus ATPase,	INVITOR Z
1			l la	Ca++ transporting, cardiac	
			l,	nuscle, slow twitch 2 (Atp2a2),	ATD
1994	12349 N	M_017290	aa ¦	nRNA. 11/22Length = 5648	ATPase, Ca++ transporting, cardiac muscle, slow
				Rattus norvegicus potassium	twitch 2
- 1			ļ. <u>.</u>	nwardy-rooties	
			["	nwardly-rectifying channel,	
1995	ลวไทเ	M_017297	ii Is	ubfamily J, member 5 (Kcnj5),	potasslum inwardly-rectifying channel, subfamily J,
	- JE 141	011231	<u>"                                     </u>	nRNA. 1/22Length = 3156	member 5
1	- 1	1	1.		
ı	- 1	-	F	Rattus norvegicus solute carrier	
1996	22025	4 047000	fa	amily 19, member 1 (Slc19a1).	solute carrier family 19 (sodium/hydrogen
1330	23025 N	M_017299	cc,dd m	RNA. 11/22Length = 242	exchanger), member 1
			] F	Rattus norvegicus potassium	overender), member 1
	- 1	1	V	oltage gated channel.	
1		1	sl	nakerrelated subfamily, beta	
			ļ.,		
1997	1028 NA	/_017304 ii		1/221 00011 47	potassium voltage gated channel, shaker related
				nzzengui - II	subfamily, beta member 2
	l			calius norvegicus Giulamaie-	
- 1	ı		Cy	steine ligase (gamma-	
	j		1 .		
			gli	utamylcysteine synthetase),	1
998	14004 NM	1 04700-	re	utamylcysteine synthetase), gulatory (Glcir), mRNA. /22Length = 1382	

TABLE	7.4	GenBank A	200	36.7	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	No.	Model Code	e Known Gene Name	1、杨秋 1.5 高级的名字编版 为唐代杨林联系统 1.5 · · · · · · · · · · · · · · · · · · ·
		,,	I Wodel, Code	s Mijown Gene Name	Unidene Seguence Cluster Title
		İ	j	Rattus norvegicus dodecenoy	
		]	ļ	coenzyme A delta isomerase	Rat mRNA for delta3, delta2-enoyl-CoA isomerase
1999	18687	NM_017306	5 hh	(Dci), mRNA. 11/22Length =	dodecenoyl-Coenzyme A delta isomerase (3,2 tra
	10007	14141_017300	, luu	987	enoyl-Coenyme A isomerase)
			1	Rattus norvegicus ATP	
				synthase, H+	
- 1				transporting, mitochondrial F	
1				complex, subunit c, isoform 1	
2000	16844	NM_017311	n,o	(Alpog1), mRNA. 11/22Length	= ATP synthase, H+ transporting, mitochondrial F0
			11,0		complex, subunit c (subunit 9), isoform 1
			ļ	Rattus norvegicus sodium-	, positivi
	J			coupled ascorbic acid	
2001	1904	NM_017315	11.0	transporter 1 (SVCT1), mRNA.	
	- 1341	077010	u,v	11/2Length = 2472	Rat VL30 element mRNA
				Rattus norvegicus cathepsin S	
2002	1894	NM_017320	b,l,m,kk	(Ctss), mRNA. 8/22Length =	
	- 150 11	017020	U,I,III,KK	133	cathepsin S
1				Rattus norvegicus	
- 1	1		1	phosphoglycerate mutase 2	
2003	24533	NM_017328	0.0	(Pgam2), mRNA. 11/22Length =	
		017020	n,o	798	Phosphoglycerate mutase 2
			1	Rattus norvegicus fatty acid	
2004	24248 N	M_017332	e,gg	synthase (Fasn), mRNA.	
				11/22Length = 9136 Rattus norvegicus CAMP	fatty acid synthase
				responsive element	
			aiknavze	responsive element modulator	
2005	355 N	IM_017334	ff	(Crem),mRNA. 1/22Length = 436	
			<del> '''</del>	Rattus norvegicus CAMP	CAMP responsive element modulator
	- 1		1	responsive element modulator	
			1	(Crem),mRNA. 1/22Length =	
2005	356 N	M_017334	a,j,k,p,q,kk	436	
T			-ijiripiqiar	100	CAMP responsive element modulator
				Rattus norvegicus myosin	
			1	regulatory light chain (MRLCB),	•
2006	16382 N	M_017343	cc,dd	ImpDNIA O/O41 11 1	
					myosin regulatory light chain
- 1				Rattus norvegicus myosin	
	_			regulatory light chain (MRLCB),	1
2006	20848 N	<u>/_017343</u>	bb,hh,jj,kk		Poi mDNA farmer
					Rat mRNA for myosin regulatory light chain (RLC)
- 1	1			Rattus norvegicus myosin	
2225				regulatory light chain (MRLCB),	j
2006	20849 NN	1_017343	99	mRNA. 6/21Length = 1139	Rat mDNA for muse!
				Rattus norvegicus glycogen	Rat mRNA for myosin regulatory light chain (RLC)
	ľ			synthase kinase 3 alpha	
2007	47705		ŀ	(Gsk3a), mRNA. 11/22Length =	}
2007	17782 NN	_017344	e	2155	IlVCOGED synthago kinner a -l-1
1	1			Larras Horvedicas Hillodell	llycogen synthase kinase 3 alpha
			6	activated protein kinase 3	ļ
2000	1500-			(Mapk3), mRNA. 11/22Length =	į
2008 1	15037 NM	_017347	e,r	1238	nitogen activated protein kinase 3
		1		Lyanas Horvedicus Chollue	mogen activated protein kinase 3
2000:	400		į t	ransporter (CHOT1), mRNA	
2009	468 NM	_017348	<u>W,X</u> [1	1/2Length = 3972	holine transporter
-	1		] [	Rattus norvegicus neural visinini	ionne dansporter
ĺ	1		ii,	ke Ca2+-binding protein type3	1
	1	1	[71	MVD 31 - DVIA	
010 2	4428 NM_	_017356	. 10	NVP-3), mRNA. 11/2Length = 15	

TABLE 1				VIVA I SAI	Atty. Ref. 44921-5090-01-WO/2105485
74.37.97	7. 144 2. 12 12 12	GenBank Acc.		And the Color of t	the transfer of the transfer o
SEQ ID	GLGO ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1				Rattus norvegicus neural visinir	
			1	like Ca2+-binding protein type2	
0044	47000			(NVP-2), mRNA. 11/2Length =	
2011	1/202	NM_017357	99	663	neural vislnin-like Ca2+-binding protein type 2
				Rattus norvegicus ras-related	
2012	20417	NM 047250	L 1 LL	protein rab1 (Rab1), mRNA.	
2012	20417	NM_017359	h,l,hh	11/2Length = 991	ras-related protein rab10
				Rattus norvegicus Pancreas zinc finger protein, see	
		1		alsoD1Bda1\2 (Znf146), mRNA.	
2013	20232	NM_017364	u,v	5/22Length = 1578	Penerne sine figure and the second se
			-,,	Rattus norvegicus PDZ and LIM	Pancreas zinc finger protein, see also D1Bda10\2
				domain 1 (Pdlim1),	1
2014	1581	NM_017365	l,p,q,s,t	mRNA.11/22Length = 1392	PDZ and LIM domain 1 (elfin)
			.,.,.	Rattus norvegicus	T be and this domain t (eiiii)
				Synaptotagmin 3 (Syt3), mRNA.	
2015	20536	NM_019122	b,l,m,u,v	11/22Length = 296	Synaptotagmin 3
				Rattus norvegicus rabaptin 5	7,
2040				(LOC5419), mRNA,	
2016	20778	NM_019124	[1]	11/22Length = 3465	rabaptin 5
				Rattus norvegicus Interferon,	
2047	20240	NM 040407		beta 1, fibroblast (Ifnb1), mRNA.	
2017	20318	NM_019127	n,o	11/22Length = 555	Interferon, beta 1, fibroblast
				Rattus norvegicus tropomyosin	
2018	455	NM_019131	b,u,v	1, alpha (Tpm1), mRNA.	_
	400	14141_013131	D,u, v	11/22Length = 14 Rattus norvegicus tropomyosin	Tropomyosin 1 (alpha)
				1, alpha (Tpm1), mRNA.	
2018	461	NM_019131	b,l,m	11/22Length = 14	Transmussin 4 (alaba)
			5,1,1.11	Rattus norvegicus Guanine	Tropomyosin 1 (alpha)
1		İ		nucleotide-binding protein G-s,	
				alphasubunit, Genbank no	·
				U51565 (Gnas), mRNA.	Guanine nucleotide-binding protein G-s, alpha
2019	15975	NM_019132	ii	11/22Length = 1738	subunit
				Rattus norvegicus early growth	
				response 4 (Egr4), mRNA.	Zinc-finger transcription factor NGFI-C (early
2020	16227	NM_019137	l,m	11/22Length = 2145	response gene)
				Rattus norvegicus protein	, , , , , , , , , , , , , , , , , , , ,
				tyrosine phosphatase, receptor	
2021	14072	NM_019140		type, D (Ptprd), mRNA.	
2021	149/3	140 19140	aa	11/22Length = 6469	Protein tyrosine phosphatase, receptor type, D
	ļ			Rattus norvegicus Fibronectin 1 (Fn1), mRNA. 11/22Length =	
2022	5618	NM_019143		(CO1), MIKINA. 11/22Length = 8329	   Fibrary and to d
		0,0140	<u>-,,</u>	Rattus norvegicus Fibronectin 1	Fibronectin 1
				(Fn1), mRNA. 11/22Length =	
2022	5622	NM_019143		8329	Fibronectin 1
				Rattus norvegicus urocortin	r moneoffit 1
				(Ucn), mRNA. 11/22Length =	
2023	278	NM_019150		579	urocortin
				Rattus norvegicus calpain 1	
				(Capn1), mRNA. 11/22Length =	
2024	20863	NM_019152	cc,dd	2917	calpain 1
				Rattus norvegicus fibulin 5	
2025	6454	NIA OAGATO		(Fbln5), mRNA. 11/22Length =	
2025	0451	NM_019153		234	fibulin 5
i	1	ĺ		Rattus norvegicus vitronectin	
2026	24362	NM_019156 j		(Vtn), mRNA. 11/22Length =	
2020	27002	##_019190	j,kk	1588	vitronectin

	14.	GenBank Ad	c.d. E. Fer		Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID.	GLGC II				TO THE REPORT OF THE PARTY OF T
الله المال	1.000,11	3 INO.	Model Code		Unigene Sequence Cluster Title
		1		Rattus norvegicus NADH	
				dehydrogenase Fe-S protein	6
0011				(Ndufs6),mRNA. 11/22Length	-
2041	2093	B NM_019223	hh	351	1
	j			Rattus norvegicus	NADH dehydrogenase Fe-S protein 6
	1	1	ł	serum/glucocorticoid regulated	4
				kinase (Sgk), mRNA.	<b>"</b>   .
2042	20433	NM_019232	p,q,kk	11/22Length = 2435	Company to the contract of the
				Rattus norvegicus procollagei	serum/glucocorticoid regulated kinase
		ļ		C-proteinase enhancer	
		1		protein(Pcoice), mRNA.	
2043	15503	NM_019237	n,o	11/22Length = 1547	
				Rattus norvegicus interferon-	procollagen C-proteinase enhancer protein
		1		related developmental regulator	
J			a.n.a.v.z bh.e	e 1 (Ifrd1), mRNA. 5/22Length =	or j
2044	17908	NM_019242	.ff	11736	l .
			<del>-1'''</del>	Rattus norvegicus	interferon-related developmental regulator 1
- 1			ł	Interest adapting 50 mg	
			1	prostaglandin F2 receptor	1
2045	21108	NM_019243	ļ.	negativeregulator (Ptgfrn),	
		1111_010240	<del></del>	mRNA. 11/22Length = 5825	prostaglandin F2 receptor negative regulator
- 1				Rattus norvegicus paired-like	
1			1	homeodomain transcription	
2046	11219	NM_019247		factor 3 (Pitx3), mRNA.	
2070	11210	14141_019247	b,u,v	11/22Length = 1253	paired-like homeodomain transcription factor 3
Í			j	Rattus norvegicus neural	
İ	[			receptor protein-tyrosine kinase	
2047	24040	NIA 040040		(Ntrk3), mRNA. 11/22Length =	
2047	24049	NM_019248	aa,bb	2682	neurotrophic tyrosine kinase, receptor, type 3
				Rattus norvegicus ral guanine	
				nucleotide dissociationstimulato	r
2040	40-04		1	(Ralgds), mRNA. 11/22Length =	
2048	18/61	VM_019250	aa	3665	ral guanine nucleotide dissociation stimulator
l				Rattus norvegicus splicing	in godinie nucleotide dissociation stimulator
	1		[ .	factor, arginine/serine-rich 5	
2040	22442		,	(Sfrs5), mRNA. 11/22Length =	
2049	23419	NM_019257	t	2781	Isplicing factor, orginized and a delication to the
	ĺ			Rattus norvegicus complement	splicing factor, arginine/serine-rich 5 (SRp40, HRS)
l l				component 1, q subcomponent,	
					complement
2050	21443 N	IM_019262	kk,li	11/22Length = 1136	complement component 1, q subcomponent, beta
	Γ			Rattus norvegicus complement	polypeptide
[			Į,	component 1, q subcomponent,	
1			li li		complement
2050	21444 N	M_019262	jj,kk	11/22Length = 1136	complement component 1, q subcomponent, beta
				Rattus norvegicus gap junction	polypeptide
			,	membrane channel protein	
			;		
2051	1143 N	M_019280	w,x	11/22Length = 3115	gap junction membrane channel protein alpha 5
				Rattus norvegicus solute carrier	(connexin 40)
- 1		1	ŧ.	amily 3, member 2	
		!	;'	01-0-01	
2052	20734 N	V_019283	,k,t,u,v,jj,kk   1	Slc3a2),mRNA. 11/22Length = 94	solute carrier family 3 (activators of dibasic and
			institution in	JT 1	neutral amino acid transport), member 2
		ļ	,	varios noi redicus sortife camer:	
		1		amily 3, member 2	
2052	20735 NIA	/_019283 i	16413	oicoaz, mŘíva. 11/22 Lengto = 1	solute carner family 3 (activators of dibasic and
	20,00141	1_019203		J <del>4</del> [,	neutral amino acid transport), member 2
1	j	1	F	varras norvedicas eceuvivi	and an openy, member 2
2053	8200	4 040000	c	yclase 4 (Adcy4), mRNA.	ľ
-000	OZUUINN	1_019285		1/001 "	Adenylyi cyclase 4

TABLE 1			:	<b></b>	Atty. Ref. 44921-5090-01-WO/2105485
050,10		GenBank Acc.	i dian		
SEQID	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
				Rattus norvegicus Actin-related	
į				protein complex 1b	
				(Arpc1b),mRNA. 11/2Length =	
2054	10015	NM_019289	n,o,jj,kk,il	143	Actin-related protein complex 1b
				Rattus norvegicus Actin-related	Present complex 18
}				protein complex 1b	
				(Arpc1b),mRNA. 11/2Length =	
2054	10016	NM_019289	a,o,jj,kk,ll	143	Actin-related protein complex 1b
				Rattus norvegicus B-cell	7 total related protein complex 10
				translocation gene 3 (Btg3),	
2055	23679	NM_019290	p,q	mRNA.11/22Length = 1259	B-cell translocation gene 3
				Rattus norvegicus carbonic	D-con translocation gene 3
1	i			anhydrase 2 (Ca2), mRNA.	
2056	15056	NM_019291	b,c	11/22Length = 1459	carbonic anhydrase 2
		0 /0_0.	5,0	Rattus norvegicus clathrin,	carbonic annyurase 2
İ				heavy polypeptide (Hc)	
ŀ				(Citc),mRNA. 11/22Length =	
2057	17507	NM_019299	f,g	671	alaibda haannada 200 au
	11001	11111_010200	פיי	Rattus norvegicus nuclear	clathrin, heavy polypeptide (Hc)
l				receptor subfamily 4, group A,	
1				member 2 (Nr4a2), mRNA.	
2058	2/67/	NM_019328		11/22Length = 22	
2030	24074	14141_019320	j,k	Rattus norvegicus Proprotein	nuclear receptor subfamily 4, group A, member 2
1				convertase subtilisin/kexin type	
i					
i				3 (paired basic amino acid	
				cleaving enzyme, funn,	
į				membrane associated receptor	
2050	40000	NN 040004		protein) (Pcsk3), mRNA.	
2059	10330	NM_019331	h,i,ii	1/22Length = 4259	Paired basic amino acid cleaving enzyme (furin)
.				Dall .	
J				Rattus norvegicus6-	
1			ļ	phosphofructo-2-kinase/fructose-	
2000	4000	040000		2,6-biphosphatase 4 (Pfkfb4),	6-phosphofructo-2-kinase/fructose-2,6-
2060	1238	NM_019333	gg	mRNA.11/22Length = 1739	biphosphatase 4
i				B.II.	
1				Rattus norvegicus Protein	
ĺ	1	1		kinase, interferon-inducible	
0004	اء	NN 04000-	,	doublestranded RNA dependent	Protein kinase, interferon-inducible double stranded
2061	52	NM_019335	<u>d</u>	(Prkr), mRNA. 11/2Length = 388	RNA dependent
		]		Rattus norvegicus regulator of	
İ		Ì		G-protein signaling 5	
605-				(Rgs5),mRNA. 11/22Length =	
2062	2088	NM_019341	aa,bb	546	regulator of G-protein signaling 5
				Rattus norvegicus glycoprotein	
				38 (Gp38), mRNA. 11/22Length	
2063	22675	NM_019358	a,n,o,kk	= 1854	glycoprotein 38
1	J			Rattus norvegicus calponin 3,	
				acidic (Cnn3), mRNA.	
2064	23491	NM_019359		5/22Length = 1932	calponin 3, acidic
1		T		Rattus norvegicus cytochrome	
				oxidase subunit VIc (Cox6c),	
2065	23225	NM_019360		mRNA. 11/2Length = 418	cytochrome oxidase subunit VIc
1	7			Rattus norvegicus palmitoyi-	
i	1	!	i,	protein thioesterase 2	
i	i	i		(Ppt2),mRNA. 11/22Length =	
2066	18819	NM_019367		· · · · · · · · · · · · · · · · ·	palmitoyl-protein thloesterase 2
-					pominto) i protoni unocotorase z

ABLE 1	4	GenBank Acc	<b>0.3</b> (2007) 172.	A THE PARTY AND A STATE OF	Atty. Ref. 44921-5090-01-WO/2105485
EQ ID	GLGC;II	No:	Model Code	Known Gene Name	Unigene Sequence Cluster Title
-				Rattus norvegicus palmitoyl-	and the second s
		1	İ	protein thioesterase 2	
2000	4000			(Ppt2),mRNA. 11/22Length =	
2066	18820	NM_019367	s,t	166	palmitoyl-protein thioesterase 2
		1		Rattus norvegicus EGL nine	
- 1		ì	1	homolog 3 (C. elegans) (Egin3)	
2067	1323	NM_019371	c,aa,bb,ii	mRNA. 11/22Length = 2825	
			0,00,00,11	111 d. 11122Leilgut - 2020	EGL nine homolog 3 (C. elegans)
1				Rattus norvegicus EGL nine	
			į	homolog 3 (C. elegans) (Egin3)	
2067	1324	NM_019371	f,g,aa,bb,kk	mRNA. 11/22Length = 2825	EGI, nine homolog 3 (C. elegans)
1				Rattus norvegicus prodynorphi	n
2000	00000			(Pdyn), mRNA. 11/22Length =	
2068	20298	NM_019374	l,m	747	prodynorphin
			1	Doffue nerveel	
		1	1	Rattus norvegicus stromai cell	1
2069	18032	NM_019380	b,l,m	derived factor receptor 1 (Sdfr1)	
	10002	11111_019000	0,1,111	mRNA. 11/22Length = 2369 Rattus norvegicus golgi	stromal cell derived factor receptor 1
- (		l	1	peripheral membrane protein	
				p65 (GRASP65), mRNA.	1
2070	2453	NM_019385	j,k	11/2Length = 2493	
			1	Rattus norvegicus tissue-type	golgi peripheral membrane protein p65
			ł	transglutaminase (Tgm2),	
2071	16	NM_019386	cc,dd,kk	mRNA.11/22Length = 3393	tissue-type transglutaminase
				Rattus norvegicus Kruppel	ussuc-type transgidtanimase
- [				associated box (KRAB) zinc	
				finger 1(Kzf1), mRNA.	
2072	904	NM_019620	р	11/2Length = 194	Kruppel associated box (KRAB) zinc finger 1
Ì				Rattus norvegicus calpactin I	calpactin I heavy chain, hydroxyacid oxidase 3
2073	57A	NM 040005		heavy chain (Anxa2), mRNA.	(medium-chain), unknown Glu-Pro dipeptide repe
20/3	3/4	NM_019905	a,h,l,z,aa,kk,ll	11/22Length = 1395	protein
- 1				Rattus norvegicus postsynaptic	
				protein Cript (Cript), mRNA.	
2074	15911	NM_019907	cc,dd	11/22Length = 1435	and a marks and the same
			1	Rattus norvegicus eukaryotic	postsynaptic protein Cript
				initiation factor 5 (eIF-5)(Eif5),	
2075	18713	NM_020075	p,q,s,t	mRNA. 11/2Length = 354	eukaryotic initiation factor 5 (eIF-5)
Ì	j			Rattus norvegicus eukaryotic	7
2075	40745	NIL 0000===		initiation factor 5 (eIF-5)(Eif5),	
2075	18/15	NM_020075	ee,ff	mRNA. 11/2Length = 354	eukaryotic initiation factor 5 (eIF-5)
	[			Rattus norvegicus a disintegrin	
	Į.		( )	and metalloproteinase	
2076	13486	NM_020306	log bb	domain17 (Adam17), mRNA.	
-0,0	10400	VIVI_UZU3U0	aa,bb	11/22Length = 4128	a disintegrin and metalloproteinase domain 17
	1		1	Rattus norvegicus thymosin, beta 1 (Tmsb1), mRNA.	
2077	20816	NM_021261	С	44001 11	thromasia bata 40
			<del>-</del>	Rattus norvegicus ribosomal	thymosin, beta 10
	ĺ			protein L35a (Rpl35a),	
2078	15335	VM_021264	w	- 5114 442661	ribosomal protein L35a
			į		mooomai protein Looa
1			1 '		
	- 1		ı	radus norvegicus transforming i	
2079	10-22	NM_021578	]	ratius norvegicus transforming growth factor, beta 1 (Tgfb1), mRNA. 11/22Length = 1585	

TABLE	1	GenBank Ac	o.	PACK MARK ARMADI AND THE	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC I	D No.	Model Code	The state of the s	潜域强烈 人名英格兰 计电路系统 医二甲基乙醇
			. INjuder Code	Known Gene Name	Unigene Sequence Cluster Title
		ļ		Rattus norvegicus activity and	
			(	neurotransmitter-induced early	1
		ļ		gene protein 4 (ania-4) (Ania4)	
2080	1894	6 NM_021584	s,t	mRNA. 11/22Length = 4831	
				Rattus norvegicus gap junctior	protein 4 (ania-4)
l		1		membrane channel protein	
				alpha 4(Gja4), mRNA.	Gan junction mombrane at a second
2081	2544	5 NM_021654	_ r	11/22Length = 12	Gap junction membrane channel, protein alpha 4 (connexin 37)
				Rattus norvegicus	ESTS. Highly similar to SVA ULIMAN Alamy (DA)
2000	00.40		ľ	neurexophilin 4 (Nxph4), mRNA	A. synthetase (Alanine-tRNA ligase) (AlaRS)
2082	2342	4 NM_021680	j,k	11/22Length = 1265	[H.sapiens]
}		1	}	Rattus norvegicus membrane-	
				associated guanylatekinase-	
2083	1066	NM_021686	1_	interacting protein (LOC59322),	membrane-associated guanylate kinase-interacting
2000	1300	111111_02 1000	n	mRNA. 3/21Length = 2691	protein
			1	Rattus norvegicus cAMP-	
- 1		1	}	regulated guanine nucleotide	}
1				exchangefactor I (cAMP-GEFI)	
2084	19667	NM_021690	lii	(Epac), mRNA, 11/2Length = 3373	cAMP-regulated guanine nucleotide exchange
			<del> </del> "	Rattus norvegicus prothymosin	factor i (cAMP-GEFI)
į				alpha (Ptma), mRNA.	
2085	22916	NM_021740	lii	11/22Length = 1182	January 1
				Rattus norvegicus CD14	prothymosin alpha
				antigen (Cd14), mRNA.	
2086	19710	NM_021744	a,j,k,q,hh,kk	11/22Length = 1591	CD14 antigen
				Rattus norvegicus Nopp14	OD 14 anugen
				associated protein (Nap65),	
2087	20035	NM_021754	a,y,z	mRNA. 11/2Length = 198	Nopp140 associated protein
1		l	1	Rattus norvegicus progesterone	
				receptor membrane component	
2088	17936	NM_021766	la	1(Pgrmc1), mRNA. 11/22Length	
2000	17300	14141_021700	d,r,gg	= 1885	progesterone receptor membrane component 1
1				I valida noi vegicus Avian	
1	1		į	sarcoma virus 17 (v-jun)	
2089	22351	NM_021835	ee,ff	oncogene homolog (Jun), mRNA. 4/22Length = 2573	
			100,111	Rattus norvegicus jun B proto-	Avian sarcoma virus 17 (v-jun) oncogene homolog
			J	oncogene (Junb), mRNA.	
2090	20161	NM_021836	j,k,p,q,r	1441001 11 1	iun D prote consume
T			<u> </u>	Rattus norvegicus fibroblast	jun B proto-oncogene
				growth factor 16 (Fgf16), mRNA.	
2091	20177	NM_021867	d,jj,kk		Fibroblast growth factor 16
- 1	- 1			Rattus norvegicus tissue	interest growth factor 10
- 1	-		ļ	inhibitor of metalloproteinase 2	
2000	040	114 004555		(Timp2), mRNA. 11/22Length =	
2092	243	VM_021989	h,l,n,o,ll	19	ESTs, tissue inhibitor of metalloproteinase 2
				Rattus norvegicus Hexokinase	of motomoproteinase 2
2093	17100	IM 000470		3 (Hk3), mRNA. 12/2Length =	
2033	17 100	NM_022179	h,l,w,x,dd	3692	dexokinase 3
!	- 1	l		Rattus norvegicus	
	- 1			topoisomerase (DNA) 2 alpha	
2094	237801	IM_022183	11 66	(Top2a), mRNA. 11/22Length =	j
	-0.001	····_UZZ 103	jj,kk	652	opoisomerase (DNA) II alpha

TABLE	1	GenBank Ad	igna (j. 1945) Maria di Santa di Santa di Santa di Santa di Santa di Santa di Santa di Santa di Santa di Santa di Santa di San	31	Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GLGC	- 1	Model Calle		Unigene Sequence Cluster Title
بدرية	0200	91140. W	Model Code	Known Gene Name	Unigene Sequence Cluster Title
	l	1		Rattus norvegicus leukemia	
				inhibitory factor (Lif), mRNA.	
2095	2020	4 NM_022196	ee,ff,kk	11/22Length = 69	leukemia inhibitory factor
				Rattus norvegicus putative	redicernia infinibility factor
	•	1	İ	chloride channel (similar to	
				MmClcn4-2) (LOC6586), mRNA	
2096	2022	5 NM_022198	b,l,m	12/2Length = 2244	
		- 11111_022100	0,4,111	Pottus popus de Ol	putative chloride channel (similar to Mm Clcn4-2)
				Rattus norvegicus Chemokine	
2097	2024	9 NM_022205	ln	receptor (LCR1) (Cxcr4), mRNA	
	2024	JINIVI_022205	_ "	5/22Length = 15	Chemokine receptor (LCR1)
		j		Rattus norvegicus neuromedin	
2000	20.45			(Nmu), mRNA. 11/22Length =	
2098	2045	NM_022239	b,l,m,u,v	832	neuromedin U
ĺ			Ì	Rattus norvegicus cytochrome	
				b5 (Cyb5), mRNA. 12/2Length =	
2099	762	NM_022245	h,i	751	
				Rattus norvegicus	cytochrome b5
		1		aminopeptidase A (Enpep),	
2100	6263	NM_022251	jj,kk	mRNA. 12/2Length = 475	
				Pattus popularious = 4/5	aminopeptidase A
l l		j		Rattus norvegicus connective	
2101	6585	NM_022266	or lete	tissue growth factor (Ctgf),	
	0000	11111_022200	q,kk	mRNA.11/22Length = 2345	connective tissue growth factor
				Rattus norvegicus sorting nexin	
0400	40756			16 (Snx16), mRNA. 12/2Length	
2102	13/58	NM_022289		= 1773	ESTs
1				+	
				Rattus norvegicus ETL protein	
2103	23511	NM_022294	n,o	(Eti), mRNA. 12/2Length = 4274	ETI protoin
				Rattus norvegicus	ETE protein
- 1				dimethylarginine	
				dimethylaminohydrolase 1	
				(Ddah4) = DNA Sign	
2104	19423	NM_022297	ļ.,,	(Ddah1), mRNA. 5/22Length =	
	10420	14141_022237	u,v	38	dimethylarginine dimethylaminohydrolase 1
			1	Rattus norvegicus alpha-tubulin	
2105	47450	1114 000000	1	(Tuba1), mRNA. 12/2Length =	
2105	1/158	NM_022298		1617	alpha-tubulin
				Rattus norvegicus alpha-tubulin	,
			1 10	(Tuba1), mRNA. 12/2Length =	
2105	17160	NM_022298	b,i,m,aa		alpha-tubulin
				Rattus norvegicus alpha-tubulin	aipna-tubuiiii
				Tuba1), mRNA. 12/2Length =	
2105	17161	NM_022298	a,z,kk	· ^ -	atala a a m
					alpha-tubulin
			.	Rattus norvegicus brain acidic	
2106	18246	NM_022300	pp   r	membrane protein (Basp1),	
2.00	.0240	1111_022300	hh r	nRNA. 12/2Length = 124	brain acidic membrane protein
[			]	Rattus norvegicus Proliferating 1	
			j lo	ell nuclear antigen	
1			1 (0	Pcna),mRNA. 11/22Length =	
245		NM_022381	d,l,m,n,o,s,t   1	16	Proliferating cell nuclear antigen
2107	11454			Rattus norvegicus Proliferating	romorading cell nuclear affugen
2107	11454		م ا	ell nuclear antigen	
2107	11454		11:		
2107	11454			Ponal mPNA 44/001	
		JM 022381	(1	Pcna),mRNA. 11/22Length =	
2107		VM_022381	s (1	Pcna),mRNA. 11/22Length = 16	Proliferating cell nuclear antigen
		NM_022381	s (1	Pcna),mRNA. 11/22Length = 16 Rattus norvegicus FXYD	Proliferating cell nuclear antigen
		VM_022381	s 1 F	Pcna),mRNA. 11/22Length = 16 Factus norvegicus FXYD omain-containing ion transport	Proliferating cell nuclear antigen
	11455 (	NM_022381 !M_022388	(I s 1 f d	Pcna),mRNA. 11/22Length = 16 Rattus norvegicus FXYD	Proliferating cell nuclear antigen

TAE	3LE 1				10,44,0	Att. Def: 4/4004, 5000 04 100 (040)
		4. 9. 0	GenBank Acc.	3 KG TO TO KANG	1 12 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Alty. Ref. 44921-5090-01-WO/2105485
SEC	ַ סוג	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
					Rattus norvegicus quinoid	The state of the s
				1	dihydropteridine reductase	
1					(Qdpr),mRNA. 11/22Length =	
	2109	13480	NM_022390	1	137	quinoid dihydropteridine reductase
					Rattus norvegicus growth	quirou dirrydropteridine reductase
i					response protein (CL-	
					6)(LOC64194), mRNA.	
<u></u> :	2110	22412	NM_022392	p,q	12/2Length = 241	growth response protein (CL-6)
1					Rattus norvegicus macrophage	
ł				}	galactose N-acetyl-	
]	l				galactosamine specific lectin	
				a,p,q,cc,dd,ee,	(MgI), mRNA. 1/22Length =	macrophage galactose N-acetyl-galactosamine
	2111	22499	NM_022393	ff,jj,kk	1358	specific lectin
	j				Rattus norvegicus scaffold	speame touri
Ι.					attachment factor B (Safb),	
<u> </u>	2112	23061	NM_022394	s,t	mRNA.11/22Length = 3113	scaffold attachment factor B
	I				Rattus norvegicus	- The state of the
		İ			mitochondrial processing	ESTs, Weakly similar to mitochondrial processing
					peptidase beta (Pmpcb), mRNA.	peptidase beta [Rattus norvegicus] [R.norvegicus],
1	2113	18221	NM_022395	cc,dd	12/2Length = 157	mitochondrial processing peptidase beta
l					Rattus norvegicus guanine	Processing peptidase beta
					nucleotide binding protein	
Ι.					gamma subunit 11 (Gng11),	guanine nucleotide binding protein gamma subunit
2	2114	23705	NM_022396	e,j,k,ii	mRNA. 12/2Length = 557	11
l						
		1			Rattus norvegicus 2-	
					oxoglutarate carrier (LOC6421),	
2	115	23300	NM_022398	jj,kk	mRNA.12/2Length = 946	2-oxoglutarate carrier
		ĺ			Rattus norvegicus calreticulin	- the grant and the carrier
_					(Calr), mRNA. 11/22Length =	
<u> 2</u>	116	24536	NM_022399	h,l,n,o	1882	calreticulin
		i			Rattus norvegicus branched	
		i			chain aminotransferase 2,	
_					mitochondrial (Bcat2), mRNA.	
2	117	24643	NM_022400	b,u,v	11/22Length = 1548	branched chain aminotransferase 2, mitochondrial
	- 1				Rattus norvegicus Aldehyde	The state of the s
	Ì	j	f	ď	dehydrogenase 1, subfamily A1	•
0	440	00045			(Aldh1a1), mRNA. 1/21Length =	
	118	∠0915	VM_022407	kk	212	Aldehyde dehydrogenase 1, subfamily A1
	·	}	l	1	reallus norvegicus territin light	
2	119	9244	ILA DODECO		chain 1 (FtI1), mRNA.	
	113	02111	NM_022500	j,kk	11/22Length = 552	ferritin light chain 1
	İ				Rattus norvegicus ferritin light	
2.	119	8212	NM_022500		chain 1 (FtI1), mRNA.	
	. 13	02121	NIVI_UZZOUU	n,i,kk,ii	11/22Length = 552	ferritin light chain 1
		. 1			Rattus norvegicus ribosomal	
21	120	A250 N	M_022504 f		protein L36 (Rpl36), mRNA.	
		72031	1W_UZZJU4		11/22Length = 364	ribosomal protein L36
		ļ	ļ	1.	Rattus norvegicus Rhesus	
21	121	8586	IM_022505	10	plood group (Rh), mRNA.	
		00001	022303	19	11/22Length = 1269	Rhesus blood group
	ļ				Rattus norvegicus Rhesus	
21	21	8587	IM_022505	),u,v [1	plood group (Rh), mRNA.	
	1	0007	022000  L		1/22Length = 1269	Rhesus blood group
		-	1	1.	Rattus norvegicus ribusumal	
	!		M 022510		protein L4 (Rpl4), mRNA.	
94	וניני	100716	(L) (L) (L) (L) (L)	;kk   1	1/22Length = 1387	ibosomal protein L4

TABLE		GenBank Ac	C.FLS 1952.5	74. √20 21. 1889 18. 13. 13. 10. 10. 10. 10. 10. 10. 10. 10. 10. 10	Atty. Ref. 44921-5090-01-WO/2105485
SEQIID	GLGC II	) No.	Model Code	Komm Com Na	2. (1) A 整理的 1. (1) A 图像 1. (1) A 图 1. (1)
	see realis	., .,	Imodei Code	Taranta I I I I I I I I I I I I I I I I I I I	Unigene Sequence Cluster Title
	İ			Rattus norvegicus profilin	
2123	210	NM_022511		(Pfn1), mRNA. 12/2Length =	
2120	210	DINN_022511	n,o,w,x	689	profilin
				Rattus norvegicus ribosomal	
2124	202	7 114 000544		protein L27 (Rpl27), mRNA.	
2124	302	NM_022514	W,X	11/22Length = 463	ribosomal protein L27
		1		Rattus norvegicus ribosomal	
2125	0000	NN4 000=4=	L	protein L24 (Rpl24), mRNA.	
2125	2696	NM_022515	cc,dd	11/22Length = 541	ribosomal protein L24
				Rattus norvegicus ribosomal	
0405	000-			protein L24 (Rpl24), mRNA.	
2125	2697	NM_022515	f,g,gg	11/22Length = 541	ribosomal protein L24
l		1		Rattus norvegicus	inscontai protein E24
		ļ		polypyrimidine tract binding	ł
				protein (Ptb), mRNA.	
2126	3900	NM_022516	s,t	11/22Length = 2723	polypyrimidine to at his di
Ţ				Rattus norvegicus	polypyrimidine tract binding protein
			1	polypyrimidine tract binding	
				protein (Ptb), mRNA.	
2126	3904	NM_022516	aa,bb,ll	11/22Length = 2723	malamata de la companya de la compan
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Rattus norvegicus	polypyrimidine tract binding protein
				polypyrimidine tract binding	
				protein (Ptb), mRNA.	
2126	162	NM_022516	e,u,v	11/22 and STO	
			C,u,v	11/22Length = 2723	malate dehydrogenase mitochondrial
				Rattus norvegicus ADP-	
2127	4145	NM_022518	jj,kk	ribosylation factor 1 (Arf1),	
	9	7111_022010	II,KK	mRNA.11/22Length = 9	ADP-ribosylation factor 1
	j			Rattus norvegicus ADP-	
2127	1151	NM_022518	h	ribosylation factor 1 (Arf1),	
	7101	NIVI_UZZ310	b,l,m	mRNA.11/22Length = 9	ADP-ribosylation factor 1
- 1			]	Rattus norvegicus omithine	
2128	1212	MA OOOEO4	[	aminotransferase (Oat), mRNA.	
2120	4242	NM_022521	b,l,m	11/22Length = 1938	omithine aminotransferase
ĺ				Rattus norvegicus CD151	
2420	4440	11.4 000-00	l. 1	antigen (Cd151), mRNA.	
2129	4412	NM_022523	l,m	11/22Length = 1668	CD151 antigen
ľ					
1	- 1			Rattus norvegicus sushi-repeat-	
0400	4004			containing protein (Srpx).	
2130	4601	NM_022524	l,m r	nRNA.11/22Length = 1827	sushi-repeat-containing protein, X chromosome
			]	Rattus norvegicus plasma	protein, A citioniosome
	l		9	lutathione peroxidase	
040	40		F	precursor(Gpxp), mRNA.	
2131	4615 N	IM_022525	cc,dd 1	2/2Length = 134	plasma glutathione peroxidase precursor
				Rattus norvegicus desmin	proving graduitone peroxidase precursor
			i (i	Des), mRNA. 11/22Length =	
2132	6100 N	IM_022531		1400	desmin
	Γ				destrini
			11	Rattus norvegicus A-raf (Araf1),	
2133	6577 N	M_022532	u,v n	Dill of the	A rof
				Rattus norvegicus	A-raf
]	1	1	ltr	anscobalamin II precursor	
	.		lő	Ccn2p), mRNA. 11/22Length =	
2134	7505 N	M_022534 i	i I	00	
			·	<u> </u>	transcobalamin II precursor
- 1	1		1.	Pattus noncosione	
2135	8097 NI	M_022536	),I   [F	Rattus norvegicus cyclophilin B Ppib), mRNA. 12/2Length = 84	

<b>)</b> ,	h ::	GenBank Ad	C.	A Section of the Section 18	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID:	GEGCIE	No.	Model Code		5. (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)
			inoaci coac	Traiowii Gene Name	Unigene Sequence Cluster Title
		1		D-11	
2135	8098	NM_022536	- I.,	Rattus norvegicus cyclophili	Į.
	- 5550	14141_022556		(Ppib), mRNA. 12/2Length =	84 cyclophilin B
	ł		'	Rattus norvegicus	
			ł	phosphatidate	1.
		[		phosphohydrolase type	
2136	9506	NIM 000500		2a(Ppap2a), mRNA. 5/22Len	gth
2130	0090	NM_022538		= 871	phosphatidate phosphohydrolase type 2a
ľ				Rattus norvegicus	- Priosphonydiolase type za
1			j	phosphatidate	
ľ			ļ	phosphohydrolase type	
2136	0507	NIN 000500		2a(Ppap2a), mRNA. 5/22Leng	gth
2130	0097	NM_022538	aa,bb,kk,li	= 871	phosphatidate phosphohydrolase type 2a
1				Rattus norvegicus	
2137	0040	<b></b>		peroxiredoxin 3 (Prdx3), mRN	A.
2137	9240	NM_022540	j,k,w,x	11/22Length = 1433	peroxiredovin 3
- 1				Rattus norvegicus rhoB gene	Parestradoxiiro
2420	05.44		İ	(Arhb), mRNA. 12/2Length =	
2138	9541	NM_022542	e,r	2183	rhoB gene
	1			Rattus norvegicus Death-	
0400				associated like kinase (Dapkl),	
2139	12422	NM_022546	n,o	mRNA. 12/2Length = 1514	Death-accorded like likes
	- 1			Rattus norvegicus thioredoxin	Death-associated like killase
2440	242-2			reductase 2 (Txnrd2),	
2140	21076	NM_022584	e,w,x	mRNA.11/22Length = 1999	thioredoxin reductase 2
				Rattus norvegicus ornithine	unoredoxiir reductase 2
				decarboxylase antizyme	
	- 1			inhibitor(Oazi), mRNA.	
2141	21062	NM_022585	gg	11/22Length = 4269	Ornithing decembers 1
				Rattus norvegicus ornithine	ornithine decarboxylase antizyme inhibitor
	ł			decarboxylase antizyme	
أسيم			ł	inhibitor(Oazi), mRNA.	
2141	21063 N	IM_022585	f,y,z	11/22Length = 4269	ornithing department and a series of the series
				Rattus norvegicus metastasis	ornithine decarboxylase antizyme inhibitor
ا				associated 1 (Mta1), mRNA.	
2142	20762 N	M_022588	r,s,t	1/21Length = 2741	metastasis associated 1
j	i			Rattus norvegicus enoyl	metastasis associated 1
	ļ		ł	coenzyme A hydratase 1	
				(Ech1), mRNA.11/22Length =	
3493	20925 N	M_022594	g,hh	197	Porovisomel en aut but at a transfer and a transfer at a t
				Rattus norvegicus cellular	Peroxisomal enoyl hydratase-like protein
			1	nucleic acid binding protein	
i				(Cnbp),mRNA. 11/22Length =	1
2144	20959 N	M_022598	d,r	164	collular puolojo paid bitalii
				Rattus norvegicus celiular	cellular nucleic acid binding protein
]				nucleic acid binding protein	
				(Cnbp),mRNA. 11/22Length =	
2144	20960 NI	M_022598	c,e,r	164	Cellular nuclois said his di
į.				Rattus norvegicus serine	cellular nucleic acid binding protein
احدیم				threonine kinase pim3 (Pim3),	
2145	21115 NA	/_022602	,k	mRNA.1/21Length = 2133	Serine throoning kinges at . S
				Rattus norvegicus protein	serine threonine kinase plm3
!			l.	phosphatase 2C (AF95927),	
2146	21206 NN	1_022606	<u> </u>	mRNA.1/21Length = 1318	protoin phosphology 80
1	ĺ	i		1010	protein phosphatase 2C
i	-	į.		Rattus norvegicus H2A histone	
- ;			İf	amily, member Z (H2afz),	
ا راحات	7661 NM	_022674 d	<u>i.gg</u> r	-Dila dame.	NOA LILL & W
			<del></del>		H2A histone family, member Z

TABLE 1			, Ri		Atty. Ref. 44921-5090-01-WO/2105485
		GenBank Acc	NATH PA	A STATE OF STREET	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1
SEQ ID	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
					The same of the sa
				Rattus norvegicus protein	
		•		phosphatase 1, regulatory	
			1	(inhibitor) subunit 1A (Ppp1r1a)	, protein phosphatase 1, regulatory (inhibitor) subunit
2148	24564	NM_022676	f	mRNA. 11/22Length = 619	11A
		1		Rattus norvegicus germinal	
04.00			1.	histone H4 gene (Hist4), mRNA	
2149	20506	NM_022686	d	1/21Length = 377	germinal histone H4 gene
			ł	Rattus norvegicus germinal	ESTs. Highly similar to 148404 histone H4 (5544) (4
	0.101		İ.	histone H4 gene (Hist4), mRNA	. is 3rd base in codon) - mouse (fragment)
2149	6121	NM_022686	d,r	1/21Length = 377	[M.musculus]
				Rattus norvegicus	
)			ļ	synaptosomal-associated	
0450	00500			protein, 23 kD(Snap23), mRNA.	
2150	20509	NM_022689	b,r,u,v	1/21Length = 633	synaptosomal-associated protein, 23 kD
1				Rattus norvegicus p15	
2454	47500	NIN 4 00000 /		coactivator (U83883), mRNA.	
2151	1/586	NM_022694	w,x	8/21Length = 3166	p105 coactivator
1 1			1	Rattus norvegicus ribosomal	
0450	47700			protein L28 (Rpi28), mRNA.	
2152	1//29	NM_022697	f,g,w,x,cc,dd	11/22Length = 466	ribosomal protein L28
1					
1 1				Rattus norvegicus bcl-2	
0450	4	NIL 000000		associated death agonist (Bad),	
2153	1//5/	NM_022698	cc,dd	mRNA. 1/21Length = 115	bcl-2 associated death agonist
				Rattus norvegicus ribosomal	
ارمدا	47000			protein L3 (Rpl3), mRNA.	
2154	1/808	NM_022699	∞,dd	11/22Length = 392	ribosomal protein L30
1				Rattus norvegicus flotillin 1	
0455	04040	NIM COOTES		(Flot1), mRNA. 11/22Length =	
2155	24346	NM_022701	99	2157	flotillin 1
				Rattus norvegicus major vault	
2450		1114 000747		protein (Mvp), mRNA.	
2156	58	NM_022715	u,v	11/22Length = 2756	major vault protein
	j			Rattus norvegicus Munc13-1	
2457	404	NILA 000004		(Unc13h1), mRNA. 1/21Length	
2157	194	NM_022861	cc,dd	= 6683	Munc13-1
	ł			Rattus norvegicus iron-	
2158	202	NIM COORCE		regulatory protein 2 (Ireb2),	
	202	NM_022863	h,l	mRNA. 1/21Length = 377	iron-regulatory protein 2
- 1				Rattus norvegicus microtubule-	
	ľ			associated proteins 1A/1B	
2159	22606	NIM OCCO		lightchain 3 (MPL3), mRNA.	
2109	23000	NM_022867	w,x	1/21Length = 861	microtubule-associated proteins 1A/1B light chain 3
1				Rattus norvegicus microtubule-	
1	1	ĺ		associated proteins 1A/1B	
2159	22600	JIM 000007		lightchain 3 (MPL3), mRNA.	
2108	23000	VM_022867		1/21Length = 861	microtubule-associated proteins 1A/1B light chain 3
		1		Rattus norvegicus nucleolar	
2160	2//2021	NM_022869	.	phosphoprotein p13 (Nopp14),	
2100	£7203	*IVI_UZZ009 !	s,t	mRNA. 1/21Length = 369	nucleolar phosphoprotein p130
1	1	į		Rattus norvegicus DnaJ-like	
2161	6801	NM_022934		protein (Hsj2), mRNA.	
2101	20911	VIVI_UZZ934 (	ee,ff	11/22Length = 161	DnaJ-like protein
			1	เพลีแนร แบเ ของเบ็นร บรู้ใบรบที่บ	
2162	2006	IM_022936		epoxide hydrolase (Ephx2),	
2102	2000;1	41A1_055290	aa l	mRNA. 1/21Length = 1992	cytosolic epoxide hydrolase

Atty, Ref. 44921-5090-01-WO.  SEQ ID GLGC ID No. Model Code Known Gene Name Unigene Sequence Cluster Tit	Z100400
SEQ ID GLGC ID No. Model Code Known Gene Name Unigene Sequence Cluster Tit	
	le .
Rattus norvegicus cytosolic	First to a second of the second
epoxide hydrolase (Ephx2),	
2162 2008 NM_022936 w,x,aa,bb mRNA. 1/21Length = 1992 cytosolic epoxide hydrolase	
Rattus norvegicus syntaxin 12	
(Stx12), mRNA. 11/22Length =	
2163 15697 NM_022939 II 819 syntaxin 12	
Rattus norvegicus suppressor	
of K+ transport defect 3	
(Skd3),mRNA. 11/22Length =	1
2164 18098 NM_022947 I 2138 suppressor of K+ transport def	ect 3
Rattus norvegicus	
tricarboxylate carrier-like	
protein(Loc6542), mRNA.  2165 18104 NM_022948 hh 1/21Length = 2699 tricarboxylate carrier-like protein	
	in
Rattus norvegicus ribosomal protein L14 (Rpl14), mRNA.	
2100 18107 NM_022949 ft,g   11/22Length = 715   ribosomal protein L14   Rattus norvegicus slit homolog	
1 (Drosophila) (Slit1), mRNA.	
2167 15727 NM_022953 u,v 11/22Length = 495 Slit1	
Rattus norvegicus vacuolar	
protein sorting protein	
33a(Vps33a), mRNA.	
2168 3337 NM_022961 a,y,z 1/21Length = 3269 ESTs	
Rattus norvegicus tRNA	
selenocysteine associated	1
protein(Secp43), mRNA.	
2169 9286 NM_023027 I,m 11/22Length = 864 tRNA selenocysteine associate	ed protein
Rattus norvegicus casein	p.o.com
kinase 1 gamma 2 isoform	
(Csnk1g2), mRNA. 2/21Length	
2170 23215 NM_023102 b,l,m = 1572 casein kinase 1 gamma 2 isofo	rm
Rattus norvegicus alpha(1)-	
inhibitor 3, variant I (Mug1),  2171 8269 NM_023103 b.i.m mRNA 2/21I ength = 462 cloba(1) inhibitor 3, variant I	
2171 8269 NM_023103 b,I,m mRNA.2/21Length = 462 alpha(1)-inhibitor 3, variant I	
Pottus population	
Rattus norvegicus CCAAT/enhancer binding	
	Iso NF-IL6, nuclear
2172 21238 NM_024125 p,q mRNA. 11/22Length = 148 factor-IL6, previously designate	id ICF5)
Rattus norvegicus	
CCAAT/enhancer binding	
p,q,r,bb,ee,ff,k protein (C/EBP), beta (Cebpb). If iver activating protein (LAP) a	ileo NE-II 6 suctos
2172 21239 NM_024125 k mRNA. 11/22Length = 148 factor-IL6, previously designate	A TOF5)
Rattus norvegicus growth arrest	u rora)
and DNA-damage-inducible 45	
alpha (Gadd45a), mRNA.	
2173 352 NM_024127 p,q 11/22Length = 711 DNA-damage-inducible transcri	pt 1
Rattus norvegicus growth arrest	
and DNA-damage-inducible 45	1
alpha (Gadd45a), mRNA.	
2173 353 NM_024127 q,ee,ff,gg 11/22Length = 711 DNA-damage-inducible transcri	pt 1
Rattus norvegicus growth arrest	
and DNA-damage-inducible 45	1
alpha (Gadd45a), mRNA.   2173   354 NM_024127   p,q,ee,ff   11/22Length = 711   DNA-damage-inducible transcri	
L 2:75; 354]NM_024127 [p,q,ee,fr [11/22Length = 711 DNA-damage-inducible transcri	nt 1

		GenBank A	CC.	新門 实际 1000 大學 1000 中華 1	Atty. Ref. 44921-5090-01-WO/2105485
EQ ID	GLGC	) No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
				Rattus norvegicus D-	
	ļ			dopachrome tautomerase (Ddt	
2174	1722	6NM_024131	b,c,u,v	mRNA. 11/22Length = 628	
		1		111 TVA: 11/22Lengu1 = 020	D-dopachrome tautomerase
	ĺ		}	Rattus norvegicus D-	
2174	4700			dopachrome tautomerase (Ddt)	),
21/4	1/22	NM_024131	c	mRNA. 11/22Length = 628	D-dopachrome tautomerase
				Rattus norvegicus guanine	
	}	1		nucleotide binding protein,	
2175	1070	NN 004400		gamma 7(Gng7), mRNA.	guanine nucleotide binding protein (G protein),
2175	10/5	NM_024138	l,m	11/22Length = 2897	gamma 7 subunit
				Rattus norvegicus Fibroblast	
i				growth factor receptor 1 (Fgfr1)	1
2176	24623	NM_024146	l lu	mRNA. 5/22Length = 2469	
			<del>"</del>	IIII VAA. OIZZLENGIN = 2409	Fibroblast growth factor receptor 1
				Rattus norvegicus	
			1 '	apurinic/apyrimidinic	
			1	endonuclease 1 (Apex),mRNA.	
2177	20801	NM_024148	d,s,t	5/22Length = 1213	apurinic/apyrimidinic endonuclease 1
İ				Rattus norvegicus ADP-	Spanniorapymindrine endondelease 1
0470	4-4-4			ribosylation factor 2 (Arf2),	)
2178	1/42	NM_024150	p,q,y,ee,ff	mRNA.11/22Length = 17	ADP-ribosylation factor 2
ł				Rattus norvegicus ADP-	1,000,100,000
2170	17547	NN 004454		ribosylation factor 4 (Arf4),	
2179	1/51/	NM_024151	f	mRNA.11/22Length = 168	ADP-ribosylation factor 4
				Rattus norvegicus ADP-	
2180	21606	NM_024152	l	ribosylation factor 6 (Arf6),	
2100	21030	INIVI_UZ4152	y,z	mRNA.11/22Length = 995	ADP-ribosylation factor 6
				Rattus norvegicus annexin VI	
2181	561	NM_024156	jj,kk	(Anxa6), mRNA. 11/22Length = 2739	
-		0_1100	Шик	Rattus norvegicus annexin Vi	annexin VI
			1	(Anxa6), mRNA. 11/22Length =	
2181	562	VM_024156	r	2739	onnovin M
				Rattus norvegicus disabled	annexin VI
				homolog 2, mitogen-	
			1	responsivephosphoprotein	
				1/6	disabled homolog 2 mitages
2182	4504	NM_024159	d	5/22Length = 317	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)
	Γ			Rattus norvegicus cytochrome	Priochiobioteit (Diosobillia)
2400				b558 alpha-subunit (Cyba),	
2183	20770	M_024160	n,o	mRNA.2/21Length = 79	cytochrome b558 alpha-subunit
				Rattus norvegicus fatty acid	A series and a series arbitrary and the series are series and series are series and series are series are series and series are seri
2404	40,450		1	binding protein 3 (Fabp3),	
2184	16476 N	IM_024162	aa	mRNA. 11/22Length = 666	Fatty acid binding protein 3, muscle and heart
				Rattus norvegicus Heat shock	g Freezest of Induoic and Healt
2185	17701	IM 0040=4		cognate protein 7 (Hsc7),	
2100	1//04/1	IM_024351	e,p,r,ee,ff	mRNA. 11/22Length = 273	heat shock 70kD protein 8
				Rattus norvegicus Heat shock	
2185	17765 1	M_024351		cognate protein 7 (Hsc7),	
-100	1770011	IVI_UZ4301	e,p,q,r,ee,ff	mRNA. 11/22Length = 273	heat shock 70kD protein 8
				Rattus norvegicus	
				Phospholipase C , beta4	
186	20933N	M_024353		(Plcb4), mRNA. 1/22Length = 5297	
		···_ UATUUU	111.1		Phospholipase C , beta4

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	GLGC II	DINO.	Model Carl	Known Gene Name	Unigene Sequence Cluster Title
<u> </u>	SECO.	J 140,	iviodei Code	Known Gene Name	Unigene Sequence Cluster Title
			ł	Rattus norvegicus GTP	
				cyclohydrolase 1 (Gch), mRNA	
2187	1534	9 NM_024356	a,y,z	11/22Length = 116	GTP cyclohydrolase 1
				Rattus norvegicus GTP	Cyclonydrolase
		1		cyclohydrolase 1 (Gch), mRNA	
2187	1535	3 NM_024356	j,k,y,z,ii	11/22Length = 116	
			1	Rattus norvegicus hypoxla	GTP cyclohydrolase 1
			j	inducible factor 1, alpha subuni	
				(Hif1a), mRNA. 11/22Length =	
2188	1146	NM_024359	y,z	3718	
			7,4	Rattus norvegicus 5-	hypoxla inducible factor 1, alpha subunit
j		1		hydroxytaintemin (a and a d	
			}	hydroxytryptamine (serotonin)	
2189	767	NM_024365	ha	receptor 6(Htr6), mRNA.	
	, 0,	THM_024303	b,c	11/22Length = 1929	5-hydroxytryptamine (serotonin) receptor 6
ĺ		1	]	Rattus norvegicus follistatin-	, , , , , , , , , , , , , , , , , , , ,
2190	15500	NIM COADCO	4-	related protein (Frp), mRNA.	
2130	10022	NM_024369	f,g	11/22Length = 137	follistatin-related protein precursor
				Rattus norvegicus follistatin-	production
2100	45000	100		related protein (Frp), mRNA.	
2190	15623	NM_024369	Г	11/22Length = 137	follistatin-related protein precursor
				Rattus norvegicus prepro bone	Process protein produsor
2424			j	inducing protein (Gdf1), mRNA.	
2191	23488	NM_024375	n,o	3/21Length = 2411	prepro bone inducing protein
1				Rattus norvegicus hairy and	propre being modeling protein
- 1			1	enhancer of split 5	
				(Drosophila)(Hes5), mRNA.	
2192	_11628	NM_024383	ь	11/22Length = 592	hoin, and only and a way
				Rattus norvegicus 3-hydroxy-3-	hairy and enhancer of split 5 (Drosophila)
1				methylglutaryl CoA lyase	
	ľ			(Hmgcl), mRNA. 3/21Length =	
2193	2811	NM_024386	cc,dd	139	
			50,00	Rattus norvegicus 3-hydroxy-3-	3-hydroxy-3-methylglutaryl CoA lyase
i	- 1			mothylalytand Co.A. Ive	
			l	methylglutaryl CoA lyase	
2193	2812	NM_024386	W X 00 44	(Hmgcl), mRNA. 3/21Length =	
		1111_024000	w,x,cc,dd	139	3-hydroxy-3-methylglutaryl CoA lyase
-	- 1			rvallus norvegicus 3-nygroxy-3-	
1	- 1			methylglutaryl CoA lyase	
2193	2042	NA COACCO		(Hmgcl), mRNA. 3/21Length =	
C 133	2013	VM_024386	b	139	3-hydroxy-3-methylglutaryl CoA lyase
1	1			rvalida norvegicus immediale	,
j				early gene transcription factor	
104				NGFI-B (Nr4a1), mRNA.	
2194	21	VM_024388	W,X	3/21Length = 2488	mmediate early gene transcription factor NGFI-B
	- 1			Lyattas Horvedicas IUMediste	and agric transcription ractor NGFI-B
				early gene transcription factor	
				NGFI-B (Nr4a1), mRNA.	
194	· 22 N	IM_024388	w,x	0/041 11 0.00	mmediate early gone transaction ( )
				Rattus norvegicus peroxisomal	mmediate early gene transcription factor NGFI-B
	1	ľ	l.	multifunctional enzyme type II	
- 1			i.	(Hsd17b4), mRNA. 3/21Length	
195	25070N	IM_024392	r,ii		
				Rattus norvegicus a disintegrin	peroxisomal multifunctional enzyme type II
1	İ		.	ratios norvegicus a disintegnin	
!	!		ļ.	and metalloproteinase with	
!	!	į	Į!	hrombospondin motifs 1	
196	بالمممما	M_024400 k	k  1	ADAMTS-1) (Adamts1), mRNA.ja	disintegrin and metalloproteinase with
14h				/22Length = 4878	nrombospondin motifs 1 (ADAMTS-1)

		GenBank A		1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	Atty. Ref. 44921-5090-01-WO/2105485
EQID	GLGC I	D No.	Model Code	Known Gene Name	Unigene Sequence Cluster, Title
				Rattus norvegicus activating	y and the state of
		f		transcription factor ATF-4	
2407	, ,,,,,,			(Atf4),mRNA. 3/21Length =	
2197	1363	3 NM_024403	e,p,q,y,z	1173	activating transcription factor ATF-4
				Rattus norvegicus activating	3 serioripaon factor ATT 4
				transcription factor ATF-4	,
2407	4202	4	1	(Atf4),mRNA. 3/21Length =	
2197	1303	4 NM_024403	a,j,k,p,q,y,z	1173	activating transcription factor ATF-4
		ĺ		Rattus norvegicus activin type	1
2100	02	0 114 004400		receptor (Acvr1), mRNA.	
2198	93	8 NM_024486	u,v	3/21Length = 178	activin type I receptor
				Rattus norvegicus GrpE-like 1	,
2199	00	20114 004407	1	mitochondrial (Grpel1),	
2133	00.	2 NM_024487	hh	mRNA.5/22Length = 961	GrpE-like 1, mitochondrial
]		1	1	Rattus norvegicus CDK5	
		1	1	activator-binding protein C53	
2200	1701	NM_024488	l.,	(C53), mRNA. 3/21Length =	
2200	11311	14IVI_UZ4468	b,v ·	1865	CDK5 activator-binding protein C53
				Rattus norvegicus cytochrome	
				b5, outer mitochondrial	
2201	348	NM_030586	u,v	membranelsoform (omb5),	cytochrome b5, outer mitochondrial membrane
		1111_000000	u,v	mRNA. 3/21Length = 845	lisoform
				Rattus norvegicus cytochrome	*
				b5, outer mitochondrial	
2201	349	NM_030586	li I	membraneisoform (omb5),	cytochrome b5, outer mitochondrial membrane
				mRNA. 3/21Length = 845	isoform
				Rattus norvegicus Glutathione peroxidase 1 (Gpx1),	
2202	1852	NM_030826	aa,gg	mRNA.11/22Length = 1539	507 51 111
				Rattus norvegicus glypican 1	ESTs, Glutathione peroxidase 1
				(Gpc1), mRNA. 11/22Length =	
2203	21746	NM_030828	c		lehining 4
					glypican 1
	Į			Rattus norvegicus growth factor	.[
				receptor bound protein 2(Grb2)	
2204	18023	NM_030846	b	mRNA. 11/22Length = 299	grouth footer recent - 1
				Rattus norvegicus epithelial	growth factor receptor bound protein 2
				membrane protein 3 (Emp3),	
2205	21509	NM_030847	h,l,n,o	mRNA.11/22Length = 737	epithelial membrane protein 3
	- 1	-		Rattus norvegicus myocyte	DESCRIPTION OF THE PROPERTY OF
2000	40000			enhancer factor 2D (Mef2d).	
2206	16292	NM_030860	cc,dd	mRNA. 11/22Length = 1557	myocyte enhancer factor 2D
			1	Rattus norvegicus moesin	
2207	4040	114 000000	1	(Msn), mRNA. 11/22Length =	
201	1048	VM_030863	s,t,hh	200	moesin
	1				
	- 1			Rattus norvegicus pyruvate	
2208	1028	NM_030872		denydrogenase kinase 2 (Pdk2),	pyruvate dehydrogenase kinase 2 subunit p45
-200	19201	VIVI_U3U0/2	s,t	mRNA.11/22Length = 227	(PDK2)
	1			Dettus	
	- 1		[	Rattus norvegicus pyruvate	
208	1929	IM_030872	hh	PRIM 11/201 and 11 201	pyruvate dehydrogenase kinase 2 subunit p45
7		000012		!!! \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	(PDK2)
			! !.	Rattus norvegicus Guanine	
				lucieotide-binding protein beta	
209	21801N	M_030987	cc,dd,ii	(Gnb1), mRNA. 4/22Length =	_
					Guanine nucleotide-binding protein beta 1

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EO ID	GLGC I	) No	Model Code	Knda College	
	OCOO II	7110.	iliviodei Code	Known Gene Name	Unigene Sequence Gluster Title
				Rattus norvegicus Guanine	
				nucleotide-binding protein beta	
2209	2180	NM_030987		1(Gnb1), mRNA. 4/22Length =	
2203	2100	14W_030967	cc,dd	2837	Guanine nucleotide-binding protein beta 1
ĺ				Rattus norvegicus	
				synaptosomal-associated	ESTs, Highly similar to LAS1_MOUSE LIM AND
2210	8819	NM_030991	an bh	protein (Snap25),mRNA.	SH3 DOMAIN PROTEIN 1 (LASP-1) (MLN 50)
	0010	1110,000001	aa,bb	11/22Length = 21 Rattus norvegicus Microtubule-	[M.musculus]
				associated protein 1a (Map1a),	
2211	1991	NM_030995	h,i	mRNA. 4/21Length = 1,12	land the same of t
	100	1414_000000	1113	Rattus norvegicus actinin,	Microtubule-associated protein 1a
1			1	alpha 1 (Actn1), mRNA.	
2212	21166	NM_031005	a,n,o	5/22Length = 2956	
		1411_001000	المارة المارة	Rattus norvegicus arachidonate	actinin, alpha 1
!		1	1	12-lipoxygenase	
Í		İ		(Alox12),mRNA. 11/22Length =	
2213	25517	NM_031010	c,v	(Alox 12), IIIRNA. 11/22Length =	111
		14111_001010	C,V	Rattus norvegicus arachidonate	arachidonate 12-lipoxygenase
				12-lipoxygenase	
- 1		ł	1	(Alox12),mRNA. 11/22Length =	1
2213	1845	NM_031010	c,v	248	111
		007070	0,0	Rattus norvegicus S-	arachidonate 12-lipoxygenase
i			1	Adenosylmethionine	
				decarboxylase 1A (Amd1a),	
2214	15682	NM_031011	n,o	mRNA. 11/22Length = 312	
		00.1071	11,0	Rattus norvegicus S-	S-Adenosylmethionine decarboxylase 1
İ				Adenosylmethionine	
- 1				decarboxylase 1A (Amd1a),	
2214	15683	NM_031011	cc,dd,gg	mRNA. 11/22Length = 312	
			oo,uu,gg	Rattus norvegicus alanyl	S-Adenosylmethlonine decarboxylase 1
				(membrane) aminopeptidase	
				(Anpep), mRNA. 1/22Length =	
2215	1540	NM_031012	n	332	
				Rattus norvegicus muscarinic	alanyl (membrane) aminopeptidase
			) )	receptor m2 (Chrm2), mRNA.	
2216	1024	NM_031016	s,u,v	4/21Length = 2483	muscarinic receptor m2
				Rattus norvegicus muscarinic	muscamine receptor mz
- 1	i		1	receptor m2 (Chrm2), mRNA.	
2216	1025	NM_031016	u,v	4/21Length = 2483	muscarinic receptor m2
			·	Rattus norvegicus cAMP	indscannic receptor inz
				response element binding	
			}	protein 1 (Creb1), mRNA.	
2217	485	NM_031017		3/22Length = 1125	cAMP response element binding protein 1
				Rattus norvegicus drebrin 1	with response element binding protein 1
	l			(Dbn1), mRNA. 11/22Length =	
2218	1719	NM_031024			drebrin 1
				Rattus norvegicus LIC-2 dynein	and t
1	l			ight intermediate chain	
,	1			53/55(Dncli2), mRNA.	
2219	16210	NM_031026		4/21Length = 43	LIC-2 dynein light intermediate chain 53/55
				Rattus norvegicus guanine	are a dynorial infermentale chain 33/33
ļ				nucleotide binding protein, alpha	
l			ļ		guanine nucleotide binding protein (G protein) alph.
ZZZU	650	VTM_031034		1450	12
-!-					16
1	!		1	Rattus norvegicus GTP-binding	
2221		NM_031035	,	protein (G-alpha-i2) (Gnai2),	

ABLE	11 1 V 1 1 1 1	GenBank Ac	: 1/3 6 1/3 8/3 (4/8)		Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GL GC II	D No.			off of the first o
الم أن	GEGO II	PINO.	Model Code	The state of the s	Unigene Sequence Cluster Title
	Į			Rattus norvegicus glycogenin	The state of the s
0000				(Gyg), mRNA. 11/22Length =	
2222	1772	7 NM_031043	C	1624 .	glycogenin
				Rattus norvegicus inositol 1,4,	5-l
	i	j		triphosphate receptor type 2	
		İ		(Itpr2), mRNA. 11/22Length =	
2223	1818	8 NM_031046	gg	1,78	incoite) to the state of the st
				Rattus norvegicus unction	inositol triphosphate receptor type 2
				plakoglobin (Jup), mRNA.	
2224	173	1NM_031047	jj,kk	4/21Length = 3177	
				Rattus norvegicus lumican	unction plakoglobin
		1		(Lim) mPNA 44/001	
2225	1595	NM_031050	c,ii	(Lum), mRNA. 11/22Length =	
	1000	14141_001000	C <sub>1</sub> II	174	lumican
				Rattus norvegicus matrix	
		ł		metalloproteinase 2 (72 KDa	
2226	24400	NIM ODIOCI		type lVcollagenase) (Mmp2),	Rattus norvegicus gelatinase A mRNA, complete
2220	21102	NM_031054	l,m	mRNA. 5/22Length = 3231	cds
				Rattus norvegicus ribosomal	
0007				protein L1a (Rpl1a),	
2227	11849	NM_031065	h,l,n,o	mRNA.11/22Length = 71	ribosomal protein L10a
		1		Rattus norvegicus PCTAIRE-1	insocomal protein £10a
- 1				protein kinase, alternatively	
			Ĭ	spliced (Pctk1), mRNA.	
2228	25600	NM_031077	b,I,m	1/22Length = 3111	DOTAIDE 4 males as a second
				Rattus norvegicus PCTAIRE-1	PCTAIRE-1 protein kinase, alternatively spliced
- 1				protein kinase, alternatively	
				spliced (Pctk1), mRNA.	
2228	6349	NM_031077	ee,ff	1/22Length = 3111	
			100,11	Rattus norvegicus cyclic GMP	PCTAIRE-1 protein kinase, alternatively spliced
				ctimulated about a live	
				stimulated phosphodiesterase	
2229	79	NM_031079	v 7 00 ff	(Pde2a), mRNA. 4/21Length =	
		001070	y,z,ee,ff	398	cyclic GMP stimulated phosphodiesterase
				Rattus norvegicus	
				phosphatidylinositol 4-kinase	
2230	1681	NM_031083	L1	(Pik4cb),mRNA. 11/22Length =	
2200	4004	14IVI_031063	b,l,m	325	phosphatidylinositol 4-kinase
J				rattus norvegicus Rab3B	
2231	10007	NB4 024004		protein (Rab3b), mRNA.	
2231	1030/	NM_031091	w,x	4/21Length = 66	Rab3B protein
-	- 1			Rattus norvegious Rab3B	,
0004	10000			protein (Rab3b), mRNA.	
2231	18308	NM_031091	w,x	4/21Lengtl: = 55	Rab3B protein
				Rattus norvegicus (Rala),	
2232	15201	NM_031093	h,l,w	mRNA. 11/22Length = 952	
				Rattus norvegicus(Rala),	
2232	15202	VM_031093	f,w,x,cc,dd	mRNA. 11/22Length = 952	
				Rattus norvegicus (Rala),	
2232	15203	VM_031093	aa,bb	mRNA. 11/22Length = 952	
				Rattus norvegicus	
İ	[			Retinoblastoma-related gene	
	i i	2.2.		(Rb2), mRNA. 11/22Length =	
2233	1376	NM_031094		4004	- u . u .
	<del>-  </del>			Rattus norvegicus	Retinoblastoma-related gene
			Ì.	Tradition Pegicus	
2234	1205	IM_031097	ike ji	aminopeptidase B (Rnpep),	
	1230	001091	j,k,r r	TIKNA, 4/21Length = 228	aminopeptidase B
	- 1			Rattus norvegicus ribosomal	
2235	12620	IM_031099	ļ	protein L5 (Rpl5), mRNA.	
· /.3:31	1.75 5811	uvi DKTNUU I	e i1	11/22Length = 169	ibosomal protein L5

ABLE		GenBank Acc		M 7 195 195 1	Atty. Ref. 44921-5090-01-WO/2105485
EQ ID	GLGCI	No.	Model Code		等性機能與機能。 · 是一個學術學的 · 是一個學術學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一個學 · 是一
	9200 12	1,00	Iniddel:code		Unigene Sequence Cluster Title
				Rattus norvegicus ribosomal	
2235	12620	NM 034000		protein L5 (Rpl5), mRNA.	
2200	1203	9 NM_031099	<u>g</u>	11/22Length = 169	ribosomal protein L5
		1		Rattus norvegicus ribosomal	
2236	20941	NM 024400		protein L1 (Rpl1), mRNA.	
2230	20012	NM_031100	g,h,l	11/22Length = 769	ribosomal protein L10
				Rattus norvegicus ribosomal	
2237	2205/	NIM COMMON		protein L13 (Rpl13), mRNA.	
2201	23034	NM_031101	f,w,x,ll	11/22Length = 722	ribosomal protein L13
				Rattus norvegicus ribosomal	
2238	20/62	NM_031102	L.	protein L18 (Rpl18), mRNA.	
	20402	14141_031102	h,l	11/22Length = 67	ribosomal protein L18
1				Rattus norvegicus ribosomal	
2239	16938	NM_031103		protein L19 (Rpl19), mRNA.	
	10300	14141_031103	g	11/22Length = 73	ribosomal protein L19
- 1		1	1	Bettus served	
		ļ		Rattus norvegicus large subuni	it
2240	22205	NM_031105	h	ribosomal protein L36a(Rpl36a)	
22.10	22200	14W_031103	b	mRNA. 4/21Length = 444	large subunit ribosomal protein L36a
				Rattus norvegicus ribosomal	
2241	20807	NM_031106	f,g	protein L37 (Rpl37), mRNA.	
	, <u>, , , , , , , , , , , , , , , , , , </u>	1414_001100	1,9	11/22Length = 366	ribosomal protein L37
ļ				Rattus norvegicus ribosomal	
2242	16847	NM_031109	h,l,x	protein S1 (Rps1), mRNA.	
	10077	14111_001100	13,1,4	11/22Length = 61	ribosomal protein S10
l				Rattus norvegicus ribosomal	
2243	10878	NM_031110	g,j,k	protein S11 (Rps11), mRNA.	
		11112001110	91114	11/22Length = 534 Rattus norvegicus ribosomal	ribosomal protein S11
				protein S21 (Rps21), mRNA.	
2244	19162	NM_031111	h,ì	11/22Length = 359	
				Rattus norvegicus ribosomal	ribosomal protein S21
	1			protein S24 (Rps24), mRNA.	
2245	25458	NM_031112	h,l	11/22Length = 466	
				Rattus norvegicus ribosomal	
				protein S27a (Rps27a),	
2246	20839	NM_031113	w,x	mRNA.4/21Length = 552	ribosemal austriu 007
			<del></del>	Rattus norvegicus S-1 related	ribosomal protein S27a
	1			protein, clone 42C (S1A1),	
2247	19040	VM_031114	a,c,h,l,y,ee,ff	mRNA. 2/22Length = 573	S 100 related arrivals at 100
				Rattus norvegicus suppression	S-100 related protein, clone 42C
- 1		ŀ		of tumorigenicity 13	
				(coloncarcinoma) Hsp7-	
		ļ		interacting protein (St13),	Suppression of turned-a-1-14 (42 ( )
2248	23568	VM_031122	•	mRNA. 4/21Length = 1694	suppression of tumorigenicity 13 (colon carcinoma Hsp70-interacting protein
	T			Rattus norvegicus suppression	Free same racing brotein
	1	Ī		of tumorigenicity 13	
	1			(coloncarcinoma) Hsp7-	
				• •	Suppression of tumoriganists 40 /
2248	23569	IM_031122 r		DNIA 41041 11 11 1-11	suppression of tumorigenicity 13 (colon carcinoma
			-	Rattus norvegicus stanniocalcin	Hsp70-interacting protein
				1 (Stc1), mRNA. 11/22Length =	
2249	882 N	IM_031123 d	ı	44	stannicación 4
				Rattus norvegicus syntaxin 3	stanniocalcin 1
				(Stx3a), mRNA. 11/22Length =	
2250	1265 N	M_031124 u		151	ountario 2
1				Rattus norvegicus sulfite	syntaxin 3
			Į,	oxidase (Suox), mRNA.	
2251	14970 N	M_031127 a	,h,l,n,o	14/00) 11 1	pulita ovidana
					sulfite oxidase

TABLE		GenBank A	cc. I	1 : ***	Atty. Ref. 44921-5090-01-WO/2105485		
SEQ,ID	GLGC I	D No.	Model Code	Known Cone Name	the first of the contract of the second		
	-	1,10.	IMODEL CODE	Known Gene Name	Unigene Sequence Cluster Title:		
		ŀ		Rattus norvegicus transcriptio	n		
	l	ļ		elongation factor B (SIII)			
	l			polypeptide 2 (18kD, elongin B	n I		
00=0				(TCEB2), mRNA. 4/21Length =	transcription elongation factor B (SIII) polypeptide		
2252	652	5 NM_031129	gg	357	(18kD, elongin B)		
		1			(TOKE), CIONGIN B)		
			1	Rattus norvegicus transformin			
			1	growth factor, beta 2 (Tgfb2),	9		
2253	1392	9NM_031131	n,o,hh	mRNA. 11/22Length = 288	TOE hate 0 and 1		
					TGF beta 2 protein		
		1		Rattus norvegicus thyroid			
				hormone receptor alpha (Thra),			
2254	181	NM_031134	l,m	mRNA.11/22Length = 246			
			- 19111	Rattus norvegicus TGFB	thyroid hormone receptor alpha		
				inducible cody court			
		ł		Inducible early growth response	9		
2255	13358	NM_031135	ام	(Tieg),mRNA. 11/22Length =			
	10000	714W_031135	d	3115	TGFB inducible early growth response		
- 1				Rattus norvegicus TGFB			
1				inducible early growth response			
2055	40050			(Tieg),mRNA. 11/22Length =			
2255	13355	NM_031135	s,t	3115	TGFB inducible early growth response		
		i		Rattus norvegicus thymosin	growth response		
2222				beta-4 (Tmsb4x), mRNA.			
2256	15052	NM_031136	c,w,x,aa,bb	4/21Length = 686	thymosin beta-4		
				Rattus norvegicus thymosin	anymosin beta-4		
			j	beta-4 (Tmsb4x), mRNA.	1		
2256	19359	NM_031136	h,i	4/21Length = 686	EST		
				Rattus norvegicus	E21		
				tripeptidylpeptidase II (Tpp2),			
2257	15485	NM_031137	l,m	mRNA. 4/21Length = 4566	lu mu		
			<del>  ''''                                </del>	Rattus norvegicus	tripeptidylpeptidase II		
			1	trinontidula = 333 = = 11 (7 )			
2257	15486	NM_031137	w,x	tripeptidylpeptidase II (Tpp2),			
	-10.00	7411_001107	W,V	mRNA. 4/21Length = 4566	tripeptidylpeptidase II		
				Rattus norvegicus ubiquitin			
- 1				conjugating enzyme			
2258	17370	NM_031138		(LOC81816),mRNA. 4/21Length			
2200	1/3/3	NIVI_031 136	r,w,x	= 1737	ubiquitin conjugating enzyme		
- 1	I			Rattus norvegicus vimentin			
2250	15405	NIM OOAAA	1	(Vim), mRNA. 11/22Length =			
2259	10185	NM_031140	n,bb,ll	1796	vimentin		
ľ				Rattus norvegicus			
				diacylglycerol kinase zeta			
			j (	(Dgkz), mRNA.11/22Length =			
2260	1638	NM_031143		350	diacylglycerol kinase zeta		
"				Rattus norvegicus cytoplasmic	diacytytycerol kinase zeta		
			la	peta-actin (Actx), mRNA.			
2261	21623	NM_031144	lc  2	1/21Length = 1128	İ		
			<del> </del>				
1			]	Rattus norvegicus calcium- and			
- 1	- 1		[ [	ntegrin-hinding protein (2)			
2262	23097	IM_031145	n,o,cc,dd 2	ntegrin-binding protein(Sip2-			
				(8), mRNA. 4/21Length = 822	calcium- and integrin-binding protein		
- 1		i		valus norvegicus for			
				roteasomal ATPase (SUG1)	. 1		
	4204	M 024440	l ko	LOC81827),mRNA. 4/21Length	· 1		
2262		M_031149	C,r =	1288	or proteasomal ATPase (SUG1)		
2263	129111						
2263	12911		T	vallus norvegicus RAB11a.	1		
2263	1291		m	nember RAS oncogene	1		
2263		M_031152	m	vallus norvegicus RAB11a.	, , , , , , , , , , , , , , , , , , , ,		

ABLE	1.7	GenBank A	CC. 15 1 1917/100	A STATE OF THE STA	Atty, Ref. 44921-5090-01-WO/2105485
EQ ID:	GLGC	D No.	Model Code	Known Gene Name	· [1] [1] [1] [2] [2] [2] [2] [2] [2] [2] [2] [2] [2
			. Injection Court	Milowii Gerie Name	Unigene Sequence Cluster Title
			1	Rattus norvegicus glutathione	S
	1			transferase, mu type 3 (Yb3)	
2265	2000	2 3 4 6 4 6 4		(Gstm3), mRNA. 4/21Length =	
2200	2000	2 NM_031154	W,X	128	glutathione S-transferase, mu type 3 (Yb3)
		1		Rattus norvegicus ubiquitin-	The second of th
	l	1	- }	conjugating enzyme E2D	
			1	3(homologous to yeast UBC4/5	5)
				(Ube2d3), mRNA. 4/21Length =	ublquitin-conjugating enzyme E2D 3 (homologou
2266	1527	3 NM_031237	aa,bb	1531	to yeast UBC4/5)
				Rattus norvegicus ubiquitin-	10 10001 0204/01
- 1			1	conjugating enzyme E2D	
				3(homologous to yeast UBC4/5	n
		1		(Ube2d3), mRNA. 4/21Length =	
2266	1527	NM_031237	la	1531	
				1001	to yeast UBC4/5)
l		1	)	Rattus norvegicus UDP-glucos	
ļ		}		dehydrogeanse (Ugdh),	e <sub>l</sub>
2267	18596	NM_031325	u,v	mRNA.4/21Length = 2318	
			10,0	III d VA.4/2   Length = 2318	UDP-glucose dehydrogeanse
		1	1	Rattus norvegicus UDP-glucos	
			aiknavzon	dehydrogeanse (Ugdh),	
2267	18597	NM_031325	),ff	mDNA 4/041 - 11 - 00 to	
		1447_001020		mRNA.4/21Length = 2318	UDP-glucose dehydrogeanse
- 1			1	Rattus norvegicus cysteine rich	
2268	11258	NM_031327		protein 61 (Cyr61), mRNA.	
	11200	14141_031327	y,z,ee,ff,gg	11/22Length = 1871	cysteine rich protein 61
				D-W	
				Rattus norvegicus	
- 1			1	heterogeneous nuclear	
2269	4005	NIA 004000	1	ribonucleoprotein A/B(Hnrpab),	
2209	4235	NM_031330	b,d,f,g,l,m	mRNA. 11/22Length = 361	heterogeneous nuclear ribonucleoprotein A/B
- 1				Rattus norvegicus voltage-	S HOURS HOUSE HOUS
i			i	dependent anion channel 1	
0070	40500			(Vdac1), mRNA. 11/22Length =	
2270	18539	NM_031353	f,g	1818	voltage-dependent anion channel 1
!				Rattus norvegicus voltage-	
	l		]	dependent anion channel 2	
				(Vdac2), mRNA. 11/22Length =	
2271	16777	NM_031354	hh	1715	Voltage dependent onlen at annal C
	Ţ	<del></del>		Rattus norvegicus ceroid-	voltage-dependent anion channel 2
.	- 1			lipofuscinosis, neuronal 2	
!	Ì			(Cln2),mRNA. 11/22Length =	
2272	20087	NM_031357	cc,dd	- 10-m	Ect-
$\neg$				Rattus norvegicus potassium	ESTs
	1			inwardly rectifying	
İ	- 1		1	channel, subfamily J, member 11	
			adry z ee ff b		
2273	18654	VM_031358	k		potassium inwardly-rectifying channel, subfamily J,
_		55 1000		Rattus norvegicus potassium	member 11
	1		] [,	nwardly so the to -	
				nwardly rectifying	
l			[	channel, subfamily J, member 11	
273	18655	IM OSTORO	[]\	Kcnj11), mRNA. 11/22Length =	potassium inwardly-rectifying channel, subfamily J,
210	100001	IM_031358	d,l,m,jj,kk	) ) )	member 11
i				Rattus norvegicus Glutathione-	
į	i		5	S-transferase, alpha type (Ya)	
	í		i (6	Gsta1), mRNA. 5/21Length =	
274	Occord-	M_031509	b,r	178	

	173	GenBank /	Acc. San and	3. 5 \$100 (2000) 1865 - 1865 - 1860 (2000)	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID.	GLGC	D No.	Acc. Model Cod	e./ Known Gene Name	Unigene Sequence Cluster Title
		3.1	DOC#10DOW 11.	A Part of the Control	Unigene Sequence Cluster Title
		1		Rattus norvegicus Glutathior	ne-
		1		S-transferase, alpha type (Ya	a)
007		1		(Gsta1), mRNA. 5/21Length =	<u> </u>
2274	63	4 NM_03150	9 d,r	11178	Clutothiana Chanas
				Rattus norvegicus Glutathior	Glutathione-S-transferase, alpha type (Ya)
		j		S-transferase, alpha type (Ya	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
	1	1		(Coto1) mBNA 5/04	)
2274	63	5 NM_031509	9  d,r	(Gsta1), mRNA. 5/21Length =	
		5/11/1_00100.	9 (0,1	1178	Glutathione-S-transferase, alpha type (Ya)
				Rattus norvegicus Isocitrate	- Jane Spe (Tu)
	İ	1	i	dehydrogenase 1, soluble	
2275	4740			(ldh1),mRNA. 5/21Length =	
22/0	1/42	NM_031510	) b,u,v	1719	Isocitrate debudrageness 4 1-1
				Rattus norvegicus Janus kina	Isocitrate dehydrogenase 1, soluble
			1	2 (a protein tyrosine	
				kinase)(Jak2), mRNA.	
2276	12580	NM_031514	a,h,l,j,k,y,z	5/211 oneth - 2704	
			G1111111111111111111111111111111111111	5/21Length = 3731	Janus kinase 2 (a protein tyrosine kinase)
j		]		Rattus norvegicus Janus kina	se
ľ		f		2 (a protein tyrosine	1
2276	10504	NIM ODERA	1	kinase)(Jak2), mRNA.	
22/0	12001	NM_031514	y,z,hh	5/21Length = 3731	Janus kinase 2 (a protein tyrosine kinase)
				Rattus norvegicus small	realise kinase z (a protein tyrosine kinase)
				inducible cytokine A2 (Scya2),	
2277	20448	NM_031530	a,d,z,ee,ff,ii,k	k mRNA. 11/22Length = 78	C
- 1				Rattus norvegicus small	Small inducible gene JE
				inducible entails - AC (C	
2277	20449	NM_031530	a,z,ee,ff,kk	inducible cytokine A2 (Scya2),	
			2,2,66,11,KK	mRNA. 11/22Length = 78	Small inducible gene JE
	1		1	Rattus norvegicus Serine	
2278	2202	NINA ODACOA		protease inhibitor (Spin2c),	
2270	3292	NM_031531	a,j,k	mRNA.11/22Length = 261	Serine protease inhibitor
1				Rattus norvegicus Solute	Total protodae illimbitol
- 1				carrier family 11 member 1	Solute corrier femily 44
				(Slc11a1), mRNA. 11/22Length	Solute carrier family 11 member 1 (natural
2279	1005	VM_031537	l,m	= 167	I September 1 Sept
				Rattus norvegicus CD36	also D9Arb3
	1		1	antigon (colleges to 1	
- 1	}		1	antigen (collagen type!	
- 1				receptor, thrombospondin	CD36 antigen (collagen type I receptor,
2280	16040	M_031541		receptor)-like 1 (Cd36l1),	thrombospondin receptor)-like 1 (scavanger
2200	100491	VIVI_031541	n,o	mRNA. 1/22Length = 2497	receptor class B type 1)
ľ	1				ype i)
1			1	Rattus norvegicus Cytochrome	
- 1	- 1			P45, subfamily 2e1(ethanol-	
				inducible) (Cyp2e1), mRNA.	Cutoshawa B450
2281	4010	IM_031543	u,v	11/22Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-
			<del>  ''</del>	1 1/22 cingui - 1024	inducible)
			1	Pattus non-set-us C : :	
- 1	i i		1	Rattus norvegicus Cytochrome	
Į			1	P45, subfamily 2e1(ethanol-	
2204	4044		]	inducible) (Cyp2e1), mRNA.	Cytochrome P450, subfamily 2e1 (ethanol-
2281	4011N	M_031543	V	11/22Length = 1624	inducible)
l				Rattus norvegicus natriuretic	inducing)
1				peptide precursor type B	
- 1				(Nppb),mRNA. 11/22Length =	
282	18389N	M_031545	a,d,y,ee,ff		
		55,540	4,4,7,56,11	628	Brain natriuretic factor
	]		, 1	radus norvegicus nuclear	
ı			ļ /	transcription factor - Y beta	
283	4000	1.00.15		(Ntyb),mRNA. 11/22Length =	
/A 11	コおンソル!!	M_031553	lii l	734	

		GenBank Acc	7	THE VATINESSEE NO SE	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGÇ I	P No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2284	2579	5 NM_031556	jj,kk	Rattus norvegicus Caveolin, caveolae protein, 22 kDa (Cav mRNA. 11/22Length = 537 Rattus norvegicus	), Caveolin, caveolae protein, 22 kDa
2285	60	2 NM_031557	11	Prostaglandin I2 (prostacyclin) synthase (Ptgis), mRNA.	
2200	03,	E[INIVI_031337	s,t,ll	11/22Length = 1618  Rattus norvegicus cd36 antige (Cd36), mRNA. 11/22Length =	·
2286	1831	NM_031561	e,u	2436 Rattus norvegicus cd36 antige	thromhospondin recenter)
2286	18316	NM_031561	е	(Cd36), mRNA. 11/22Length = 2436	CD36 antigen (collagen type I receptor,
2286	18317	NM_031561	r,aa,bb,ii	Rattus norvegicus cd36 antige (Cd36), mRNA. 11/22Length = 2436	CD36 antigen (collagen type I receptor.
2286	18310	NM_031561		Rattus norvegicus cd36 antige (Cd36), mRNA. 11/22Length =	CD36 antigen (collagen type I receptor.
2287		NM_031570	w,x,cc,dd	2436 Rattus norvegicus ribosomal protein S7 (Rps7), mRNA. 11/22Length = 65	thrombospondin receptor)
			Mixioojaa	Rattus norvegicus Phosphorylase kinase, gamma	ribosomal protein S7
2288	546	NM_031573	h,ii	1 (Phkg1), mRNA. 11/21Length = 1388 Rattus norvegicus P45	Phosphorylase kinase, gamma 1
2289	1918	NM_031576	gg	(cytochrome) oxidoreductase (Por), mRNA. 11/22Length = 2441	P450 (cytochrome) oxidoreductase
2289	1920	NM_031576	s	Rattus norvegicus P45 (cytochrome) oxidoreductase (Por), mRNA. 11/22Length = 2441	
				Rattus norvegicus P45 (cytochrome) oxidoreductase	P450 (cytochrome) oxidoreductase
2289	1921	NM_031576	j,k,s,t	(Por), mRNA. 11/22Length = 2441 Rattus norvegicus growth	P450 (cytochrome) oxidoreductase
2290	942 1	NM_031577		hormone releasing hormone (Ghrh),mRNA. 11/22Length = 616	
				Rattus norvegicus growth hormone releasing hormone	growth hormone releasing hormone
2290	25793	NM_031577	li .	(Ghrh),mRNA. 11/22Length = 616 Rattus norvegicus testis	
2291	21715	IM_031578		specific protein kinase 1 (Tesk1), mRNA. 11/22Length =	
			1	Rattus norvegicus protein tyrosine phosphatase 4a1	testis specific protein kinase 1
5385	24219 N	M_031579	,p,q,y,z,kk	(Ptp4a1),mRNA. 11/22Length = 2638 Rattus norvegicus glucose-6-	protein tyrosine phosphatase 4a1
2293	E400	N 004555		phosphatase, transport protein 1 G6pt1), mRNA. 11/22Length =	
2231	5496 N	M_031589 a		100	glucose-6-phosphatase, transport protein 1

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SEQ ID	GLGC I	D No.	Model Gode	Known Gene Name	· 排入数据: 《数据》 (数字) (4)
				Rattus norvegicus glucose-6-	Unigene Sequence Cluster Title
	1			phosphatase transport	4
				phosphatase, transport protein	1
2293	549	7 NM_031589	lii	(G6pt1), mRNA. 11/22Length =	
		11111_001003		193	glucose-6-phosphatase, transport protein 1
		1		Rattus norvegicus squamous	
		1	1	cell carcinoma antigen	
		İ	1	ceir carcinoma antigen	
2294	1454	2 NM_031596	_	recognized by T-cells 1 (Sart1)	i i i i i i i i i i i i i i i i i i i
	1107	211111_031390	<u> </u>	mRNA. 11/22Length = 2532	cells
				Bottus	
- 1				Rattus norvegicus squamous	
ŀ		•		cell carcinoma antigen	
2294	1151	3 NM_031596	<b></b>	recognized by T-cells 1 (Sart1),	squamous cell carcinoma antigen recognized by
2207	1404	2 141VI_03 1596	b,u,v	mRNA. 11/22Length = 2532	cells
1			1	Rattus norvegicus tyrosine 3-	
- 1				monooxygenase/tryptophan 5-	
ŀ			1	monooxygenase activation	
		1		protein, epsilon polypeptide	tyrosine 3-monooxygenase/tryptophan 5-
000=				(Ywhae), mRNA. 11/22Length =	monooxygenase activatioprotein, epsilon
2295	19341	NM_031603	h,l	1771	nolynentide
				Rattus norvegicus ATPase, H+	ILNb-hago
- 1				transporting, lysosomal	
ł				noncatalytic accessory protein	ATPase, H+ transporting, lysosomal (vacuolar
- 1				1a (Atp6n1a), mRNA.	proton pump) noncatalytic accessory protein 1
2296	20840	NM_031604	cc,dd	11/22Length = 3876	(110/160 kDa)
					(110/100 KDa)
			1	Rattus norvegicus phosphatase	
			1	and tensin homolog (Pten),	
2297	11296	NM_031606	f	mRNA.11/22Length = 1212	phosphatase and tensin homolog (mutated in
- 1				Rattus norvegicus	multiple advanced cancers 1)
- 1				neuroblastoma, suppression of	
				tumorigenicity1 (Nbi1), mRNA.	la11
2298	19022	NM_031609	s,t,jj,kk	11/22Length = 1788	Neuroblastoma, suppression of tumorigenicity 1
			Original	Rattus norvegicus thioredoxin	(DNA segment human D1S1733E)
				reductase 1 (Txnrd1),	
2299	24234	NM_031614	r,y,z,jj,kk	mPNA 11/201 and 000	
		30,014	1.12.12.1311VV	mRNA.11/22Length = 336 Rattus norvegicus thioredoxin	thioredoxin reductase 1
				reductore 4 (Type 44)	
2299	24235	NM_031614	ly z kk	reductase 1 (Txnrd1),	
	200	001014	y,z,kk	mRNA.11/22Length = 336	thioredoxin reductase 1
	ļ			radius norvegicus mitogen-	
				activated protein kinase 6	
2300	14957	NM_031622	·	(Mapk6), mRNA_11/22Length =	
	1 7001	vi_00 1022		3662	mitogen-activated protein kinase 6
- 1				Rattus norvegicus growth factor	
				receptor bound protein 14	
2301	15767	NIM OSTEOS		(Grb14), mRNA. 11/22Length =	
2001	10/0/	NM_031623		195	growth factor receptor bound protein 14
	1	ſ		ratius norvegicus	
	1	ļ		immunoglobulin binding protein	
2202	24770	114 004004	]	1 (lgbp1), mRNA. 11/22Length =	
2302	21/12	NM_031624		1239	immunoglobulin (CD79A) binding protein 1
j				ratius norvegicus nuclear	y which y shiding protein i
ı		1	ļı	receptor subfamily 4. group A,	
0000			<u> </u>	member 3 (Nr4a3), mRNA	
2303	567 1	IM_031628	p,q :	1.1001-07gt. = 4	nuclear receptor subfamily 4, group A, member 3
-				Rattus norvegicus core	ndoledi receptor subrannily 4, group A, member 3
ļ		İ	lr.	promoter element binding	
			از	protein (Copeb), mRNA.	
2304	1727 N	IM_031642		141001	core promoter element binding protein
				···	ZIE UIOMOTEL Element blading protein

TABLE	1000	GenBank Ac	c. 157 - 177 - 3		Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	DINO.		Known Gene Name	自己的复数的复数的复数 经基本经济的 医皮肤 化二甲基二甲二甲基
			. Moder Code		Unigene Sequence Cluster Title
	ł	1		Rattus norvegicus receptor	
	1			(calcitonin) activity modifying	
2305	1606	2 NM_031646	n,o	protein 2 (Ramp2), mRNA.	
	1		11,0	11/22Length = 751	receptor (calcitonin) activity modifying protein 2
	1			Rattus norvegicus MYB bindir	10
2306	1744	8 NM_031668	h,i	protein 1a (Mybbp1a), mRNA.	
		91.111_001000	1111	11/22Length = 3834 Rattus norvegicus actinin alph	MYB binding protein (P160) 1a
	ł	1		4 (Actn4), mRNA. 11/22Length	la l
2307	535	8 NM_031675	l <sub>r</sub>	= 2996	
			- <del> </del>	Rattus norvegicus transgelin 3	Actinin, alpha 4
				(Tagln3), mRNA. 1/22Length =	
2308	1990	NM_031676	l <sub>ii</sub>	12	
		1	- <del>  </del>	Rattus norvegicus four and a	EST
	[	1	1	half LIM domains 2 (FhI2),	
2309	1840	NM_031677	d,jj,kk	mRNA.11/22Length = 84	£
		T	- 4,11,	Rattus norvegicus period	four and a half LIM domains 2
			1	homolog 2 (Per2), mRNA.	
2310	15041	NM_031678	ji,kk	11/22Length = 5761	nowled harmal and on the same
			1"	acongui - 0/01	period homolog 2 (Drosophila)
		1		Rattus norvegicus solute carrie	ar.
1			}	family 29, member 1 (Slc29a1),	1
2311	20743	NM_031684	a,x,z,kk	mRNA. 11/22Length = 1766	solute carrier family 29 (nucleoside transporters), member 1
- 1				Rattus norvegicus crystallin,	member 1
1				beta B3 (Crybb3), mRNA.	
2312	8844	NM_031690	b	11/22Length = 747	covetellin hate D2
- 1				Rattus norvegicus	crystallin, beta B3
			1	sialyltransferase 5 (Siat5),	
2313	16663	NM_031695	s	mRNA. 11/22Length = 2725	sialyìtransferase 5
- 1				Rattus norvegicus ribophorin 2	Sicilyiti arisierase 5
2011				(Rpn2), mRNA. 1/22Length =	
2314	21575	NM_031698	W,X	2234	ribophorin II
1				Rattus norvegicus ribosomal	as opionin ii
2245	40004	LIL 00 1 mag		protein S8 (Rps8), mRNA.	
2315	16204	NM_031706	f,g,jj,kk	11/22Length = 696	ribosomal protein S8
- 1	- 1			Rattus norvegicus ribosomal	
2215	40000	NII 004770	l [	protein S8 (Rps8), mRNA.	
2315	16205	NM_031706	jj,kk	11/22Length = 696	ribosomal protein S8
				Rattus norvegicus homer,	,
	1		]	neuronal immediate early gene,	
2316	1805	NM_031707		1(Homer1), mRNA. 11/22Length	
2010	10004	MM_031/0/		= 45	RuvB-like protein 1
				Rattus norvegicus homer,	
	ł		] [	neuronal immediate early gene,	
2316	18057	VM_031707	[_	1(Homer1), mRNA. 11/22Length	
<del></del>	13007	111_001101		= 45	RuvB-like protein 1
				Rattus norvegicus homer,	
1	l	1	[]	neuronal immediate early gene,	
2316	18059	IM_031707	D. 7.00 #	(Homer1), mRNA. 11/22Length	
		001707		= 45	RuvB-like protein 1
		)	1_	Rattus norvegicus adhesion	
2317	240811	IM_031708	e in	egulating molecule 1 (Adrm1),	
			- II	nRNA. 11/22Length = 1444	glycoprotein 110
				Rattus norvegicus ribosomal	
2318	16918	M_031709	۱۶ 1 g, <u>h</u> ,l,w,x	rotein S12 (Rps12), mRNA.	
		551703		1/22Length = 499	ribosomal protein S12
		l	1.	Rattus norvegicus olfactory	
2319	20210N	M_031710	۱۱,۷ ا	eceptor 41 (Olfr41), nRNA.11/22Length = 984	
		··· <u>··</u> ···		#XIVM.   1///   QD/III = QQ/I	olfactory receptor 41

1 1	1	GenBank A	oc I	V 18	Atty: Ref. 44921-5090-01-WO/2105485
SEQ:ID	GLGC	IDINO	∞.   Model Code		
	1-1-0-0	is into:	INJUGE! COURS	1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Unigene Sequence Cluster Title
	}			Rattus norvegicus	10.00
	}	1		phosphofructokinase, muscle	
				(Pfkm), mRNA.11/22Length =	
2320	) 13	40 NM_031715	jj,kk	2757	phoophofmetal
	}			Rattus norvegicus chloride	phosphofructokinase, muscle
	1		[	channel, nucleotide-sensitive,	,
				14/Chada) Date	
2321	1904	18 NM_031719	jj,kk	1A(Cins1a), mRNA.	
	100	10/11/1/19	)),KK	11/22Length = 1399	chloride channel, nucleotide-sensitive, 1A
	ļ	1			7 ( ) ( )
	l	1	1	Rattus norvegicus	
2222	4550		Ì	serine/threonine kinase 3 (Stk3	spine/threonine kinase 3 (Ste20, yeast homolog)
2322	1550	7 NM_031735	u	mRNA.11/22Length = 261	STK3
	1			Rattus norvegicus activated	
			1	leukocyte cell adhesion	1
			1	molecule (Alcam), mRNA.	1
2323	2072	4 NM_031753	a	11/22Length = 2866	
				11/22Lengui = 2000	activated leukocyte cell adhesion molecule
į		1	1	Rattus posteriore	
				Rattus norvegicus matrix	
ì		Í		metalioproteinase 24	
2324	4000	NINE 004		(membrane-inserted) (Mmp24),	
2324	1000	3 NM_031757	С	mRNA. 11/22Length = 4245	matrix metalloproteinase 24 (membrane-inserted)
1		1		Rattus norvegicus guanine	matrix metalloproteinase 24 (membrane-inserted)
		İ	}	deaminase (Gda), mRNA.	
2325	14184	NM_031776	kk	11/22Length = 1568	ananin d
1				Rattus norvegicus guanine	guanine deaminase
1			1	deaminase (Gda), mRNA.	
2325	14185	NM_031776	kk	11/22Length = 1568	
			<del></del>	Pottus portos ana	guanine deaminase
- 1			[	Rattus norvegicus potassium	
		j		channel regulatory protein	
2326	1225	NM_031784	1.	KChAP (83614), mRNA.	
2020	4020	111111_031764	d	12/21Length = 2927	potassium channel regulatory protein KChAP
1			1 1	Rattus norvegicus ATPase, H+	
- 1		ł	1	transporting, lysosomal(vacuolar	-
		ł	]	proton pump), subunit 1	
			1	/41 0 41	ATPasa Un transporting business (
2327	16178	NM_031785	f	289	ATPase, H+ transporting, lysosomal (vacuolar
				Rattus norvegicus NF-E2-	proton pump), subunit 1
				related factor 2 (Nfe2i2),	
2328	1169	NM_031789	ld )		
-			† <del></del>	Rattus population NE FO	NF-E2-related factor 2
	l		Į .	ratius norvegicus NF-E2-	
2328	1170	NM_031789	dim #12.	related factor 2 (Nfe2l2),	
		1111_00 11 08	d,l,m,jj,kk j	mRNA.5/21Length = 237	NF-E2-related factor 2
2329	4400	NIM ADATOS		Rattus norvegicus citron (Cit),	
2029	1182	NM_031790	b,I,m r	DNA 44/001	postsynaptic density protein (citron)
- 1	1				
	- 1		1	Rattus norvegicus kangai 1	ESTs, Kangal 1 (suppression of tumorigenicity 6,
1	ì		t le	14 141	prostato: CD22 onlines (D2)
2330	15864	NM_031797		- I	prostate; CD82 antigen (R2 leukocyte antigen,
[	T				antigen detected by monoclonal and antibody IA4))
- 1	- 1		] ],	Rattus norvegicus solute carrier	
l	1		e.	amily 12 mombas 2 (2) 42 a	
2331	2114	VM_031798	as bh	amily 12, member 2 (Slc12a2),	
		,_001730	aa,bb n	RNA. 11/22Length = 642	solute carrier family 12, member 2
- 1	- 1	ì	<u> </u>	vallus norvegicus detensin	
2222	10455	NA 0040:-	b	eta 1 (Defb1), mRNA.	•
2332	101551	NM_031810	<u>ii                                   </u>	/22Length = 416	tefensin beta 1
- 1	1		F	Rattus norvegicus	Signature I
- 1	- 1	}		steomodulin (osteoadherin)	-
1			lic	Omd), mRNA. 5/21Length =	
2333	15840IN	IM_031817	h,i 18	-00	
					steomodulin (osteoadherin)

1.1		GenBank	Acc.		Atty. Ref. 44921-5090-01-WO/2105485
seo id	GLGC	D No.	Model Cor	4.2 P. · · · · · · · · · · · · · · · · · ·	A CONTRACT OF CASE OF THE PARTY
			, induction		Unigene Sequence Cluster Title
	1	ł		Rattus norvegicus serum-	
2334	200	E NIL ODAG	<u>.</u> .	inducible kinase (Snk), mRNA.	, [
2004	200	55 NM_03182	21 d	111/22Length = 2781	serum-inducible kinase
	1			Rattus norvegicus lectin,	- I I I I I I I I I I I I I I I I I I I
		İ		galactose binding, soluble	
				3(Lgals3), mRNA. 5/22Length	=
2335	2232	1 NM_03183	2 a,h,i,n,o,x,i	kk 948	
				Rattus norvegicus	lectin, galactose binding, soluble 3
		}		sulfotransferase family 1A,	
			ſ	phenol-preferring, member 1	i
		1		(Sult1a1), mRNA. 1/22Length =	
2336	474	8 NM_03183	s,t,aa,bb	1227	The state of the s
			. 011,00,00	Rattus norvegicus	member 1
- 1		1	ľ	culfotronofora a facility	
i		j		sulfotransferase family 1A,	
				phenol-preferring, member 1	Aryl sulfotransferase cytosolic, 1A, phenol-
2336	1710	NM_031834		(Sult1a1), mRNA. 1/22Length =	preferring, member 3, sulfotransferase family 1A,
2000	4/4	U31834	t,bb	11227	phenol-preferring, member 1
ļ				Rattus norvegicus vascular	Freezening moniber 1
ľ			1	endothelial growth factor	
0007		J		(Vegf),mRNA. 11/22Length =	1
2337	8384	NM_031836	gg,il	645	Wassellar and that all all all all all all all all all a
]				Rattus norvegicus vascular	vascular endothelial growth factor
- 1		J		endothelial growth factor	
				(Vegf),mRNA. 11/22Length =	
2337	8385	NM_031836	s,t,gg	645	
			191139	Rattus norvegicus vascular	vascular endothelial growth factor
			1	and the list are the first are the	
				endothelial growth factor	
2337	8386	NM_031836	- I.,	(Vegf),mRNA. 11/22Length =	
-2007	0000	14141_03 1030	<u> </u>	645	vascular endothelial growth factor
- 1			ļ	Rattus norvegicus ribosomal	growth taolor
2220	40000	1114 004000		protein S2 (Rps2), mRNA.	
2338	10269	NM_031838	h,l,w,x	11/22Length = 817	ribosomal protein S2
- 1				Rattus norvegicus stearoyi-	Protectival protecti OZ
				Coenzyme A desaturase 2	
				1/O - 10\	Rat DNA polymores alebe a Data as
2339	15077	NM_031841	lii	555	Rat DNA polymerase alpha mRNA, 3' end, stearoy
				Rattus norvegicus Calmodulin 1	Coenzyme A desaturase 2
				(phosphorylase kinase, delta)	
			1	(Calm1), mRNA. 11/22Length =	
2340	19190	NM_031969	h,i	10040	
			<del></del>		Calmodulin 1 (phosphorylase kinase, delta)
	i			I . www.co moraedicas callifodfilly 11	
ł	- 1			(phosphorylase kinase, delta)	
2340	19101	VM_031969	<u> </u>	(Caim1), mRNA. 11/22Length =	
-070	1919111	AINI_021909	h,l	3513	Calmodulin 1 (phosphorylase kinase, delta)
1			1	I read not vegicus Califiodulin 11	Tricopilor Jidos Killase, della)
- 1			1	(phosphorylase kinase, delta)	
2246	404		f	(Calm1), mRNA. 11/22Length =	
2340	19195	IM_031969	h,l,ll	3513	Calmodulin 1 (phoophands and the control of the con
				Rattus norvegicus Calmodulin 1	Calmodulin 1 (phosphorylase kinase, delta)
	- 1			(phosphorylase kinase, delta)	
				(Calm1), mRNA. 11/22Length =	
2340	25802 N	IM_031969	h,l,aa,bb,ll	10540	N. I. A. W
			,,,	12.11	Calmodulin 1 (phosphorylase kinase, delta)
			1	1 Tallos Holvegicus Heat Shock	:STS, Moderately similar to hypothetical protein
2341	17734N	M_031970	20000 414	14 100 and Table 11 T	AGC10974 [Homo sapiens] [H.sapiens], heat shock
	54/10	001810	a,o,q,ee,#,kk	5	iko protein (
- 1				Railus norvegicus Heat shock   F	STs, Moderately similar to hypothetical protein
341	47705	M_031970	a,z,ee,ff,kk	27 kDa protein (Hsp27), mRNA. M 11/22Length = 787	IGC10974 [Homo sapiens] [H.sapiens], heat shock

		GenBank A	lcc.	7 N. W. C.	Atty, Ref. 44921-5090-01-WO/2105485
SEQI	GLGC I	⊃No.	Model Cod	e Known Gene Name	Barrier & Branch & Commencer
		<del>                                     </del>	inigao, coa	2 Indown Gene Name	
	1		1	Rattus norvegicus Heat shock	ESTs, Moderately similar to hypothetical protein
234	11 1773	6 NM_031970	0   -1	27 kDa protein (Hsp27), mRNA	MGC10974 [Homo sapiens] [H.sapiens], heat sho
	1770	3/14/4/_03/19/(	0 a,I,o,q,ee,ff		27kD protein 1
				Rattus norvegicus Heat shock	The state of the s
234	2 447	-	.	protein 7-1 (Hspa1a),	ESTS Highly similar to C404 DAT 8 405
204	14/3	NM_031971	a,p,q,ee,ff	mRNA.5/21Length = 2455	ESTs, Highly similar to S10A_RAT S-100 protein,
				Rattus norvegicus Heat shock	alpha chain [R.norvegicus], Heat shock protein 70-
00.4	<u> </u>	1	ĺ	protein 7-1 (Hspa1a),	
234	2 8661	NM_031971	e,ee,ff,gg	mRNA.5/21Length = 2455	lustration and the second
				Rattus norvegicus Heat shock	Heat shock protein 70-1
	1		1	protein 7-1 (Hspa1a),	
2342	2 8662	NM_031971	ee,ff,gg	mPNIA FOAL II.	
			- cc,n,gg	mRNA.5/21Length = 2455	Heat shock protein 70-1
	1			Rattus norvegicus Heat shock	
2342	8663	NM_031971	#	protein 7-1 (Hspa1a),	
	- 0003	NIVI_031971	ee,ff,gg	mRNA.5/21Length = 2455	Heat shock protein 70-1
		İ		Rattus norvegicus Aldehyde	5.100K protent 70-1
				dehydrogenase family 3	
	]		1	subfamily A1 (Aldh3a1), mRNA.	•
2343	24644	NM_031972	cc,dd		in a constant of the constant
					Aldehyde dehydrogenase class 3
	1 1			i l	
			ł	Rattus norvegicus clathrin, light	
2344	17075	NM_031974	1	polypeptide (Lca) (Clta),mRNA.	
	17075	NIVI_U31974	99	11/22Length = 1124	clathrin light chain
				Lyamas horvedicas	- Cathiring it Grain
0045	,			parathymosin (Ptms), mRNA.	
2345	17556	NM_031975	j,k	111/201	ma-11.
- 1				1 3	parathymosin
			1	Rattus norvegicus protein	
- 1	[			kinase, AMP-activated, beta	
Ī				1222 - Alvir-activated, beta	
2346	17601	NM_031976	a li kk	1non-catalytic subunit (Prkab1),	
		007070	a,jj,kk	mRNA. 11/22Length = 1978	5'-AMP-activated protein kinase, beta subunit
- 1	1			The first oglogo ogibility	Protein initiate, beta suburit
2347	19400 N	IA 024004	1	(Caib1), mRNA. 11/22Length =	
207/	10455	IM_031984	aa,bb	228	Perehellar Ca hinding projety age
ļ				Rattus norvegicus calbindin 1	perebellar Ca-binding protein, spot 35 protein
				(Calh1) mPNA 44/001	
				NOGIDII, IIIKNA 11/2/I ONAIN - I	
2347	18500 N	M_031984	bb	(Calb1), mRNA, 11/22Length =	
2347	18500 N	M_031984	bb	[228 ] <sub>C</sub>	erebellar Ca-binding protein, spot 35 protein
2347	18500 N	M_031984	bb	228   C   Rattus norvegicus S6 kinase	erebellar Ca-binding protein, spot 35 protein
				228   C   Rattus norvegicus S6 kinase   (Rps6kb1), mRNA. 5/21Length	
2347		M_031984 M_031985	il	Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287	
				228   C   Rattus norvegicus S6 kinase   (Rps6kb1), mRNA. 5/21Length   = 2287   S   Rattus norvegicus S6 kinase	erebellar Ca-binding protein, spot 35 protein
2348	18898 N	M_031985	ii	228   C   Rattus norvegicus S6 kinase   (Rps6kb1), mRNA. 5/21Length   = 2287   S   Rattus norvegicus S6 kinase	
	18898 N			228   C     Rattus norvegicus S6 kinase     (Rps6kb1), mRNA. 5/21Length     = 2287   S     Rattus norvegicus S6 kinase     (Rps6kb1), mRNA. 5/21Length     = 2287   S	6 kinase
2348	18898 N	M_031985	ii	228   C     Rattus norvegicus S6 kinase     (Rps6kb1), mRNA. 5/21Length     = 2287   S     Rattus norvegicus S6 kinase     (Rps6kb1), mRNA. 5/21Length     = 2287   S	
2348	18898 N	M_031985 M_031985	ji gg	228   C     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   S     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   Si     Rattus norvegicus syntenin	6 kinase
2348	18898 N	M_031985 M_031985	ji gg	228   C     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   S     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   Si     Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length     277	6 kinase
2348	18898 N	M_031985 M_031985	ji 99	228   C     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   S     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   St     Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length     277   Sv	6 kinase
2348	18898 N	M_031985 M_031985	ii gg f,g,cc,dd	228   C     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   S     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   St     Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length     277   Sy     Rattus norvegicus carnitine O-	6 kinase
2348 2348 2349	18898 NI 18899 NI 19768 NA	M_031985 M_031985 M_031986	ii gg f,g,cc,dd	228   C     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   S     Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length     = 2287   St     Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length     277   Sy     Rattus norvegicus carnitine O-octanoyltransferase (Crof).	6 kinase
2348	18898 N	M_031985 M_031985 M_031986	ii gg f,g,cc,dd b,l,m,aa,cc,dd	228   Cattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287   S	6 kinase 6 kinase votenin
2348 2348 2349	18898 NI 18899 NI 19768 NA	M_031985 M_031985 M_031986	ii gg f,g,cc,dd b,l,m,aa,cc,dd	228   Cattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287   S	6 kinase
2348 2348 2349	18898 NI 18899 NI 19768 NN 20554 NN	M_031985 M_031985 M_031986 M_031987	ii gg f,g,cc,dd b,l,m,aa,cc,dd	228   Cattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287   S	6 kinase 6 kinase rntenin
2348 2348 2349	18898 NI 18899 NI 19768 NA	M_031985 M_031985 M_031986 M_031987	ii f,g,cc,dd b,l,m,aa,cc,dd	Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length = 277  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681	6 kinase  rntenin  rnitine O-octanoyltransferase
2348 2348 2349	18898 NI 18899 NI 19768 NN 20554 NN	M_031985 M_031985 M_031986 M_031987	ii f,g,cc,dd b,l,m,aa,cc,dd	228   Cattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287   S	6 kinase 6 kinase votenin
2348 2349 2350	18898 NI 18899 NI 19768 NN 20554 NN	M_031985  M_031985  M_031986  M_031987	ii f,g,cc,dd b,l,m,aa,cc,dd j,k	228   Cattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287   S	6 kinase  rntenin  rnitine O-octanoyltransferase
2348 2349 2350	18898 NI 18899 NI 19768 NN 20554 NN	M_031985  M_031986  M_031987  M_031987	ii gg f,g,cc,dd b,l,m,aa,cc,dd j,k	Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus S9 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length = 277  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus RalA binding orotein 1 (Ralbp1),	6 kinase  Intenin  Intine O-octanoyltransferase  Intine O-octanoyltransferase
2348 2348 2349	18898 NI 18899 NI 19768 NN 20554 NN	M_031985  M_031986  M_031987  M_031987	ii gg f,g,cc,dd b,l,m,aa,cc,dd j,k	Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus S7 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length = 277  Rattus norvegicus carnitine O- octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus carnitine O- octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus RalA binding orotein 1 (Ralbp1), mRNA.5/21Length = 3622	6 kinase  Intenin  Intine O-octanoyltransferase  Intine O-octanoyltransferase
2348 2349 2350	18898 NI 18899 NI 19768 NN 20554 NN	M_031985  M_031986  M_031987  M_031987	ii gg f,g,cc,dd b,l,m,aa,cc,dd j,k	Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length = 277  Rattus norvegicus carnitine O- octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus carnitine O- octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus RalA binding orotein 1 (Ralbp1), mRNA.5/21Length = 3622  Rattus norvegicus RalA binding	6 kinase  rntenin  rnitine O-octanoyltransferase
2348 2349 2350 2350	18898 NI 18899 NI 19768 NN 20554 NN	M_031985  M_031985  M_031986  M_031987  M_031987	ii gg f,g,cc,dd b,l,m,aa,cc,dd j,k	Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus S9 kinase (Rps6kb1), mRNA. 5/21Length = 2287  Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length = 277  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus camitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681  Rattus norvegicus RalA binding orotein 1 (Ralbp1),	6 kinase  Intenin  Intine O-octanoyltransferase  Intine O-octanoyltransferase

- CUD		GenBank A			Atty, Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC;	D No.	Model Code	Known Gene Name	
-				Rattus norvegicus synaptojar	Unigene Sequence Cluster Title
		1		2 (Syri2) = DNA 44/00	nin
2352	117	1 NM_032071		2 (Synj2), mRNA. 11/22Lengti	
		1111/2002071	y,z	533	synaptojanin II
	l	1		Rattus norvegicus aldehyde	
2353	1220	000440		dehydrogenase 2 (Aldh2),	
_2000	1229	9 NM_032416	C	mRNA. 11/22Length = 1889	aldehyde dehydrogenase 2, mitochondrial
				Rattus norvegicus vesicle	de deny drogenase 2, millochononal
				associated protein (VAP1),	
2354	2110	2 NM_033021	11	mRNA.7/21Length = 4422	Voniele anne diet it.
				Rattus norvegicus vesicle	vesicle associated protein
				associated protein (VAP1),	
2354	2110	3 NM_033021	s	mRNA.7/21Length = 4422	
			<u> </u>	Pattus paris siena	vesicle associated protein
			1	Rattus norvegicus vesicle	
2354	2110	NM_033021		associated protein (VAP1),	
	2110	11111_033021	s,t	mRNA.7/21Length = 4422	vesicle associated protein
- 1			j	Rattus norvegicus Protein	Proton
- 1				phosphatase type 1B (formely	
i		1	ľ	2C), Mg-dependent, beta	
				isoform (Ppm1b), mRNA.	Protoin phoopheters to 42 //
2355	25529	NM_033096	ln,o	7/21Length = 3257	Protein phosphatase type 1B (formely 2C), Mg-
			<u> </u>	Rattus norvegicus Protein	dependent, beta isoform
ĺ				phosphatase type 1B (formely	
- 1		1		2C) Ma dependent to the	
		ļ		2C), Mg-dependent, beta	
2355	25560	NM_033096		isoform (Ppm1b), mRNA.	Protein phosphatase type 1B (formely 2C), Mg-
		14141_033090	ļ	7/21Length = 3257	dependent, beta isoform
i				Rattus norvegicus Protein	7
				phosphatase type 1B (formely	
			]	2C), Mg-dependent, beta	
				isoform (Ppm1b), mRNA.	Protoin whose but the second
2355	19148	NM_033096	h,i	7/21Length = 3257	Protein phosphatase type 1B (formely 2C), Mg-
ľ	- 1			Rattus norvegicus Hemoglobin,	dependent, beta isoform
			1 1	beta (Hbb), mRNA. 12/21Length	
2356	25468	NM_033234	b,c,v	= 62	
					Hemoglobin, beta
	ŀ		1 .	Rattus norvegicus Hemoglobin,	
2356	17820	NM_033234	1_	beta (Hbb), mRNA. 12/21Length	
2000	17028	NVI_033234		= 62	Hemoglobin, beta
	- 1			Rattus norvegicus Hemoglobin,	
0250	,,,,,		j jt	peta (Hbb), mRNA. 12/21Length	
2356	17832	VM_033234	b,c,v =		
				Rattus norvegicus Hemoglobin,	Hemoglobin, beta
	1		1 6	peta (Hbb), mKNA. 12/21Length	
2356	25469	NM_033234	b,c,v	: 62	
				Rattus norvegicus Proteasome	
	· 1			Process Services Proteasome	
1	1		·	prosome, macropain) 26S	
2357	2577	IM_033236	_  S	ubunit, ATPase (Psmc2),	Proteasome (prosome, macropain) 26S subunit,
-501	2011	IIV_U33230	r m	" " " " " " " " " " " " " " " " " " "	ATPase
	- 1			Rattus norvegicus galanin	
250	007:-		(0	Gal), mRNA. 11/22Length =	
358	23/15 N	M_033237	j,k,y,z,jj,kk  6:	99	galanin
İ			F	Rattus norvegicus Fc receptor,	Acidilli
- 1	]		lin	G, alpha chain transporter	-
			1/5	Cont) mRNA 44200	
359	12364N	M_033351	9 17 90 #	cgrt), mRNA. 11/22Length =	
		000001		552	c fragment immunoglobulin G receptor
- 1		ļ	Į.B	initias itot vegious no teceptor. T	- January Compton
	1	1	H <sub>e</sub>	Spelphershalm transporter	
359	40005	M_033351	(F	cgrt), mRNA. 11/22Length =	

<u> </u>	the state	GenBank A	icc,	NOTE OF THE STATE	Atty. Ref.:44921-5090-01-WO/2105485
SEQ ID	GLGC	ID No.	Model Code		7 12 2 2 1 7 3 124 3 7 3 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1
		37 8	livionei cone	AND THE PROPERTY OF THE PARTY O	Unigene Sequence Cluster Title
		1		Rattus norvegicus ATP-bindir	ng
	1	1	1	cassette, sub-family D (ALD),	
2360	147	14 2114 0000		member 2 (Abcd2), mRNA.	
2300	117	14 NM_033352	2 kk	11/22Length = 5531	ESTs
	1			Rattus norvegicus PRKC,	10,0
		1		apoptosis, WT1, regulator	
	ľ		1	(Pawr), mRNA.11/22Length =	
2361	2389	95 NM_033485	i laa	2122	Drawkel
				Rattus norvegicus eukaryotic	Prostate apoptosis response protein 4
				translation elongation factor	
				1alpha 2 (Eef1a2), mRNA.	
2362	2442	0 NM_033539	jj,kk,ll	11/22Length = 144	
			min min	Rattus populations and dis	eukaryotic translation elongation factor 1 alpha 1
				Rattus norvegicus eukaryotic	
				translation elongation factor	
2362	2///1	9 NM_033539		1alpha 2 (Eef1a2), mRNA.	
	441	O 1414 O 2 2 2 2 3 2 3 9	jj,kk	11/22Length = 144	eukaryotic translation elongation factor 1 alpha 1
			1	Rattus norvegicus Insulin-like	and a supplied to the supplied
2363	2507	NIN 07005	l	growth factor 1 receptor (lgf1r).	
2303	2007	NM_052807	j,k	mRNA. 1/21Length = 4696	Insulin-like growth factor 1 receptor
		1		Rattus norvegicus Pancreatitis-	- Inc growth factor i receptor
- 1				associated protein 1	ESTs, Weakly similar to R02D3.2.p
				(Pap1),mRNA. 11/21Length =	Cooperhold to a least to the state of the st
2364	15867	NM_053289	a,h,l,w,x	781	[Caenorhabditis elegans] [C.elegans], Pancreatitis
				Rattus norvegicus	associated protein 1
ĺ				Phosphoglycerate kinase 1	
1				(Pgk), mRNA. 11/22Length =	1
2365	1311	NM_053291	e	1675	
					phosphoglycerate kinase 1
- 1				Rattus norvegicus Adenosine	
2366	1596	NM_053294		A2a-receptor (Adora2a), mRNA.	
-500	1000	14141_000284	- 1	4/22Length = 2373	Adenosine A2a-receptor
- 1		İ			
			i	Rattus norvegicus	
2367	20225	NIM OFFICE	1	adrenomedullin receptor (Admr),	ESTs, Weakly similar to dual-specificity
2007	20200	NM_053302	cc,dd	*********	phosphatase [Mus musculus] [M.musculus]
- 1				Rattus norvegicus homer,	a
	- 1			neuronal immediate early gene,	
0000				2(Homer2), mRNA. 11/22Length	
2368	15748	NM_053309	<u>lii</u>	= 1994	homer neuronal immediate a l
	ĺ			Rattus norvegicus enigma	homer, neuronal immediate early gene, 2
			] [	homolog (Enh), mRNA.	
2369	7207	NM_053326	hh	441041	oniama hamala
-	T			Rattus norvegicus basic helix-	enigma homolog
	ĺ			loop-helix domain	
			] [	Containing older Do (D) II : -:	
2370	1063	VM_053328	le li	containing,class B2 (Bhihb2),	
				mRNA. 11/22Length = 2388	basic helix-loop-helix domain containing, class B2
			]	. warrage trout acditional timosottistis	
2371	14927	IM_053330	]_	protein L21 (Rpl21), mRNA.	
	17321	vivi_U3333U	e	11/22Length = 554	ibosomal protein L21
1	- 1			Rattus norvegicus ribosomal	provent table
2274	44000	11.1 0555	l ir	orotein L21 (Rpl21), mRNA.	
2371	14929 1	IM_053330	<u>[h,l                                    </u>	1/22Length = 554	ibosomal protein L21
1		•		Rattus norvegicus resistin like	ioosomai protein LZ1
. 1			la	Ilpha (Retnla), mRNA.	
372	2674 N	M_053333	99 1	1/201 00015	
7			<u> </u>	Rattus nonvectore Dan di	esistin like alpha
	- 1	}		Rattus norvegicus Ras-related	
ļ			la //	ssociated with diabetes	Í
373	1609 N	M_053338	j.p.q,y,z 1	Rrad),mRNA. 11/22Length =	
	1000114	·**_VUUJJO	1.O.O V.7	421 In	as-related associated with diabetes

		GenBank A		Atty. Ref. 44921-5090-01-WO/2105485
SEQIL	GLGC	ID No.	cc. Model (	archialter a complicate to the College Colle
			, signocor,	
1		1		Railus norvegicus general
	j	j	l	transcription factor IIa, 2
237	1 100	10/11/ 050015	.	(12kDsubunit) (Gtf2a2), mRNA.
201	109	49 NM_053345	ii	111/21Length = 33   general transcription for the line of t
				Rattus norvegicus nuclear   general transcription factor IIa, 2 (12kD subunit)
				distribution gene E
007			1	homolog(Aspergillus) (Nude),
237	935	52 NM_053347	u,v	
				mkNA. 11/22Length = 2153 nuclear distribution gene E homolog (Aspergillus
	j	į		Rattus norvegicus procollagen,
				type I, alpha 2 (Col1a2),mRNA.
2376	615	4 NM_053356	f,g	
			1.0	11/22Length = 4474 procollagen, type I, alpha 2
				Raffus nonceigus and all
		1	- 1	Rattus norvegicus procollagen,
2376	615	5 NM_053356	a	type I, alpha 2 (Col1a2),mRNA.
		1	9	11/22Length = 4474 procollagen, type I, alpha 2
	l	1	]	
i	ľ			Rattus norvegicus procollagen,
2376	6159	NM_053356	_	type I, alpha 2 (Col1a2),mRNA.
	0.00	-11 1W_00000	g	11/22Length = 4474 procollagen, type I, alpha 2
ĺ			1	Rattus norvegicus procollagen,
2376	6457	1114 050000	1.	type I, alpha 2 (Col1a2).mRNA
2370	0137	NM_053356	f,g	11/22Length = 4474 procollagen, type I, alpha 2
			1	Rattus norvegicus procollagen,
0070	02404		1	type I, alpha 2 (Col1a2),mRNA.
2376	25184	NM_053356	f	11/22Length = 4474
- 1				Rattus norvegicus fatty acid
				binding protein 4 (Fabp4),
2377	19512	NM_053365	lii	mDNA 44/001
				Rattus norvegicus transcription
				factor 4 (Tcf4), mRNA.
2378	622	NM_053369	a,j,k	14/901
	1			Rattus norvegicus transcription   transcription factor 4
1	1		i	factor 4 (Tcf4), mRNA.
2378	623	NM_053369	r,hh	14/001 11 0
				transcription factor 4
- 1	- 1			Rattus populario populario di
1	j			Rattus norvegicus nerve growth
				factor receptor (TNFRSF16)
2379	16017	NM_053401	o,aa	associated protein 1 (Ngfrap1),
	- 1		vjuu	mRNA. 11/22Length = 519 brain expressed X-linked 3
1	1	ſ		
j	1			Rattus norvegicus nerve growth
		İ		factor receptor (TNFRSF16)
2379	16018N	IM_053401	h c	associated protein 1 (Ngfrap1),
		000701	b,c	mRNA. 11/22Length = 519 brain expressed X-linked 3
	}	!		ratios not vegicus
				diacylglycerol O-acyltransferase
2380	14621 N	M_053437		1 (Dgat1), mRNA. 11/22Length
	1702 111	IVI_00043/	e,hh	= 1751
1	- 1	i		Trattus noi vegicus histone
2204	6740	4 050 115	<b>.</b>	deacetylase 3 (Hdac3), mRNA
2381	6/12 N	M_053448 c	c,dd	11/22Length = 1799   history departs.   0
- 1				Rattus norvegicus nucleobindin
		M_053463		(Nucb), mRNA. 11/22Length =
382				

	35 , 15.	GenBank Ac	C.   :   :   :   :   :   :   :   :		Atty: Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	No.	Model Code	11 2 2 (2 )	
			i model gode	Known Gene Name	Unigene Sequence Cluster Title
		1		Rattus norvegicus cytochrom	e
2383	21000	NIM OFOATO		c oxidase, subunit 4b (Cox4b)	
2000	21000	NM_053472	u,v	mRNA. 11/22Length = 74	cytochrome c oxidase, subunit IVb
		ŀ		Rattus norvegicus spinophilin	2 Oxidado, Subdilit IVD
2004				(LOC84686), mRNA.	1
2384	21498	NM_053474	_ lgg	11/21Length = 455	spinophilin
					Spirioprimiti
				Rattus norvegicus karyopherir	
		İ		(importin) alpha 2 (Kpna2),	•
2385	15556	NM_053483	kk	mRNA. 11/22Length = 1886	land to the second seco
				Rattus norvegicus calcium	karyopherin (importin) alpha 2
		1	ı	binding protein A6	
	'		i	(calcyclin)(S1a6), mRNA.	1
2386	16394	NM_053485	h,l,w,x	11/21 carth 201	
		1111_000400	1111,441	11/21Length = 291	calcium binding protein A6 (calcyclin)
1				Rattus norvegicus transporter-	
2387	14004	NM_053492		like protein (Ctl1),	
-50/	17304	14141_000492	s,t	mRNA.11/21Length = 2849	transporter-like protein
- 1				Rattus norvegicus unknown Gl	U
	1			Pro dipeptide repeat	
2000	40.00			protein(LOC85383), mRNA.	
2388	16135	NM_053516	aa,bb	11/21Length = 1876	unknown Glu-Pro dipeptide repeat protein
1				Rattus norvegicus	dringtown Glu-P10 dipeptide repeat protein
1	}		1	homocysteine-inducible,	
- 1				endoplasmic reticulum stress-	ł
- 1				inducible, ubiquitin-like domain	)
				member 1 (Herpud1), mRNA.	
2389	18826	NM_053523	bb	11/21Length = 1857	homocysteine-inducible, endoplasmic reticulum
			<del> </del>	Pattus populations /	stress-inducible, ubiquitin-like domain member 1
	ı		İ	Rattus norvegicus Kruppel-like	
2390	14380	VM_053536		factor 15 (Kif15), mRNA.	
	140001	VIVI_000000	e,y,z	11/22Length = 2458	Kruppel-like factor 15 (kidney)
!				Rattus norvegicus solute carrier	
:	}			family 22 (organic anion	
	-			transporter), member 7	
2391	. ام		i.	(Sic22a7), mRNA, 1/22Length =	solute carrier family 22 (organic anion transporter),
23911	37/1	M_053537	b	191	member 7
ļ					THOMBO! I
j	j			Rattus norvegicus pyruvate	
			e,n,o,p,q,r,aa,	dehydrogenate kinase 4 (Pdk4),	
2392	15829 N	M_053551	bb	mRNA.11/22Length = 1435	munusia datuut
. !				Rattus norvegicus synaptogyrin	pyruvate dehydrogenase kinase, isoenzyme 4
I				2 (Syngr2), mRNA. 11/21Length	
2393	17298 N	M_053553	cc,dd	I 440	
			,	Rattus norvegicus vesicle-	synaptogyrin 2
1	. 1			accorded many	
			ļ	associated membrane protein 5	
2394	11843 NI	M_053555		(Vamp5), mRNA. 11/21Length =	
2007	10-010	w_00000	n,o,s	39	vesicle-associated membrane protein 5
1				warras univediras undest KWV I	
1	- 1	1	1	helicase, DECD variant of	
2205				DEADbox family (Ddxl), mRNA	nuclear RNA helicase, DECD variant of DEAD box
2395	4327 NI	M_053563	a,n,o,y,z,jj,kk	11/21Length = 1511	family
	}			Rattus norvegicus cytokine	anny
ł		i	li li	inducible SH2-containing protein	
				3 (Cish3), mRNA. 11/21Length	
2396	15708 NA	/i_053565	o,q,y,z	000	
1	1				cytokine Inducible SH2-containing protein 3
1	!	]	[.	ratios not regions phosphate	
1	1		lo	cytidylyltransferase 2,	
	مارمون ا	1_053568 f	Je	ethanolamine (Pcyt2), mRNA. 11/21Length = 1846	
				4 (0.4)	

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EQ ID.	GLGC I	D No.:	Model Code	Koowo Coho M	Unigene Sequence Cluster Title
			Thioriei Code	Nijown Gene Name	Unigene Sequence Cluster Title
	1			Rattus norvegicus	4
2398	1025	2414 050570	1	peroxiredoxin 5 (Prdx5), mRN/	A.
2090	1925	2 NM_053576	а	1/22Length = 1414	peroxiredoxin 5
		Ī		Rattus norvegicus fatty acid	
2200	-			transport protein (Sic27a1),	
2399	65	3 NM_053580	aa,bb	mRNA. 11/21Length = 398	fatty acid transport protein
				Rattus norvegicus	
				glucocorticoid-inducible protein	
0400				(gis5),mRNA. 11/21Length =	
2400	3049	NM_053582	j,k,t,kk	1869	glucocorticoid-inducible protein
				Rattus norvegicus	giosocorticold-iriducible protein
				glucocorticoid-inducible protein	
				(gis5),mRNA. 11/21Length =	
2400	3050	NM_053582	j,k,t,kk	1869	diseased to the control of
T				Rattus norvegicus Oif-1/EBF	glucocorticoid-inducible protein
		1	1	associated Zn finger protein	1
		1	1	Roaz(Roaz), mRNA.	
2401	24875	NM_053583	ii,jj,kk	11/21Length = 4665	OK 4 PPP P
			1.7,3,7.4.	Rattus norvegicus MAP-kinase	Olf-1/EBF associated Zn finger protein Roaz
				activating death domain	
				(Madd) mDNA 44/04)	
2402	21170	NM_053585	s,t	(Madd),mRNA. 11/21Length = 5249	
			10,1		MAP-kinase activating death domain
			1	Rattus norvegicus S1 calcium-	
			1	binding protein A9(calgranulin	
2403	21445	NM_053587	201755#	B) (S1a9), mRNA. 11/21Length	1
	170	000001	a,e,y,z,ee,ff	= 494	S100 calcium-binding protein A9 (calgranulin B)
				Rattus norvegicus	(Saigi Gradiff D)
			1	Deoxyuridinetriphosphatase	
2404	20808	NM_053592	L.	(dUTPase) (Dut), mRNA.	
	20000	1111 000082	h,i	5/22Length = 952	Deoxyuridinetriphosphatase (dUTPase)
	1			Rattus norvegicus cyclin-	(2011 000)
2405	Sugna	NM_053593	1_	dependent kinase 4 (Cdk4),	
- 150	20002	14141_000093	r	mRNA.11/21Length = 1232	cyclin-dependent kinase 4
	İ		1	Rattus norvegicus Endothelin-	
2406	21700	MA DESCO		converting enzyme 1 (Ece1),	
-400	21709	NM_053596	j,k,y,li	mRNA.5/22Length = 4469	Endothelin-converting enzyme 1
	-			Rattus norvegicus ribosomal	The stand on Eyme 1
1407	2400	114 050		protein S27 (Rps27), mRNA.	
2407	2103	VM_053597	g	11/22Length = 336	ribosomal protein S27
				Rattus norvegicus Matrix	
400	44-04			metalloproteinase 23 (Mmp23).	
408	11794	NM_053606	ii	mRNA. 11/21Length = 1444	Matrix metalloproteinase 23
				Rattus norvegicus casein	metanoproteniase 23
400	000:-	•• • • • • •		kinase 1, alpha 1 (Csnk1a1).	
409	20243 N	IM_053615	aa,bb	DNA 44041 II I	casein kinase 1, alpha 1
				Rattus norvegicus fatty acid	occom milase i, alpha i
ļ				Coenzyme A ligase, long chain	
				4 (Facl4), mRNA. 11/22Length =	
410	13005 N	M_053623	j,k,y,z	4000	fatty gold Coopers - A 1
	T			Rattus norvegicus G elongation	fatty acid-Coenzyme A ligase, long chain 4
			į.	factor (EF-G), mRNA.	
411	1228 N	M_053625	j,k	44/04)	
$\neg$				Rattus norvegicus potassium	G elongation factor
	İ	ļ	[,	voltage-gated channel,	
			!	Total State Charles,	
- 1	ı	1	1:	member 4 (Kcnh4), mRNA.	
- 1					
412	15777 NI	M_053630	b,u,v	(4/04)	otassium voltage-gated channel, subfamily H (eag- elated), member 4

TABLE	1	GenBank A	icc I	The Committee of the Co	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC II	No.	Model Code	· · · · · · · · · · · · · · · · · · ·	2. 関心では診断が、作品で乗ってはいるできません。
, , , , , , , , , , , , , , , , , , ,	OLOG II	JN0	Model Code	Known Gene Name	Unigene Sequence Cluster Title
	1			Rattus norvegicus early growth	1
0440		1		response 2 (Egr2), mRNA.	
2413	85	7 NM_053633	y,z,ee,ff	11/21Length = 2976	early growth rooms and
				Rattus norvegicus beta-	early growth response 2
	ł	1		carotene 15, 15-dioxygenase	
i				(Bcdo),mRNA. 11/22Length =	
2414	1864	NM_053648	3 bb	227	
	.004	714W_00004C	טט		beta-carotene 15, 15'-dioxygenase
ľ		]		Rattus norvegicus dynamin 1-	78
2415	4446	NA 050055		like (Dnml1), mRNA.	
2413		NM_053655	и	11/22Length = 3845	dynamin 1-like
- 1			j	Rattus norvegicus purinergic	
f			1	receptor P2X, ligand-gated ion	
			1	channel, 2 (P2rx2), mRNA.	
2416	1316	NM_053656	s,t,ii	1/22Length = 1831	
				Rattus norvegicus cyclin L	purinergic receptor P2X, ligand-gated ion channel,
l				(Con) - DNA 44/044	
2417	3454	NM_053662	ln a	(Ccnl), mRNA. 11/21Length =	
	0704	14141_000002	p,q	292	cyclin L
ł		]	1	Rattus norvegicus cyclin L	
244-	0.45-		1	(Ccnl), mRNA. 11/21Length =	
2417	3455	NM_053662	p,q,gg	292	cyclin L
				Rattus norvegicus YME1	O CONTRACTOR OF THE CONTRACTOR
			1	(S.cerevisiae)-like 1 (Yme1I1),	
2418	2063	NM_053682	le ·	mRNA.11/21Length = 2727	V/454 /0
				Rattus norvegicus Cbp/p3-	YME1 (S.cerevisiae)-like 1
			ľ	interacting transactions	
				interacting transactivator,	
- 1				withGlu/Asp-rich carboxy-	
2419	46400	NILL OFFICE		terminal domain, 2 (Cited2),	Cbp/p300-interacting transactivator, with Glu/Asp-
2419	10122	NM_053698	p,q,ee,ff	mRNA. 11/21Length = 1155	rich carboxy-terminal domain, 2
				Rattus norvegicus Cbp/p3-	non carboxy terrimal domain, 2
ſ			1	interacting transactivator,	
	-		1	withGlu/Asp-rich carboxy-	,
- !	1				Ch-/-2001
2419	16123	VM_053698	d,p,q,jj,kk		Cbp/p300-interacting transactivator, with Glu/Asp-
			-iPidilikur	Rattus norvegicus mitogen-	rich carboxy-terminal domain, 2
			1 1	ratios noivegicus mitogen-	
i	i			activated protein kinase kinase	
2420	6604	114 052702	[,. ]	6(Map2k6), mRNA. 11/22Length	
2420	0004	VM_053703	kk	= 169	mitogen-activated protein kinase kinase 6
	J			Light of the Property of the P	O SERVICE PROPERTY VILLAGE VILLAGE O
			1	factor 4 (gut) (Klf4),	
2421	13622	IM_053713	aa,bb,ii		Kninnal like feeten & (m.)
-				Rattus norvegicus Kruppel-like	Kruppel-like factor 4 (gut)
	I		1 1	factor 4 (gut) (Kif4),	
2421	22411	IM_053713	d,t	D111 444001	
242::				mRNA.11/22Length = 2393	Kruppel-like factor 4 (gut)
2421			1 1.	Rattus norvegicus Kruppel-like	
242:	- 1			factor 4 (gut) (Klf4),	
	25270	M OF2740		(3-9 (7 4) 7)	
	25379 N	M_053713	_t,li	mRNA.11/22Length = 2393	Kruppel-like factor 4 (out)
	25379 N	M_053713	t,II I	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1	Kruppel-like factor 4 (gut)
	25379 N	M_053713	t,II I	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1	Kruppel-like factor 4 (gut)
2421			[t,ll	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1 coiled-coil, myosin-like BCL2-	
2421		M_053713 M_053739	t,	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1),	eclin 1 (coiled-coil, myosin-like BCL2-interacting
2421			t,	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198	
2421			t,     (	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198 Rattus norvegicus	eclin 1 (coiled-coil, myosin-like BCL2-interacting
2421			t,	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198 Rattus norvegicus phosphotidylinositol transfer	eclin 1 (coiled-coil, myosin-like BCL2-interacting
2421	15269 N	M_053739	t,	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198 Rattus norvegicus phosphotidylinositol transfer protein, beta(Pitpnb), mRNA	eclin 1 (coiled-coil, myosin-like BCL2-interacting
2421	15269 N		t,	mRNA.11/22Length = 2393 Rattus norvegicus beciin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198 Rattus norvegicus phosphotidylinositol transfer protein, beta(Pitpnb), mRNA. 1/22Length = 268	eclin 1 (coiled-coil, myosin-like BCL2-interacting rotein)
2421	15269 N	M_053739	t,	mRNA.11/22Length = 2393 Rattus norvegicus beciin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198 Rattus norvegicus phosphotidylinositol transfer protein, beta(Pitpnb), mRNA. 1/22Length = 268 Rattus norvegicus celt division	eclin 1 (coiled-coil, myosin-like BCL2-interacting
2421	15269 N	M_053739	t,	mRNA.11/22Length = 2393 Rattus norvegicus beciin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198 Rattus norvegicus phosphotidylinositol transfer protein, beta(Pitpnb), mRNA. 1/22Length = 268 Rattus norvegicus celt division	eclin 1 (coiled-coil, myosin-like BCL2-interacting rotein)
2421	15269 N	M_053739	t,	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198 Rattus norvegicus phosphotidylinositol transfer protein, beta(Pitpnb), mRNA. 1/22Length = 268 Rattus norvegicus cell division ycle 37 homolog (S.	peclin 1 (coiled-coil, myosin-like BCL2-interacting protein) hosphotidylinositol transfer protein, beta
2421	15259 N	M_053739	t,     (	mRNA.11/22Length = 2393 Rattus norvegicus beclin 1 coiled-coil, myosin-like BCL2- nteracting protein) (Becn1), nRNA. 11/21Length = 198 Rattus norvegicus chosphotidylinositol transfer protein, beta(Pitpnb), mRNA. 1/22Length = 268 Rattus norvegicus celt division ycle 37 homolog (S. erevisiae) (Cdc37), mRNA.	eclin 1 (coiled-coil, myosin-like BCL2-interacting rotein)

TABLE		GenBank Ac	C. 1	A A	Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GLGC I		Model Code	***	
	1,0200 1	3/110.	INOGEL CODE	the factory of the contract of	Unigene Sequence Cluster Title
	i	1		Rattus norvegicus succinate-	
		1		CoA ligase, GDP-forming,	
	1	1		alphasubunit (Suclg1), mRNA.	
2425	1817	5 NM_053752	aa,bb	11/21Length = 1684	guadinala Ca A II
				Rattus norvegicusUDP-N-	succinate-CoA ligase, GDP-forming, alpha subun
	1	1	Ī	acetylglucosamine-2-	
				epimerase/N-	
			1	acelylmannosamine kinase	
	1	1	1		l
2426	7027	NM_053765	ا ا	(Uae1),mRNA. 11/22Length =	UDP-N-acetylglucosamine-2-epimerase/N-
	1321	141VI_033703	d	258	acetylmannosamine kinase
				Rattus norvegicus protein	
				tyrosine phosphatase, non-	
0.40=				receptortype 16 (Ptpn16),	
2427	15996	NM_053769	cc,dd	mRNA. 11/22Length = 198	protein tyrosine phosphatase, non-receptor type 1
				Rattus norvegicus Arg/Abi-	Protein tyrosine phosphatase, non-receptor type 1
		1	]	interacting protein	
				ArgBP2(Argbp2), mRNA.	
2428	14015	NM_053770	hh	11/21Length = 6331	A. JALLE
				Rattus norvegicus Arg/Abl-	Arg/Abl-interacting protein ArgBP2
- 1				interesting protein	
				interacting protein	
2428	14017	NM_053770	44	ArgBP2(Argbp2), mRNA.	
2720	14017	14141_053770	hh	11/21Length = 6331	Arg/Abl-interacting protein ArgBP2
- 1				Rattus norvegicus protein	
0400	4040			kinase inhibitor, alpha (Pkia),	
2429	1016	NM_053772	r,gg	mRNA.11/21Length = 1183	protein kinase inhibitor, alpha
	1			Rattus norvegicus interferon	protein kinase inhibitor, aipria
				gamma receptor (Ifngr), mRNA.	
2430	9059	NM_053783	j,k,kk	11/21Length = 186	Interference
			77-1	Rattus norvegicus kinase D-	interferon gamma receptor
1	- 1		1	interacting substance of 22 kDa	
i i				(Kiding 22) mDNA 2/00/	
2431	11606	NM_053795	lgg l	(Kidins22), mRNA. 3/22Length = 714	
	- 11555	0007.00	99		kinase D-interacting substance of 220 kDa
- 1	[			Rattus norvegicus aspartyl-	
2432	25504	NM_053799		tRNA synthetase (Dars),	
2702	200041	MM_000799	jj,kk,ii	mRNA.11/21Length = 2143	aspartyl-tRNA synthetase
- 1					
0400	45545			Rattus norvegicus thioredoxin	
2433	15615	NM_053800	h,l	(Txn), mRNA. 11/22Length = 33	thioredovin
			1	Rattus norvegicus Rho	W. C. COOAIII
			<u> </u>	interacting protein 3 (Rhoip3),	•
2434	25262 N	M_053814	b,u,v,cc,dd	- Dila datori	Pho internating westers a
		-		Rattus norvegicus tissue	Rho interacting protein 3
ĺ	- 1		İ	inhibitor of metalloproteinase 1	<del></del>
			alknovzbh	Timn1) mDNA 44 mai	
2435	15002 N	IM_053819	⊆,י,י,י,י,∪,∧,∠,⊞  ( }}	(Timp1), mRNA. 11/21Length =	
	.5552	000013		74	tissue inhibitor of metalloproteinase 1
1	ĺ		l.	ratius itorvegicus tissue	
j	1		ļi	nhibitor of metalloproteinase 1	
2425	45000		a,ı,ĸ,n,o,x,z,hh (	Timp1), mRNA. 11/21Length =	
2435	15003N	M_053819	,kk   7	74   <sub>1</sub>	tissue inhibitor of metalloproteinase 1
				Rattus norvegicus v-ral simian	The same of the canopide hase 1
- 1		ŀ	lie lie	eukemia viral oncogene	
			lh.		rol almion leukemie wiest
2436	20421 N	M_053821	ji j	D414 441044	/-ral simian leukemia viral oncogene homolog B
	1			Rattus norvegicus S1 calcium-	ras related)
		ļ	إ,إ	Salus noivegious 5 i calcium-	
- 1			د	Money protein Adjudgaration	
2437	16173 NI	M_053822	e,y,z,ee,ff =	) (S1a8), mRNA. 11/21Length	
	10110111	vUUJOZZ   6	• v 7 88 ft  -	361	6100 calcium-binding protein A8 (calgranulin A)

			GenBank A	CC: 1 i i i i i	11.	the second of the second	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	ΙD	No.		el Code	Known Gene Name	
						Associate Marile	Unigene Sequence Cluster Title
	1	ĺ				Rattus norvegicus dathrin, lig	
						polypeptide (Lcb) (Cltb),mRN	gnt
2438	3 171	54	NM_053835	b,gg		11/22 oneth - 020	
		-	000000	10,99		11/22Length = 982	clathrin, light polypeptide (Lcb)
	1	- 1		-		Pottus personal and 1 in a	
	1			- 1		Rattus norvegicus clathrin, lig	ht
2438	3 171	55	NM_053835	10		polypeptide (Lcb) (Citb),mRNA	l.
	<del>                                     </del>	-	1111_000000	g		11/22Length = 982	clathrin, light polypeptide (Lcb)
	]	- 1				Pottus I I I I	
		- 1		ł		Rattus norvegicus clathrin, lig	ht
2438	180	65	VM_053835	_		polypeptide (Lcb) (Cltb),mRNA	h.
	100	991	VIVI_000000	C		11/22Length = 982	clathrin, light polypeptide (Lcb)
						Rattus norvegicus adaptor-	
	!	1				related protein complex 2, mu	1
2439	400	یار		1.		subunit (Ap2m1), mRNA.	
2439	100	191	M_053837	f,r,cc,	dd	11/21Length = 1816	adaptor-related protein complex 2 4 1
							adaptor-related protein complex 2, mu 1 subunit
	!					Rattus norvegicus Fc receptor	
				1		lgG, low affinity II) (Fcgr3),	'
2440	2086	1 8	M_053843	kk	ł	mRNA. 11/22Length = 1318	Formonton In C. Annua W. H. W.
						gai 1010	Fc receptor, IgG, low affinity III
j				1		Rattus norvegicus Fc receptor,	
					l	lgG, low affinity III (Fcgr3),	
2440	2086	9 N	M_053843	w,x,kk	- 1	mRNA. 11/22Length = 1318	e
		1				Rattus norvegicus neurexin 2	Fc receptor, IgG, low affinity III
		1		1	- 1,	Nrxn2), mRNA. 11/21Length =	
2441	178	oln	M_053846	u,v	12	3436	
		7				Rattus norvegicus calcium	neurexin 2
1		1		1	ا	hannel, voltage-dependent,	
ŀ					,	oeta Scuburit (Carto)	
2442	101	ılnı	M_053851	le	14	peta 2subunit (Cacnb2), mRNA. 1/22Length = 3927	
		$\top$		<del>                                     </del>	<del></del>	1/22Lerigur = 392/	calcium channel, voltage-dependent, beta 2 subuni
1				i	1,	Rattus norvegicus N-	
- 1		1		1		cotyltransfermed 4 /	
				j	١	cetyltransferase 1 (arylamineN	
2443	16361	INN	/L_053853	cc,dd	a	cetyltransferase) (Nat1),	N-acetyltransferase 1 (arylamine N-
		<del>                                     </del>	000000	100,00		RNA. 11/22Length = 2533	acetyltransferase)
-					1.5	Rattus norvegicus eukaryotic	
- 1		l		1	jtr.	anslation initiation factor4E	
2444	1570	NIA	1_053857	<b>.</b> .	þ	nding protein 1 (Eif4ebp1),	eukaryotic translation initiation factor 4E binding
-7-17	13/0	INIV	1_00000/	s,t	m	RNA. 11/22Length = 843	protein 1
				ļ	Į.F	Rattus norvegicus eukaryotic	
				l	tra	anslation initiation factor4E	
المدادد	4 4		. 0000		bi	nding protein 1 (Eif4ebp1).	eukaryotic translation initiation factor 4E binding
2444	15/1	NN	_053857	e,t,kk	m	RNA. 11/22Length = 843	protein 1
					R	attus norvegicus valosin-	1
2445	400		0=0==		CC	ntaining protein (Vcp), mRNA	
2445	18357	MM	_053864	n,o	11	/OOI!! OO	valosin-containing protein
					R	attus norvegicus	valoan-containing protein
- 1						ospholipase A2, activating	
					Dro	otein (Plaa),mRNA.	
2446	<u>114</u> 05	NM.	_053866	f	111	1041 11	shows 12 April 12
T					R	attus norvegicus dynein,	phospholipase A2, activating protein
- 1	ı		1		Crt	oplasmic, intermediate	
	[				l no	voentide 2 /Dto:	1
2447	1352	MV	_053880	22	Ipol	ypeptide 2 (Dnci2), mRNA.	
	- 502	****	_000000	aa	$-\frac{11}{5}$	21Length = 2538	dynein, cytoplasmic, intermediate polypeptide 2
- 1	- 1				Ra	attus not vegicus A i Pase.	
ſ					11100	WOIGH 44 I/D /AL O	
2448	20030	18.4	053884	39	Ivac	cuolar, 14 kD (Atp6s14), kNA. 11/21Length = 667	ļ

	1 (2)	GenBank Acc	En la la la la la la la la la la la la la	The state of the state of	Atty. Ref. 44921-5090-01-WO/2105485
ÈQ ID	GLGC II	D No:	Model Code	122-11-10-11-11	※ 作品 (30年) ありのかがら、「サールマート」
	92.00%	<u> </u>	Nionel Code:		Unigene Sequence Cluster Title
				Rattus norvegicus arginine-	
	l			glutamic acid dipeptide (RE)	
0440			İ	repeats(Rere), mRNA,	
2449	38	5 NM_053885	b,o,u,v,ee,ff,kk	11/21Length = 6659	arginine-glutamic acid dipeptide (RE) repeats
				Rattus norvegicus Proteinase-	
		]		activated receptor-2, G protein-	. [
				coupled receptor 11 (F2rl1),	
2450	75	NM_053897	ee,ff,gg	mRNA. 5/22Length = 1428	Proteinase-activated receptor-2, G protein-couple receptor 11
			1	1420	
			1	Rattus norvegicus peroxisomal	
ł				biogenesis factor 12 (Pex12),	
2451	15706	NM_053921	lu	mRNA. 11/21Length = 2347	
			<del> "</del>	Rattus norvegicus eukaryotic	peroxisomal biogenesis factor 12
1				translation initiation factor 2B	
			i .		
2452	1400	NIM OFFICE		(Eif2b), mRNA. 11/21Length =	
2702	1420	NM_053950	aa	1634	eukaryotic translation initiation factor 2B
			1	Rattus norvegicus MCF.2 cell	
- 1		1		line derived transforming	
0,55				sequence-like (Mcf2i), mRNA.	
2453	531	NM_053951	gg	11/21Length = 4354	MCF.2 cell line derived transforming sequence-lik
- 1				Rattus norvegicus endoplasmic	
				retuclum protein 29 (Erp29),	
2454	16552	NM_053961	h,l,n,o	mRNA. 11/21Length = 4529	endoplasmic retuclum protein 29
					endoprasmic reductum protein 29
i				Rattus norvegicus endoplasmic	
- 1				retuclum protein 29 (Erp29),	
2454	16553	NM_053961	h,l	mRNA. 11/21Length = 4529	
			11,11	Rattus norvegicus matrix	endoplasmic retuclum protein 29
				metallogratelages 40 (Mars 40)	
2455	16654	NM_053963	n,o	metalloproteinase 12 (Mmp12),	
			11,0	mRNA. 11/21Length = 1632	matrix metalloproteinase 12
ľ				Rattus norvegicus solute carrier	
			l .	fomily 25(com/l/m / mile Carrier	
			1	family 25(carnitine/acylcarnitine	
				ranslocase), member 2	
2450	40540	NA 050005		Slc25a2), mRNA.11/21Length =	solute carrier family 25 (carnitine/acylcarnitine
2456	10040	NM_053965	hh	1231	translocase), member 20
- 1				Rattus norvegicus solute carrier	
l				amily 25(carnitine/acylcamitine	
ſ	ľ		t	ranslocase), member 2	
	1		ı İ.	01-05-0)	•
			l (	Sic25a2), mRNA.11/21Lenath =1	Solute carrier family 25 (carniting/appleanting)
2456	16547	NM_053965	<u> </u>	231	solute carrier family 25 (carnitine/acylcarnitine
2456	16547	NM_053965	<u> </u>	231	solute carrier family 25 (carnitine/acylcamitine translocase), member 20
2456	16547	NM_053965	1111	Rattus norvegicus G protein	solute carrier family 25 (carnitine/acylcamitine translocase), member 20
2456 2457			r F	Rattus norvegicus G protein pathway suppressor 1 (Gps1),	translocase), member 20
			d n	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794	solute carrier family 25 (carnitine/acylcamitine translocase), member 20  G protein pathway suppressor 1
			đ n	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal	translocase), member 20
2457	6357	NM_053969	d n	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA.	translocase), member 20 G protein pathway suppressor 1
	6357	NM_053969	d n h,l,n,o,w,x 1	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963	translocase), member 20
2457	6357	NM_053969	d r	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal	translocase), member 20 G protein pathway suppressor 1
2457	6357 15135	NM_053969 NM_053971	d r h,l,n,o,w,x 1	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA.	translocase), member 20  G protein pathway suppressor 1  ribosomal protein L6
2457	6357 15135	NM_053969 NM_053971	d r h,l,n,o,w,x 1 h,l,w,ii 1	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963	translocase), member 20 G protein pathway suppressor 1
2457	6357 15135	NM_053969 NM_053971	d r h,l,n,o,w,x 1 h,l,w,ii 1	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal Rattus norvegicus ribosomal Rattus norvegicus ribosomal	translocase), member 20  G protein pathway suppressor 1  ribosomal protein L6
2457 2458 2458	6357 15135 15136	NM_053969 NM_053971 NM_053971	d p	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA.	translocase), member 20  G protein pathway suppressor 1  ribosomal protein L6
2457	6357 15135 15136	NM_053969 NM_053971 NM_053971	d p h,l,n,o,w,x 1 h,l,w,ii 1 h,l,w,ii 1 h,l,w,ii 1	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963	G protein pathway suppressor 1  ribosomal protein L6  ribosomal protein L6
2457 2458 2458	6357 15135 15136	NM_053969 NM_053971 NM_053971	d r h,l,n,o,w,x 1 h,l,w,ii 1 h,l,w,ii 1 h,l f	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus Ras-related	translocase), member 20  G protein pathway suppressor 1  ribosomal protein L6
2457 2458 2458	6357 15135 15136	NM_053969 NM_053971 NM_053971	d p h,l,n,o,w,x 1 h,l,w,ii 1 h,l,w,ii 1 h,l 1	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus Ras-related Rattus norvegicus Ras-related Rattus norvegicus Ras-related	G protein pathway suppressor 1  ribosomal protein L6  ribosomal protein L6
2457 2458 2458	6357 15135 15136 122183	NM_053969 NM_053971 NM_053971	d p h,l,n,o,w,x 1 h,l,w,ii 1 h,l,w,ii 1 h,l 1	Rattus norvegicus G protein pathway suppressor 1 (Gps1), nRNA.11/21Length = 1794 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963 Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 1/21Length = 963	G protein pathway suppressor 1  ribosomal protein L6  ribosomal protein L6

ABLE	1	GenBank Ac	10 to 10 to		Atty. Ref. 44921-5090-01-WO/2105485
EQ ID	GLGC II	D No.			(4) (2) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4
		7 1.19.	" Fladonei Code	Known Gene Name	Unigene Sequence Cluster Title
	1			Rattus norvegicus RAB28,	
	ľ	-		member RAS oncogene family	,
0400				(Rab28), mRNA. 11/21Length	=
2460	1879	8 NM_053978	h,l,n,o	1483	
				Rattus norvegicus ribosomal	RAB28, member RAS oncogene family
		1	1	protein S15a (Rps15a),	
2461	1546	8 NM_053982	j,w,x,jj,kk	mRNA.11/21Length = 449	
			<i>J. J. J.</i>	Rattus norvegicus H3 histone	ribosomal protein S15a
				family 3B (H3f3b), mRNA.	•
2462	15642	2 NM_053985	d	11/21Length = 117	
			<del>-  </del>	Pottus = 27/	H3 histone, family 3B
				Rattus norvegicus H3 histone,	
2462	15646	NM_053985	١.	family 3B (H3f3b), mRNA.	
2402	13040	MINIT 09989	đ	11/21Length = 117	H3 histone, family 3B
		ł		Rattus norvegicus myosin Ib	
2402	47050			(Myo1b), mRNA. 11/22Length	=
2463	1/653	NM_053986	cc,dd	367	myosin IB
{				Rattus norvegicus progestin	- John LD
		1		induced protein (dd5), mRNA.	1
2464	18025	NM_053989	w,x	11/21Length = 318	Prognotin indused and a
			T		progestin induced protein
i			1	Rattus norvegicus 3-	1
1			1	hydroxybutyrate dehydrogenasi	
				(hand mitable denydrogenas)	
2465	17730	NM_053995	l_	(heart, mitochondrial) (Bdh),	3-hydroxybutyrate dehydrogenase (heart,
2.00	17700	14141_000990	g	mRNA. 11/21Length = 142	mitochondrial)
1				Rattus norvegicus protein	
				phosphatase 2 (formerly 2A),	
- 1				regulatory subunit B (PR 52).	
				alpha isoform (Ppp2r2a),	protein phosphotose 2 (farment, out
2466	16962	NM_053999	u,v	mRNA. 11/21Length = 2142	protein phosphatase 2 (formerly 2A), regulatory
				Rattus norvegicus CD36	subunit B (PR 52), alpha isoform
	1			antigen (collagen type I	
!			[	receptor,thrombospondin	
ĺ	ĺ		1	receptor, the or to depos	
2467	25249	NM_054001	n,o	receptor)-like 2 (Cd36l2),	
		004001	11,0	mRNA. 11/21Length = 1938	
i				<b>5</b>	
!				Rattus norvegicus TBP-	
2468	46560	111 051001		interacting protein 12A (Tip12A),	
2400	100001	VM_054004	hh	mRNA. 11/21Length = 4383	TBP-interacting protein 120A
1				Rattus norvegicus integral	TOTAL TENT
. !	- 1		j	membrane-associated protein	
			j l	1(Itmap1), mRNA. 11/21Length	
2469	1108	NM_054005	b,l,m	= 2282	intogral manufactures and the second
				Rattus norvegicus unr protein	integral membrane-associated protein 1
	· 1		ļ	(unr), mRNA. 11/21Length =	
2470	174311	IM_054006		3755	
					unr protein
		ļ	l l	Rattus norvegicus Rgc32	
2471	17326 4	IM_054008	[[	protein (Rgc32), mRNA.	
-T/ I	110201	IVI_004008		11/21Length = 889	Rgc32 protein
- 1	1			Rattus norvegicus Rgc32	
أيدي	47000		];	protein (Rgc32), mRNA.	
2471	1/330 N	M_054008	aa,bb	14/04111 000	Rgc32 protein
- 1				Rattus norvegicus vesicle-	rigooz protent
ļ.	1	j	. ا	associated membrane protein 3	
1	1		.	Vamp3/ mps/4 44/00/	
i	برامعمد	Mi_057097	r,g   (	Vamp3), mRNA. 11/22Length =	
7/6		··· []	เมื่อเ	742	vesicle-associated membrane protein 3
776	2020011			0	residic associated intelliptable protein 3
776	2020011			Rattus norvegicus growth arrest	vosidio associated membrane protein 3
			s	Rattus norvegicus growth arrest pecific 6 (Gas6), nRNA.11/22Length = 2573	vosidio-associated membrane protein 3

		GenBank Ac	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC I	D No.	Model Code	Known Gene Name	Unigene Sequence Clüster Title
				Rattus norvegicus Cytochrome	
	1	İ		P45, subfamily XXI (steroid 21-	<b>*</b>
	1	1		hydroxylase) (Cyp21), mRNA.	
2474	1770	9 NM_057101	u,v	1/22Length = 1964	T 1 M
				Rattus norvegicus A kinase	Tenascin X
		İ		(PRKA) anchor protein (gravin)	
	1			12(Akap12), mRNA.	
2475	1965	8 NM_057103	gg	11/22Length = 5236	A 11
		1	99	Rattus norvegicus	A kinase (PRKA) anchor protein (gravin) 12
				ectonucleotide	
	ĺ	1	ł		
	1			pyrophosphatase/phosphodiest	
2476	052	8 NM_057104	1_	rase 2 (Enpp2), mRNA.	ectonucleotide pyrophosphatase/phosphodiesteras
2410	332	0/14/05/104	- <u>                                    </u>	11/22Length = 3216	2
				Rattus norvegicus UDP	
	1	1		glycosyltransferase 1	
				family,polypeptide A6 (Ugt1a6),	IDP alvoquitronsferred 4 feet"
2477	1512	5 NM_057105	jj,kk,il	mRNA. 1/22Length = 1593	
			,,,,,	Rattus norvegicus	UDP glycosyltransferase 1 family, polypeptide A7
		1		peroxiredoxin 1 (Prdx1), mRNA.	
2478	15391	NM_057114	d	11/21Length = 882	
				Rattus norvegicus splicing	peroxiredoxin 1
]		1	j	factor, arginine/serine-	
1			ľ	rich(transformer O.D.	
				rich(transformer 2 Drosophila	
2479	23307	NM_057119		homolog) 1 (Sfrs1), mRNA.	splicing factor, arginine/serine-rich (transformer 2
	20001	14141_007 118	e	11/21Length = 1978	Drosophila homolog) 10
1			İ	Rattus norvegicus splicing	
i				factor, arginine/serine-	
				rich(transformer 2 Drosophila	
2479	02240			homolog) 1 (Sfrs1), mRNA.	splicing factor, arginine/serine-rich (transformer 2
24/9	23310	NM_057119	e,s,t	11/21Length = 1978	Drosophila homolog) 10
				Rattus norvegicus protease	- J
- 1		ļ	1	(prosome, macropain) 26S	
				subunit, ATPase 1 (Psmc1),	protease (prosome, macropain) 26S subunit,
2480	727	NM_057123	s,t	mRNA. 11/21Length = 1556	ATPase 1
1					
1	,	•		Rattus norvegicus peroxisomal	
1				biogenesis factor 6 (Pex6),	
0.4-1	919	NM_057125	l,m	mRNA.11/21Length = 3169	peroxisomal biogenesis factor 6
2481				Rattus norvegicus	F-1-1-100min progenicala idulul 0
2481				Trattus Horvegicus	
2481				heterogeneous nuclear	
				heterogeneous nuclear	
2481		NM_057141	b,g,n,o.u.v	heterogeneous nuclear ribonucleoprotein K (Hnrpk),	
			b,g,n,o,u,v	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563	heterogeneous nuclear ribonucleoprotein K
			b,g,n,o,u,v	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus	
			ხ,g,n,o,υ,ν	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear	
2482	2413	NM_057141		heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear ribonucleoprotein K (Hnrpk),	heterogeneous nuclear ribonucleoprotein K
	2413		b,g,n,o,u,v	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563	
2482	2413	NM_057141		heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich	heterogeneous nuclear ribonucleoprotein K
2482	2413 2416	NM_057141 NM_057141	t	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear nibonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA.	heterogeneous nuclear ribonucleoprotein K heterogeneous nuclear ribonucleoprotein K
2482	2413 2416	NM_057141		heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear nibonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA. 11/22Length = 853	heterogeneous nuclear ribonucleoprotein K
2482	2413 2416	NM_057141 NM_057141	t	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear nibonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA. 11/22Length = 853 Rattus norvegicus oxidation	heterogeneous nuclear ribonucleoprotein K heterogeneous nuclear ribonucleoprotein K
2482 2482 2483	2413 2416 1892	NM_057141 NM_057141 NM_057144	t a,o,x,ee,ff,kk	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear nibonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA. 11/22Length = 853 Rattus norvegicus oxidation resistance 1 (Oxr1), mRNA.	heterogeneous nuclear ribonucleoprotein K heterogeneous nuclear ribonucleoprotein K
2482	2413 2416 1892	NM_057141 NM_057141 NM_057144	t	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear nibonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA. 11/22Length = 853 Rattus norvegicus oxidation resistance 1 (Oxr1), mRNA. 11/21Length = 1896	heterogeneous nuclear ribonucleoprotein K heterogeneous nuclear ribonucleoprotein K cysteine-rich protein 3
2482 2482 2483	2413 2416 1892	NM_057141 NM_057141 NM_057144	t a,o,x,ee,ff,kk	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear nibonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA. 11/22Length = 853 Rattus norvegicus oxidation resistance 1 (Oxr1), mRNA. 11/21Length = 1896	heterogeneous nuclear ribonucleoprotein K heterogeneous nuclear ribonucleoprotein K
2482 2482 2483	2413 2416 1892	NM_057141 NM_057141 NM_057144	t a,o,x,ee,ff,kk	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear nibonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA. 11/22Length = 853 Rattus norvegicus oxidation resistance 1 (Oxr1), mRNA. 11/21Length = 1896	heterogeneous nuclear ribonucleoprotein K heterogeneous nuclear ribonucleoprotein K cysteine-rich protein 3
2482 2482 2483	2413 2416 1892 19481 I	NM_057141 NM_057141 NM_057144 NM_057153	t a,o,x,ee,ff,kk	heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus heterogeneous nuclear nibonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563 Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA. 11/22Length = 853 Rattus norvegicus oxidation resistance 1 (Oxr1), mRNA. 11/21Length = 1896	heterogeneous nuclear ribonucleoprotein K heterogeneous nuclear ribonucleoprotein K cysteine-rich protein 3

TABLE		GenBank Ad	<b>2</b>	Dark Control Oracle Control	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	ID No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
			The Midwell Sound	Pattus serverious	Unigene Sequence Cluster Title
	-		i	Lyanna Horvedions salcowello	
	i	1	- }	muscle protein	
2485	154	61 NM_057191	ee,ff	(Sarcosin),mRNA. 11/21Lengt	1
	- 10 11	2.7.111_007 131	100,11	= 2316	sarcomeric muscle protein
		İ	i	Rattus norvegicus 2,4-dienoy	
				CoA reductase 1, mitochondria	aí
2486	1540	08 NM_057197	_  f,g,l,m	(Decr1), mRNA. 11/22Length =	
		101102	1,9,,,,,	Rattus norvegicus 2,4-dienoyl	2,4-dienoyl CoA reductase 1, mitochondrial
				CoA reductase 1, mitochondria	
				(Decr1), mRNA. 11/22Length =	<sup>31</sup>
2486	1540	9 NM_057197	f,g	119	
		5007 107	1,9	119	2,4-dienoyl CoA reductase 1, mitochondrial
ľ				Pathus populations to the state of	
]		1	İ	Rattus norvegicus tropomyosii	וי
2487	1812	2 NM_057208	h,l	3, gamma (Tpm3), mRNA.	1.
		557 200	1191	11/21Length = 111 Rattus norvegicus synaptic	tropomyosin 3, gamma
ł				vesicle glycoprotein 2 a	
				(Sv2s) mBNA 44/041	
2488	174	3 NM_057210	hh	(Sv2a),mRNA. 11/21Length = 3844	
			····	Rattus norvegicus Kruppel-like	synaptic vesicle glycoprotein 2 a
- 1				factor 9 (Kif9), mRNA.	
2489	864	NM_057211	bb	11/22Length = 2721	le
				17722Lerigui - 2721	Kruppel-like factor 9
1		1	j	Rattus norvegicus brain specifi	
				binding protein (LOC117582),	9
2490	11632	NM_057212	ь	mRNA. 11/22Length = 999	la de la companya de
				Rattus norvegicus cytokine	brain specific binding protein
				inducible SH2-containing protein	
				2 (Cish2), mRNA. 11/22Length	1
2491	15707	NM_058208	d	= 918	autili ti un aus
				Rattus norvegicus ribosomal	cytokine inducible SH2-containing protein 2
				protein S23 (Rps23), mRNA.	1
2492	10498	NM_078617	c,g,w,x	11/22Length = 432	ribonomal protein 000
				Rattus norvegicus Smhs1	ribosomal protein S23
			1	protein (Smhs1), mRNA.	İ
2493	8820	NM_080399	j,k,ee,ff,jj,kk	12/21Length = 117	Smhe1 protein
			]	Rattus norvegicus melanoma	Smhs1 protein
			]	antigen, family D, 2	1
- 1				(Maged2),mRNA. 12/21Length =	
2494	2541	NM_080479	aa,bb	1993	melanoma antigen, family D, 2
		<del></del>		Rattus norvegicus adaptor-	mounta anagen, faililly D, Z
			ľ	related protein complex 2, beta	
				1 subunit (Ap2b1), mRNA.	
2495	17958	NM_080583	gg	11/22Length = 5413	adaptor-related protein complex 2, beta 1 subunit
J	ļ			Rattus norvegicus adaptor-	
- 1			ļ	elated protein complex 2, beta	
2400	47000	Nu acces		i subunit (Ap2b1), mRNA.	
2495	1/960	NM_080583	<u>r</u>	11/22Length = 5413	adaptor-related protein complex 2, beta 1 subunit
,				Rattus norvegicus gamma-	rolated protein complex 2, beta i subunit
- 1	- 1		į a	aminobutyric acid (GABA) A	
2400	500	114 000=5	r	eceptor,gamma 1 (Gabrg1).	gamma-aminobutyric acid (GABA) A receptor,
2496	506	VM_080586	<u>ii  </u> r	nRNA. 1/22Length = 1739	gamma 1
i	- 1			Rattus norvegicus dynein light	J
احمدا	47000		ic	hain-2 (Dic2), mRNA.	
2497!	:7662 N	M_080697	cc,dd 1	/22Length = 51	dynein light chain-2
				Dotters	-yo ngrit orialit-z
i	í	1	[1	ratius norvegicus fibromodulin 1	
i		IM_080698	{(	Rattus norvegicus fibromodulin Fmod), mRNA. 11/22Length = 96	

	1	GenBank /	Accil	Atty. Ref. 44921-5090-01-WO/2105485
SEO IN	GLGC	DING	100,-	Atty. Ref. 44921-5090-01-WO/2105485  Je Known Gene Name Unigene Sequence Cluster Title
OLG, (D,	OLGCI	DINO.	iviodel Cod	de Known Gene Name Unigene Sequence Cluster Title
	1			Rattus norvegicus purinergic
	İ	1	l	receptor P2X, ligand-gated ion
		1		channel, 5 (P2rx5), mRNA.
2499	36	3 NM_08078	0 d,e,p,q,ee,	
		1	- (-)-,-,-,-,-	purinergic receptor P2X, ligand-gated ion channel
	ł	ŀ	1	
	j	1		Rattus norvegicus
	ľ		- 1	BCL2/adenovirus E1B 19 kDa-
2500	2202	3 114 00000	_	interactingprotein 3-like (Bnip3I), BCL2/adenovirus E1B 19 kDa-interacting protein 3
2000	2303	3 NM_08088	g ir	
				Rattus norvegicus hypoxia
0504				induced gene 1 (Hig1), mRNA.
2501	995	2 NM_080902	cc,dd	14/001 11
				hypoxia induced gene 1
		1	1	Rattus norvegicus Dihydrofolate
		1	1	reductase 1 (active) (Dhfr1),
2502	4739	NM_130400	aa,bb	
			- 144,50	mRNA. 1/22Length = 761 Dihydrofolate reductase 1 (active)
ĺ				Trattus not vegicus protein
ı		1	}	phosphatase 1,
		1		regulatory(inhibitor) subunit 14a
2502	0000	NINA 400	<b>I</b>	(Ppp1r14a), mRNA. 1/22Length protein phosphatase 1, regulatory (inhibitor) subuni
2503	9033	NM_130403	jj,kk	= 559 (Minibile) Subuli
- 1				Rattus norvegicus coronin,
- 1				actin binding protein 1A
			- 1	(Coro1a),mRNA. 1/22Length =
2504	21695	NM_130411	c	14000
			<del>-  </del>	Rattus norvegicus heat shock coronin, actin binding protein 1A
ŀ	İ			27kD protoin 2 (Heato) - Put
2505	11709	NM_130431	s	27kD protein 2 (Hspb2), mRNA.
		100401	-	11/22Length = 549 heat shock 27kD protein 2
			1	Rattus norvegicus guanine
- 1	1		1	nucleotide binding protein,
1	l			betapolypeptide 2-like 1
2500	440=0	NIA : 46		(Gnb2l1), mRNA. 11/22Length = guanine nucleotide binding protein (G protein), beta
2506	14959	NM_130734	w,x	IDDIVIDADIDA 2-146 1
	1	-		Rattus norvegicus lipocalin 2
1			1	(Lcn2), mRNA. 11/22Length =
2507	1809	NM_130741	l,k	1070
			1	Rattus norvegicus solute carrier
- 1	ŀ			family 5 mombes 6
ļ	ł		1	family 5, member 6
2508	1502	NM_130746	100	(Slc5a6),mRNA. 11/22Length = solute carrier family 5 (sodium-dependent vitamin
	1302	100/40	aa	
	1			Rattus norvegicus solute carrier
				family 5, member 6
2502	4500	10.0	1.	(Slc5a6),mRNA. 11/22Length = solute carrier family 5 (sodium-dependent vitamin
2508	1503	M_130746	d	391 Itransporter) member 6
				Rattus norvegicus ATPase,
				Ca++-sequestering (Atp2c1),
2509	20738 N	IM_131907	c	
			T	Rattus norvegicus mltogen
i	1			activated protein Linear II
İ	- 1		1	activated protein kinase kinase
2510	17564 N	M 122202	1	2(Map2k2), mRNA. 11/22Length
2010	17 304 1	M_133283	hh	= 1376 mitogen activated protein Mineral Manager
- 1				Natus noi vegicus zinc finger
			1	protein 36 (Zfp36), naPAIA
2511	25730 N	M_133290	j,k,p,q	144/001 11 000
			1	zinc finger protein 36
_ [				carboxylesterase 3 (Ces3),
วรงวไ	20870 1	M_133295	I	Amboylesiciase 3 (Cess)!
2512	2007 3119	W 133795	hh	mRNA. 11/22Length = 1935 carboxylesterase 3

TABLE		IGen	Bank Acc		<b>建</b>	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC I	DINO	Dank Acc	Model Code	Known Gene Name	\$
	,,,,,,,,,,,	7,110.		Intoneicone	Known Gene Name	Unigene Sequence Cluster Title
	1	1			Rattus norvegicus glycoprote	
					(transmembrane) nmb (Gpnm	In I
2513	1945	6 NM	133298	h,l,w,x	mPNA 2/201 or at 1000	
		1	100200	11,1,1,1,1	mRNA. 2/22Length = 232	glycoprotein (transmembrane) nmb
					Pattus populacione altra anno 1	
					Rattus norvegicus glycoprotei	n
2513	404	BINM	133298	h,l,n,o,w,x	(transmembrane) nmb (Gpnml	
		11111	100230	III,II,IU,W,X	mRNA. 2/22Length = 232	glycoprotein (transmembrane) nmb
	1			1	Pottus non-select	
					Rattus norvegicus glycoprotei	ח
2513	4049	MAIN .	133298	c,h,l,n,o,w,x	(transmembrane) nmb (Gpnmb	
	1010	11111	100230	C,H,H,R,O,W,X	mRNA. 2/22Length = 232	glycoprotein (transmembrane) nmb
-					Rattus norvegicus basic helix-	
,		1			loop-helix domain	
2514	1064	NINA 4	33303		containing, class B3 (Bhlhb3),	
2017	1001	IAIAI_	33303	p,q,hh	mRNA. 11/22Length = 311	basic helix-loop-helix domain containing, class B,
ŀ					Rattus norvegicus oxidised lov	/ Cass b,
ļ		l			density lipoprotein(lectin-like)	
2545	4040				receptor 1 (Olr1), mRNA,	oxidised low density lipoprotein (lectin-like) receptor
2515	4318	NM_1	33306	p,q	11/22Length = 375	11
1					Rattus norvegicus Interleukin 4	
25.40					receptor (II4r), mRNA.	
2516	657	NM_1	33380	J,k,y,z	3/22Length = 3576	Interleukin 4 receptor
j					Rattus norvegicus sphingosine	micheukii 4 receptor
					kinase 1 (Sphk1), mRNA.	
2517	7700	NM_1	33386	ee,ff	11/22Length = 2648	sphingosine kinase 1
i					Rattus norvegicus integrin-	Springosine kinase 1
	l				linked kinase (Ilk), mRNA.	
2518	16713	NM_1	33409	b	3/22Length = 1359	intonia liale d li
					Rattus norvegicus dyskeratosis	integrin-linked kinase
			j		congenita 1, dyskerin	
			ľ		(Dkc1),mRNA. 3/22Length =	J
2519	19326	NM_13	3419	u,v,jj,kk	183	de la contraction de la contra
					Rattus norvegicus splicing	dyskeratosis congenita 1, dyskerin
1				İ	factor YT521-B (YT521), mRNA	
2520	10660	NM_13	3423	∍,cc,dd	3/22Length = 2968	
				,	Rattus norvegicus adenylate	splicing factor YT521-B
	- 1		1		cyclase activating polypeptide 1	
				1		
2521	24775	VM_ 13	3511	: 1	11/22Length = 2681	adenylate cyclase activating polypeptide 1 receptor
					Rattus norvegicus transcription	1
İ			- 1	Į,	factor E20 (Tet-2-)	
2522	25543	IM 13	3524 s		factor E2a (Tcfe2a),	
		10			mRNA.3/22Length = 216	
j					Rattus norvegicus	
					ransmembrane 4 superfamily	
2523	20890 N	M 13	3526 li	1.	member 3(Tm4sf3), mRNA.	
		100	, JEO   I		3/22Length = 1182	transmembrane 4 superfamily member 3
				[_	r varras norvedicas	
			1	Į.	preimplantation protein 3	
2524	2788 N	M 123	1520	. 19	Prei3), mRNA. 3/22Length =	
<del></del>	210011	w_135	3528 s,		2513	preimplantation protein 3
	-			[.	Rattus norvegicus general	
	1		- 1	tr	anscription factor III C	
2525	4704		l	1	(Gtf3c1), mRNA. 3/22Length =	
2020	1791 N	W_133	541	.  6	878	general transcription factor III C 1
1				F	varras noi vedicris bloteiu	general surficient factor fill C
i	İ			[ty	rosine phosphatase 2E	I
2526	1824 N			(F	Ptp2E), mRNA. 3/22Length =	}
			545 j,k	1.5	543	

TABLE	1.1.1.		GenBank A	CC.	14 3 2 3 4	Atty.: Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	اأما	No.	Model Code	Knowe Company	等性 1967年 (1967年) 1967年 (1967年) 1967年 (1967年) 1967年 (1967年) 1967年 (1967年) 1967年 (1967年)
		: <u>-</u> F		Iwodei Oode	** Latin Court define	Unigene Sequence Cluster Title
	1				Rattus norvegicus myeloid	10 1 11 1
	ł			1	differentiation primary	ļ
2527	111	ماده	NA 400546		responsegene 116 (Myd116),	
2021	114	001	VM_133546	j,k,p,q,kk	mRNA. 3/22Length = 2225	myeloid differentiation primary response gene 11
		- 1		}	Rattus norvegicus myeloid	primary response gene 11
					differentiation primary	
2527	400	٠,			responsegene 116 (Myd116),	
2527	1804	13/1	NM_133546	s,t,ll	mRNA. 3/22Length = 2225	myeloid differentiation primary
					Rattus norvegicus	myeloid differentiation primary response gene 11 EST, Weakly similar to FGD1_MOUSE Putative
				İ	phospholipase A2, group IVA	IDUO/BSC OUSDING BUOGOSTISS
					(Cytosolic, calcium-dependent)	
		1		a,j,k,y,z,ee,fi	k (Pla2g4a), mRNA. 1/22Length	
2528	24	4 N	M_133551	k	2858	
		Т			Rattus norvegicus proprotein	IVA (cytosolic, calcium-dependent)
ļ					convertase subtilisin/kexin type	
					4 (Pcsk4), mRNA. 11/22Length	
2529	2536	9 N	M_133559	l,m	= 2458	
		T			Rattus norvegicus cell division	proprotein convertase subtilisin/kexin type 4
		1			cycle 25B (Cdc25b),	
2530	182	7 N	M_133572	r,u,v	mRNA.3/22Length = 284	
		$\top$		7,0,1	Rattus norvegicus cell division	cell division cycle 25B
j		1		1	cycle 3ED (Odeos)	
2530	1830	ואוכ	M_133572	lv	cycle 25B (Cdc25b),	
		-	1000/ 2	- <del> </del>	mRNA.3/22Length = 284	cell division cycle 25B
- }					Rattus norvegicus cell division	
2530	1831	IN	M_133572	1.,	cycle 25B (Cdc25b),	
		1	n_100012	V	mRNA.3/22Length = 284	cell division cycle 25B
					Rattus norvegicus RN protein	
2531	24600	NIA	/_133585		(LOC171116), mRNA.	
	24000	TIVIN	/_133365	cc,dd	3/22Length = 1619	RN protein
1		1			Rattus norvegicus adaptor-	
					related protein complex AP-3,	
2532	1971	NIN	1_133593		mu 1 subunit (Ap3m1), mRNA.	
2002	12/1	INIV	1_133593	a,ee,ff,jj,kk	4/22Length = 2146	adaptor-related protein complex AP-3, mu 1 subuni
ļ					Rattus norvegicus hydroxyacyl-	
- 1				1	Coenzyme A dehydrogenase/3-	
					ketoacyl-Coenzyme A	
1	ì			1	thiolase/enoyl-Coenzyme A	
					hydratase (trifunctional protein)	hydroxyacyl-Coenzyme A dehydrogenase/3-
امد	<b>,_</b>				beta subunit (Hadhb), mRNA	ketoacyl-Coenzyme A thist-set is 1.0
2533	1728	<u> </u>	_133618	w,x	3/22Length = 1928	ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A
-					Rattus norvegicus guanylate	hydratase (trifunctional protein), beta subunit
	ĺ			1	binding protein 2,interferon-	
					inducible (Gbp2), mRNA.	
2534	14995	NM_	_133624	la	2/001 - 11	manual-1-11 b
	T				Rattus norvegicus cathepsin D	guanylate binding protein 2, interferon-inducible
					(Ctsd), mRNA. 11/22Length =	
2535	1463	MV	_134334	u,v,gg	1004	
			<del></del>	1.199	Rattus norvegicus RAP1B,	cathepsin D
İ					member of BAC	
					member of RAS oncogene	
2536	16456	JM	134346		family (Rap1b), mRNA.	
			.107040	<u> </u>	3/22Length = 1874	RAP1B, member of RAS oncogene family
i	- 1				Traiting Horvedicus (MAXOAILIIS	
	- 1		į		(influenza virus) resistance 3	•
2537	517	I A A	134350	_ i'	(Mx3), mRNA. 3/22Length =	
		ı IVI	1 3/1 (6) 1	s l	2443	nyxovirus (influenza virus) resistance 3

		GenBank Ac	xc. T	10 (10 19 10 ) 以 (10 10 10 10 10 10 10 10 10 10 10 10 10 1	Atty. Ref. 44921-5090-01-WO/2105485
EQ ID	GLGC I	No.	Model Code	Known Gene Name	
		11777	Intodes code	Pottus serie Marie:	Unigene Sequence Cluster Title
		1		Rattus norvegicus methionine	
	ļ	1		adenosyltransferase II, alpha	
2538	17337	NM_134351	1.1.	(Mat2a), mRNA. 3/22Length =	
	17331	1401_134331	j,k	1337	ESTs
				Rattus norvegicus Plasminoge	en
	1		1	activator, urokinase receptor	
2539	600	101050	l .	(Plaur), mRNA. 5/22Length =	
2009	600	NM_134352	a,y,z	1277	Plasminogen activator, urokinase receptor
		l		Rattus norvegicus poly(A)	gen deardier, droidingse receptor
			-	binding protein, cytoplasmic	
0540			1 .	1(Pabpc1), mRNA. 3/22Length	
2540	19840	NM_134353	n ·	= 219	poly(A) binding protein, cytoplasmic 1
				Rattus norvegicus diacetyl/L-	polyty binding protein, cytopiasmic 1
				xylulose reductase (glb), mRN/	<u> </u>
2541	8692	NM_134387	hh_	3/22Length = 879	
				310	diacetyl/L-xylulose reductase
			l	Rattus norvegicus LL5 protein	
2542	1530	NM_134397	a,e,jj,kk	(LI5), mRNA. 3/22Length = 376	5 1 1 5 protoin
$\Box$			1	1 - 3/1 0/22Lettgti1 = 3/6	o LLo protein
٠.	}			Rattus norvegicus cytosolic	
			1	sorting protein PACS-1 (Pacs1)	
2543	7164	NM_134406	jj,kk	mRNA. 3/22Length = 4198	
			,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	Rattus norvegicus collagen,	cytosolic sorting protein PACS-1
	1		1	type V, alpha 1 (Col5a1),	
2544	25237	NM_134452	l <sub>r</sub>	mPNA 11/201 and	
		101102	<del> </del>	mRNA.11/22Length = 5551	collagen, type V, alpha 1
	ļ		1	Rattus norvegicus chemokine	
			1	(C-X3-C motif) ligand 1	1
2545	10077	NM_134455		(Cx3cl1),mRNA. 1/22Length =	
-570	13011	104400	aa,bb	344	small inducible cytokine subfamily D, 1
	1		J	Rattus norvegicus late	
2546	10904	VM_138518	<b>L</b>	gestation lung protein 1 (Lgl1),	
	13/13/4/1	RICOCI TINIA	t,ii	mRNA.4/22Length = 352	late gestation lung protein 1
			i	Rattus norvegicus associated	V F
			1	molecule with the SH3 domain	
25/7	4400	114 400-0		ofSTAM (Amsh), mRNA.	
2547	4422	NM_138531	gg	11/22Length = 1544	associated molecule with the SH3 domain of STAN
	1			Rattus norvegicus glutamate	Molecule with the SHS domain of STAN
	- 1		1	receptor interacting protein 2	
			l	(Grip2), mRNA. 4/22Length =	
2548	5283 N	IM_138535	gg	5433	distanate recentor interestina and the
!				Rattus norvegicus synaptic	glutamate receptor interacting protein 2
				glycoprotein SC2 (SC2), mRNA.	
2549	25479 N	M_138549	jj,kk	14/001	pymontic absence to a coc
T				Rattus norvegicus	synaptic glycoprotein SC2
.				Metallothionein (Mt1a), mRNA.	
2550	15189 N	M_138826	j,k,y,z,ee,ff,kk		3.4-1. D. d.1
			A THILLD CHILLY	Rattus norvegicus	Metallothionein
		l		Metallothionals (1445)	
2550	15190N	M_138826	ikvzii	Metallothionein (Mt1a), mRNA.	
-	.5.55	100020	j,k,y,z,ii	11/22Length = 389	Metallothionein
j	i	ì	-	Rattus norvegicus solute carrier	
				family 2,member 1	
554	16040	4 40000-		(Slc2a1),mRNA. 1/22Length =	Solute carrier family 2 a 1 (facilitated glucose
2551	10248 N	M_138827	y,z	2571	transporter) brain
	}	1		Rattus norvegicus solute carrier	
i	i	;	!	family 2,member 1	
				/OLO 41	Solute carrier family 2 a 4 (familiary 4 - 1)
551	16249 NI	M. 138827	.k	0574	Solute carrier family 2 a 1 (facilitated glucose
33 H	10540141	", 1000£; "		23/ L	ransporter) brain

TABLE	1	GenBank Acc	2 (1983) 12.		Atty. Ref. 44921-5090-01-WO/2105485
SEO ID	GL GC II			THE WOLLD A A	2011年19日 - 東京書館 - 東京書 - 東京 - 東京
OLG,ID	GLGC II	O No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
	l			Rattus norvegicus	The state of the s
	•		1	apolipoprotein E (Apoe), mRN	A
2552	1640	0 NM_138828	cc,dd	11/22Length = 936	
			100,00	1 1/22Lengin = 936	Apolipoprotein E,
	1		J	Rattus norvegicus	
2552	1010	1		apolipoprotein E (Apoe), mRN/	A.
2002	1640	1 NM_138828	gg	11/22Length = 936	
				Rattus norvegicus vacuole	
		i		Membrane Protein 1 (Vmp1),	
2553	23166	NM_138839	y,z,ee,ff,kk	mRNA.11/22Length = 183	
			77-10-11-11-11	Rattus norvegicus	Vacuole Membrane Protein 1
- 1				Const	
]				Saccharomyces cerevisiae	
2554	0700	1114 4000 1-	1	Nip7p homolog(pEachy),	
2554	9/96	NM_138847	j,k	mRNA. 4/22Length = 1175	Saccharomyces cerevisiae Nip7p homolog
ľ				Rattus norvegicus prolactin-like	e Caccharoniyees cerevisiae Nip/p nomolog
- 1				protein K (Pripk), mRNA.	
2555	8468	NM_138861	b	11/22Length = 865	
			<del> </del>	1 1/22Length = 865	prolactin-like protein K
İ				Rattus norvegicus Diaphorase	
				(NADH) (cytochrome b-5	
				reductase)(Dia1), mRNA.	
2556	17530	NM_138877	n,o,ìi	4/22Length = 1893	Dispherene (MADLE) ( )
- 1				Rattus norvegicus Diaphorase	Diaphorase (NADH) (cytochrome b-5 reductase)
- 1				(NADH) (cytochrome b-5	
				(NADA) (Cytochrome b-5	
2556	17522	NM 420077	1.,	reductase)(Dia1), mRNA.	
2000	17332	NM_138877	j,k	4/22Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
- 1			1	Rattus norvegicus Diaphorase	(10 to 1) (O) to childre b-5 reductase)
- 1				(NADH) (cytochrome b-5	
	-			reductase)(Dia1), mRNA.	
2556	25039	NM_138877	ee,ff	Alogi and - 4000	
			56,11	4/22Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
1	i			Rattus norvegicus Best5 proteir	1
0557	4504			(Best5), mRNA. 4/22Length =	
2557	4594	NM_138881	С	3628	Best5 protein
				Rattus norvegicus	Desito protein
	ŀ			phosphatidy/serine-specific	
	i			phospholipaseA1 (Pspla1),	
2558	945	VM_138882	j,k,s,t	PriospholipaseA (Psplat),	
		111_100002		mRNA. 11/22Length = 1743	phosphatidylserine-specific phospholipase A1
				Rattus norvegicus ATP	, , , , , , , , , , , , , , , , , , , ,
ł	İ		[:	synthase, H+transporting,	
	j		į.	mitochondrial F1 complex. O	
ľ	- 1	1	ا		ATP synthese 11, terms in the same in the
			12		ATP synthase, H+ transporting, mitochondrial F1
2559	7395lN	IM_138883	, <u> </u>	nPNA 4/221	complex, O subunit (oligomycin sensitivity
		55555	· <u> </u>	<u> </u>	conferring protein)
			l.	Rattus norvegicus polyubiquitin	
2560	2045		(	Loc192255), mRNA.	
2560	3075/	IM_138895	aa,bb 4	//22Length = 1115	polyubiquitin
J				Rattus norvegicus	L-3-andmini
			İn	hospholipase B (Loc192259),	
2561	1168 N	M_138898	e,n   'n	•DNA 4/001	
			-,	Pattue populations	phospholipase B
1	1	- 1		Rattus norvegicus complement	
		ł	Įċ	omponent 1, s subcomponent	
2560	10007	14 400000	[(0	C1s), mRNA. 11/22Length =	
2562	1000/N	M_138900 b	),C 2	98	complement component 1, s subcomponent
	1		11	Rattus norvegicus stress-	Promont component 1, 5 subcomponent
	1	į	lin	duced-phosphoprotein 1	
		i		den7/Hen0 organists	
			155	Hsp7/Hsp9-organizing protein)	
2563	118/0 1	M_138911 e	[5	30p1), milden. 4/22Langth -	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-
	11040 1	м_138911 е		JUZ 102	organizing protein)
ı		1	Ţ.	Rattus norvegicus ribosomal	5 Protokil
			10	oteln L41 (Rpl41), mRNA.	•
2564	15380 N	И_139083 <b>ไ</b> น	v,cc,dd 11	1001 11	ibosomal protein L41

WO 2004/063334

		GenBank Ac	5.4	Name and the second of the	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC IC	No.	Model Code		
			38.7 ( 1.1 % %)	Rattus norvegicus CTD-bindir	Unigene Sequence Cluster Title
				SR-like protein rA8	19
				(LOC245926), mRNA.	İ
2565	734	NM_139094	99	5/22Length = 4794	OTD 11 11 OD III
			33	Rattus norvegicus ATP	CTD-binding SR-like protein rA8
- 1		1		synthase, H+ transporting,	
			İ	mitochondrial F1 complex,	
		i		epsilon subunit (Atp5e), mRNA	1 A
2566	17203	NM_139099	g,hh	5/22Length = 44	
			SI	Rattus norvegicus ATP	complex, epsilon subunit
- 1				synthase, H+ transporting,	•
J				mitochondrial F1 complex,	
			1	epsilon subunit (Atp5e), mRNA	ATD 4
2566	17204	NM_139099	g	5/22Length = 44	
				Rattus norvegicus CD48	complex, epsilon subunit
	İ			antigen (Cd48), mRNA.	
2567	17854	NM_139103	lii	5/22Length = 1422	0040
			1	Rattus norvegicus Estrogen-	CD48 antigen
- 1			1	regulated protein CBL2, 2.4kD	ECTo Manharday
				(LOC245963), mRNA.	ESTs, Weakly similar to T09065 hypothetical
2568	17868	NM_139104	r,s,t	5/22Length = 1888	protein - mouse [M.musculus], Estrogen-regulated
				Rattus norvegicus	protein CBL20, 20.4kD
				ribonuclease/angiogenin	
	1			inhibitor (Rnh1),mRNA.	
2569	18108	NM_139105	a,n,o,ll	11/22Length = 1664	ribanusia lauda da a a a a a a a a a a a a a a a a
				Rattus norvegicus G protein-	ribonuclease/angiogenin inhibitor
l	ı			coupled hepta-helical receptor	
-	1		[	Ig-Hepta (Ig-Hepta), mRNA.	
2570	14463	NM_139110	ii	5/22Length = 4951	G protoin counted best at the
				Rattus norvegicus stem cell	G protein-coupled hepta-helical receptor Ig-Hepta
			•	derived neuronal survival proteir	
- !				precursor (Sdnsf), mRNA.	
2571	22595 N	M_139253	cc,dd	5/22Length = 1771	stem cell derived neuronal survival protein precursor
	1			Rattus norvegicus	precuisor
	ĺ		' l:	mannosidase, alpha, class 2C,	
			ļ.	member 1(Man2c1), mRNA.	
2572	1803 N	M_139256	<u>c </u> !	5/22Length = 336	mannosidase alpha aless 20 mg t
l	1			Rattus norvegicus brain-	mannosidase, alpha, class 2C, member 1
ł		}		enriched SH3-domain protein	
			E	Besh3 (Besh3), mRNA.	
2573	9775 N	M_139334	C 1	1/22Length = 2362	brain-enriched SH3-domain protein Besh3
ĺ				Rattus norvegicus LRP16	
0	40.		ļr	rotein (Lrp16), mRNA.	Rattus norvegicus LRP16-like protein mRNA,
2574	12450 N	M_139337	c,hh  1	1/22Length = 13	complete cds
	1			Rattus norvegicus	
		ļ	h	omocysteine respondent	
2575	24040	14 4000 :-	p	rotein HCYP2 (Hcyp2), mRNA.	Rattus norvegicus homocysteine respondent proteir
2575	ZIBIBIN	M_139342 I	ob 1		HCYP2 mRNA, complete cds
ļ	[	1			
i	i	ļ	ļ F	Rattus norvegicus Rho GTPase	ESTs, Moderately similar to RHG4_HUMAN Rho-
2576	12004	4 444740	ıس	Severing protein 4 (Alligab4).	GTPase-activating protein 4 (Rho-GAP
23/0	12004 1	M_144740 i	m m	RNA. 11/22Length = 325	hematopoletic protein C1) (P115) [H.sapiens]
i			Į F	remos norvedicos agribocate	i machenis
İ		ļ	ļα	omplement related protein of	ESTs, Weakly similar to 1917150A
£77	12710		3	(Da (Acrp3), mRNA.	collagen:SUBUNIT=alpha1:ISOTYPE=VIII [Raftus
<u> </u>	13/12/NA	<u>1_144744</u> ji	1·	1/22L611911 - / 0/	norvegicus] [R.norvegicus]
i	i	İ	F	allus norvegicus hypothetical (	- 1 F adiogol
578	22756 11	1_145084 g	pr	otein RMT-7 (Rmt7),	Rattus norvegicus hypothetical protein RMT-7
	: M M IMB	<u>1_145084</u>  g	a I	RNA.11/22Length = 1855	nRNA, complete cds

	" (2 d	GenBank A	CC 1 To 1 To 1		Atty. Ref. 44921-5090-01-WO/2105485
	GLGC I	DINO.		And the second s	Frank British and Committee and the Committee an
,5-4 10	OLCO!	DINO.	Model Code	The second of th	Unigene Sequence Cluster Title
	İ			Rattus norvegicus pyruvate	
			1	dehydrogenase phosphatase	
			İ	isoenzyme2 (Pdp2), mRNA.	
2579	1576	1 NM_145091	cc,dd,jj,kk	11/22Length = 175	Rattus norvegicus pyruvate dehydrogenase
			- Jojou jjjinat	Raffus populations land	phosphatase isoenzyme 2 mRNA, complete cds
	1			Rattus norvegicus lamina-	, , , , , , , , , , , , , , , , , , , ,
	1			associated polypeptide 1C	
2580	101	NIM 445000		(Lap1c), mRNA. 11/22Length	= Rattus norvegicus lamina-associated polypeptide
	194	8 NM_145092	b,l,m	231	
				Rattus norvegicus zinc finger	to (2 trio) mittal, complete cas
				DHHC domain containing	
			1	2(Zdhhc2), mRNA. 11/22Leng	th Detter
2581	673°	NM_145096	hh	= 1487	I State of Itali tee (Siec) Illicity, Compi
				140/	cds
		]		Pottus nemicalisms	
		ĺ		Rattus norvegicus peroxisoma	al
ĺ			t	Ca-dependent solute carrier-lik	ke
2582	6000	NINA 4470		protein (Pcscl), mRNA.	
2002	0900	NM_145677	j,k	11/22Length = 315	ESTs
				Rattus norvegicus Max	12013
			ĺ	dimerization protein 3 (Mad3),	
2583	305	NM_145773	u,v	mRNA.11/22Length = 989	<b>.</b>
				Rattus norvegicus nuclear	Rattus norvegicus Myx mRNA, complete cds
				reacter and facility and clear	
				receptor subfamily 1, group D,	
2584	15640	NM_145775	1,	member 1 (Nr1d1), mRNA.	1
2004	10040	145/75	h,i,j,k,r	11/22Length = 2297	Rat Rev-ErbA-alpha protein mRNA, complete cds
1				Rattus norvegicus nuclear	A COMPlete Cds
				receptor subfamily 1, group D,	
			ĺ	member 1 (Nr1d1), mRNA.	
2584	15641	NM_145775	h,i	11/22Length = 2297	
			1.7	Pottus portestant la la	Rat Rev-ErbA-alpha protein mRNA, complete cds
				Rattus norvegicus tubulin,	
2585	22972	NM_145778		gamma 1 (Tubg1), mRNA.	
		140770	е	11/22Length = 142	Rattus norvegicus mRNA for tubulin, complete cds
ł	1			Rattus norvegicus G protein-	o to the tabain, complete cus
	ſ			coupled receptor 37-like 1	
0500				(Gpr37i1), mRNA. 11/22Length	
2586	20106	VM_145784	ļii	= 2451	ESTs
	- 1			Rattus norvegicus G protein-	ESIS
- 1	- 1			coupled receptor 37-like 1	
			1	(Cpr37/4) DAIA 44/00	
2586	20515 N	M_145784	la l	(Gpr37I1), mRNA. 11/22Length	
		111_140704	10	= 2451	ESTs
i	- 1			Rattus norvegicus G protein-	
- 1	į			coupled receptor 37-like 1	
0500				(Gpr37I1), mRNA. 11/22Length	
2586	19976	IM_145784	jj,kk	= 2451	ECT
				Rattus norvegicus G protein-	ESTs
			[	coupled receptor 37-like 1	
				(Gnr2711) mDNA 44/00	
2586	20046 N	M_145784		(Gpr37I1), mRNA, 11/22Length	
		1-707 04		= 2451	ESTs
1	1			Rattus norvegicus fatty acid	
	i		11	pinding protein 5, epidermal	
0=0=			d,j,k,t,bb,gg,kk (	Fabp5), mRNA. 11/22Length =	Pattus nonregious O
2587	20740 N	M_145878	,11	264	Rattus norvegicus Sprague-Dawley lipid-binding
				Rattus norvegicus PLRR-4	protein mRNA, complete cds
1	}	[	-	10) vmombio loveine - ' '	
1			(F	olymorphic leucine-rich repeat	
2588	5005 NI	M_147140	P	rotein (Pirr4), mRNA.	Rattus norvegicus clone PLRR-4 polymorphic
<del></del>	30331141	14/140	u,v 14	***************************************	eucine-rich repeat protein mRNA, complete cds
		ł	11	Rattus norvegicus ischemia	not repeat protein mixina, complete cds
		ŀ	re	elated factor vof-21	
- 1			la	-OC259228), mRNA.	I
			17.		
589 2	25435 NN	<u>/_</u> 147208	s,t  1	1/22Length = 4885	

TABLE		GenBank Ac	C. 18948 17 67		Atty, Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	ID No.	Model Code	NOTE : NOTE 1889 A TO THE STATE OF THE STATE	《·劉德···································
	<del></del>		mgasi odac	The transfer of the state of th	Unigene Sequence Cluster Title
			1	Rattus norvegicus nuclear	
	i			receptor subfamily 1, group D	
259	ol 🤄	90 NM_147210	h,i	member 2 (Nr1d2), mRNA.	Rattus norvegicus nuclear receptor Rev-ErbA-bo
	<del>`</del>	2011112111	11,1	11/22Length = 1996	mRNA, partial cds
	1		}	Detture a la como de	
	1	1		Rattus norvegicus SH3 doma	
259°	1 176	0 NM_147211	d,kk	binding protein CR16 (CR16),	Rattus norvegicus SH3 domain binding protein
		70 1411 141211	U,KK	mRNA.11/22Length = 4359	(CR16) mRNA, complete cds
				Rattus norvegicus outer	
	1			mitochondrial membrane	
2592	1054	4 NM_152935		receptor rTOM2 (LOC26661),	Rattus norvegicus outer mitochondrial membrane
2002	1004	4 INIVI_152935	s,t,u,v	mRNA. 11/22Length = 976	receptor rTOM20 mRNA, complete cds
	ł			Rattus norvegicus pancreatic	
	1	İ		secretory trypsin inhibitor type	ıı <b>)</b>
2502	4070			(PSTI-II) (LOC26662), mRNA.	Rat pancreatic secretory trypsin inhibitor type II
2593	12/0	0 NM_152936	h,I	11/22Length = 379	IIPS II-III MPNIA complete - 3.
	1	1		Rattus norvegicus heat shock	7
000			1	kDa protein 4 (Hspa4), mRNA.	
2594	1571	1 NM_153629	lp_	1/22Length = 4521	Rattus norvegicus ischemia responsive 94 kDa
				1021	protein (irp94) mRNA, complete cds
				Rattus norvegicus paired	ECTO FOT- 18 11 h m
				mesoderm homeobox 1 (Pmx1)	ESTs, ESTs, Highly similar to S37300 glycogen
2595		NM_153821	h,I	mRNA.1/22Length = 1375	, Ipnosphorylase (EC 2.4.1.1), brain - rat
2596	19888	S56464	cc,dd	111 (VA. 1/22Lengin = 13/5	[[R.norvegicus]
			1-3,00	glutamate receptor, ionotropic,	ESTs
2597	15693	S56679	aa,bb	AMPA1 (alpha 1)	
2598	25495	S59892	b,i,m	(alpha 1)	glutamate receptor, ionotropic, AMPA1 (alpha 1)
2599	25496	S59893	b,i,m		
2600		S61960	jj,kk	ferritin light chain 1	
2601		S63519	a,c,r,w,x	Terrair light chain 1	ferritin light chain 1
2602		S69206	ii	mast cell protease 1	ESTs
			i	mast cell protease 1	mast cell protease 1
2603	18647	S69316	d,e		ESTs, Weakly similar to HS9B_RAT Heat shock
2604	25066	S75280	r		protein HSP 90-beta (HSP 84) [R.norvegicus]
2605	25538	S76466	gg		•
					FOX- IV II
1					ESTs, Highly similar to MLES_RAT Myosin light
2606	24469	S77858	'u		Chain alkali, smooth-muscle isoform (MI C3SM)
			<del>"</del>		[[K.norvegicus]
2607	21583	S77900	bb,kk		ESTs, Highly similar to A37100 myosin regulatory
2607			jj,kk		light chain A, smooth muscle - rat [R.norvegicus]
			<sub>111</sub> , at		. 3.000
		}	İ		
2608	17626	S78556	gg	İ	ESTs, Highly similar to I56581 dnaK-type molecula
2608	25547		n,cc,dd,ii		chaperone grp75 precursor - rat [R.norvegicus]
				protein phosphatase 1,	
2609	25550	379213	d	regulatory /inhibited and the	
2610	25556		hh	egulatory (inhibitor) subunit 2	
2611	25571 8	398336	1,V		
2612	25075 (	J01347	,m		
2613	25572 L	J02534	)		
2614	15462 L			rotoln S	
					protein S
2615	16675 L	17565	,ii	nini chromosome maintenance	mini chromosome maintenance deficient 6 (S.
261ô	25589 U		,,, lo	eficient 6 (S. cerevisiae)	perevisiae)
2617	22196 U				
2618	25590 U		h		STs
2619					
		00010	,l,m		
2620	25593 U	26310 g	a	ensin	

TABLE		GenBank	<del></del>	L. Out	Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC	ID No		i silika i kita da katalan iliya kili ilikali salah k	<ul> <li>J. Charles and M. C. C. Charles and J. Charles and J. C. Charles and J. C. Charles and J. C. Charles and J. C. Charles and J. C. Charles and J. C. Charles and J. C. Charles and J. C. Charles and J. C. Charles and J. Charles and J. Charles and J. Charles and J. Charles and J. C. Charles and J. Charles and J. Charles and J. C. Charles and J. Charl</li></ul>
262			Model Code	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	Unigene Sequence Cluster Title
202	<del>'' </del>	99 U31668	p,q	E2F transcription factor 5	E2F transcription factor 5
202				proprotein convertase	- Sanosinpuoli labiol 0
262	2 202	24 U47014	b,u,v	subtilisin/kexin type 5	proprotoin convertees subject to
	ł				proprotein convertase subtilisin/kexin type 5
	_				P nominations 114 OUD. The second
262	3 145	54 U48828	ln		R.norvegicus H1SHR mRNA, Rattus norvegicus
	1				retroviral-like ovarian specific transcript 30-1 mR
262	4 216	54 U53184	a.e.i.k.g.v.z.k	k LPS-induced TNF-alpha factor	
				C induced TVF-alpha facto	
262	5 12	83 U61729	cc,dd,ll		Rattus norvegicus proline rich protein mRNA,
2626		18 U64705	r		complete cds
2626		19 U64705	<del>-  -</del>	<del></del>	
2627		36 U68562	cc,dd	hast start at the start at	
2628		29 U70270	n,o	heat shock protein 60 (liver)	heat shock protein 60 (liver)
2629		5 U72660			
	<del>                                     </del>	0/2000	a,jj,kk	Ninjurin	Ninjurin
2630	215	3 U75404		A kinase (PRKA) anchor protei	n
2631		2 U75405	u,v	(gravin) 12	A kinase (PRKA) anchor protein (gravin) 12
2632	2000	01175000	9		12 (Gravity Tiener protein (Gravity) 12
2002	2003	8 U75923	gg	isoleucine-tRNA synthetase	
0000	4-0-	01.17005		G protein-coupled receptor VTF	3
2633		6 U76206	jj,kk	15-20	
2634		3 U77829	cc,dd	growth arrest specific 5	G protein-coupled receptor VTR 15-20
2634		7 U77829	d	growth arrest specific 5	ESTs
2635		7 U83119	9,99	grandi direct specific o	E018
2636		3 U89745	u,ii	unknown protein	
2637	2328	2 U90725	hh	lipoprotein-binding protein	
2638		9 U95157	b,I,m	nyapodina recent a l	lipoprotein-binding protein
2639		3 X02904	ii	ryanodine receptor type II	
2640		X03347		glutathione S-transferase, pi 2	glutathione S-transferase, pi 2
		7,00047	p,q	FDI	
2641	1018	X06769		FBJ murine osteosarcoma viral	FBJ murine osteosarcoma viral (v-fos) oncogene
2642	14966	X07551	p,q	(v-fos) oncogene homolog	homolog
2643	2567	X07686	c,w,x,cc,dd		
2010	2007	707000	g		
2644	2/6/	X13411		Eph receptor B2 (ELK-related	Eph receptor B2 (ELK-related protein tyrosine
2017	240-	X13411	u,v_	protein tyrosine kinase)	kinase)
2645	20010	X14181	1.		ESTs, Highly similar to R5RT18 ribosomal protein
2040	20010	A14181	f,g,w,x		L18a, cytosolic [validated] - rat [R.norvegicus]
2646	40544	V4 407 4			ESTs, Highly similar to RL26_RAT 60S
2040	16541	X14671	g		RIBOSOMAL PROTEIN L26 [R.norvegicus]
				Rattus norvegicus	LZO [K.norvegicus]
	04455			mitochondrial genome.	
12	21152	X14848	bb	9/22Length = 16.3	golgi SNAP receptor com-1
				<u> </u>	golgi SNAP receptor complex member 1 ESTs, Highly similar to RL7A_HUMAN 60S
					tibesomal protein 1.7- (0) ( )
2647		X15013	f,g,w,x		ribosomal protein L7a (Surfeit locus protein 3) (PLA
2647	25679	X15013	f,g,aa		X polypeptide) [R.norvegicus]
					COTA I Palette de la
2648	15626	X17665	w,x	ribosomal protein S16	ESTs, Highly similar to R3RT16 ribosomal protein
T			<del>      '</del>	niscositiai proteiit 310	516, CVIOSOliC [validated] - rat IR populational
2649		X51536	_ gg ´  ı	a	ESTS, Highly similar to RS3 MOUSE 40S
2649		X51536		ribosomal protein S3	ribosomal protein S3 [R.norvegicus]
			, politi	rbosomai protein 53	
2650	18250	X51706	w,x	ihonomal nestetu to	ESTs, Highly similar to RL9_RAT 60S RIBOSOMAL
			- **·^	ibodomai protein L9	PROTEIN L9 [R.norvegicus]
2651	20872	X51707	1,44		STs, Highly similar to R3RT19 ribosomal protein
	16715	(53054	l,w,x r	ibosomal protein S19	519, cytosolic [validated] - rat [R.norvegicus]
26521			cc,dd,ii		Rat mRNA for RT1.D beta chain
		(530E)			AND THE PERSONAL PROPERTY OF THE PROPERTY OF T
2652 2652 2653	16716 2 20427 2		c n	bosomal protein S13	Rat mRNA for RT1.D beta chain

		GenBank Acc.	1 10, 75020	4. (19.71) Fig. (20.88) A GRAPE, 14.	Atty. Ref. 44921-5090-01-WO/2105485
SEQID	GLGC ID	No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2654	18606	X53504	g,w,x		ESTs, Highly similar to RL12_RAT 60S
2654		X53504	g	<del> </del>	RIBOSOMAL PROTEIN L12 [R.norvegicus]
2655		X53581	hh		
2655		X53581	g		
			19	Transporter 1, ABC (ATP	
2656	1037	X57523	d	binding cassette)	Tennanda 4 ABO (ABB )
			<del> </del>	Dinding casselle)	Transporter 1, ABC (ATP binding cassette)
			1		ECT- Webbert 7 4 Date was
2657	15106	X57529	h,l,aa		ESTs, Highly similar to RS18_HUMAN 40S
2658		X58200	g	ribosomal protein L29	ribosomal protein S18 (KE-3) (KE3) [R.norvegicus
2658		X58200	h,l,w,x	ribosomal protein L23	ribosomal protein L29
2659	25702	X58465	g,w,x	Ribosomal protein S5	Diberry
2659		X58465	g,w,x	Ribosomal protein S5	Ribosomal protein S5
2660		X59375	b,d,l,kk	Tribosomai protein 55	Ribosomal protein S5
2661		X59864			
		7.00004	<del>"</del>		
- 1	İ			}	
2662	17176	X60212	f.		R.norvegicus ASI mRNA for mammalian equivaler
	- 17 17 0	700212	1	amulaid bata (A.O.	of bacterial large ribosomal subunit protein L22
ì				amyloid beta (A4) precursor	
2663	25711	X60468		protein-binding, family B,	amyloid beta (A4) precursor protein-binding, family
2664		X61295	s,t	member 1	B, member 1
2004	23/10	A01295	c,g,hh		
2665	21657	X61381		}	Rattus norvegicus interferon-inducible protein
2005	21007	X01381	d,j,k,m,y,z,kk		variant 10 mRNA, complete cds
0000	45075	1/004.45			ESTs, Highly similar to RL8_HUMAN 60S ribosom
2666	158/5	X62145	h,r	ribosomal protein L8	protein L8 [R.norvegicus]
000-					ESTs, Highly similar to RL3_RAT 60S RIBOSOMA
2667	13646	X62166	n,o,w,x,kk,ll		PROTEIN L3 (L4) [R.norvegicus]
				4	ESTs, Highly similar to R3RT25 ribosomal protein
2668	15387	X62482	W,X	*	S25, cytosolic [validated] - rat [R.norvegicus]
				HMm:glutathione S-transferase,	ESTs, Highly similar to S23433 glutathione
2669	16780	X62660	c,f,g	alpha 4	transferase (EC 2.5.1.18) 8 - rat [R.norvegicus]
1	1			Inhibitor of nuclear factor of	- Tar [Tanorvegicus]
	-			kappa light chain gene enhancer	
2670	25090	X63594	j,k	in B-cells, alpha	
					ESTs, Highly similar to R3RT3A ribosomal protein
2671	20844	X65228	f,g,cc,dd		L23a, cytosolic [validated] - rat [R.norvegicus]
					R.norvegicus mRNA for cytosolic resiniferatoxin-
2672		X67877	c,s,t,gg		binding protein
2673		X68101	ee,ff		R.norvegicus trg mRNA
2674		X70369	c,g,bb	procollagen, type III, alpha 1	procollagen, type III, alpha 1
2675		X70667	l,m	melanocortin 3 receptor	prosonagon, type m, aiptia t
2676	16725		e,jj,kk	- I Josephor	R.norvegicus mRNA for Fc gamma receptor
2677	24232			Cyclin D1	
2678	16272		u,v	-,	Cyclin D1
2679	25741			CD9 antigen (p24)	
2680	25094		bb	J Gridgeri (PZT)	
2681	25743		aa,bb		
2682	18621)			RT1 class ib gene	DT4 along the com-
2683	25752		b,l,m	11 1 orașa în Acite	RT1 class lb gene
2684	25761		,k		
2685	25765	100	D,C,U,V		
2686	18031	10.45-1		laminin gamma 4	
	/			laminin, gamma 1	laminin, gamma 1
2687	12978		B,j,k,p,q,y,z,ce #		ESTs, Highly similar to S33363 gly96 protein -
2687	25770 3		ff		mouse [M.musculus]
**		· <i>≘</i> ·⊶⊙/	o,c,u,v,y		
2588	19279 Y	(00350		uroporphyrinogen	
· 20)	132/3 1	0000U 8	a,aa,bb,jj,kk	decarboxylase	uroporphyrinogen decarboxylase

TABLE 1		• • . • • •	3 37	42	Atty: Ref. 44921-5090-01-WO/2105485
SEQ ID.	ĞLĞC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2689	17146	Y07534	aa	Serine protease inhibitor	Serine protease inhibitor
2690	25777	Y08355	i,m	oxidative stress induced	oxidative stress induced
2691	18352	Z12298	aa,bb	decorin	decorin
2692	25790	Z21935	b,u,v	mitogen activated protein kinase 4	
2693		Z48444	cc,dd	A disintegrin and metalloprotease domain (ADAM) 10	A disintegrin and metalloprotease domain (ADAM)
2694	17481	Z49761	w,x		R.norvegicus mRNA for RT1.Ma
2695			y,z,ee,ff		ESTs, Moderately similar to T17342 hypothetical protein DKFZp586K1924.1 - human (fragment) [H.sapiens], R.norvegicus hsp70.2 mRNA for heat shock protein 70
2696	15569	Z78279	c,g,bb		procollagen, type I, alpha 1
2696	15570		c,f,g,j,k		procollagen, type I, alpha 1

TABLE		GenBank Ac	<del></del>	Atty, Ref. 44921-5090-01-WO/21054
SEQ in	GLGC ID	No.		
4 10	OLGC ID	No.	Model Code	i i durinays
4040	0046-			Actions of Nitric Oxide in the Heart, Arginine and proline metabolism, Hypox
1649	20127	AJ011116	j, k, n, o	Inducible Factor in the Cardiovascular System
2037	18569	NM_019212	f, w, x, hh	Actions of Nitric Oxide in the Heart, Integrin Signaling Pathway
2284	25795	NM_031556	jj, kk	Actions of Nitric Oxide in the Heart, Integrin Signaling Pathway
				Pathway
			1	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling
				through the T Cell Recentor Active tion of AAAD
				through the T Cell Receptor, Activation of cAMP-dependent protein kinase,
[			1	PKA, Attenuation of GPCR Signaling, CCR3 signaling in Eosinophils,
				ChREBP regulation by carbohydrates and cAMP, Erk1/Erk2 Mapk Signaling
2019	15975	NM_019132	lii	Ipouritally I mospholipase C-ensilon nathway Signaling Dath
		010102		Proving Gillings, Transcription tector CDED and the auto- and
	Ì		]	The state of the s
1			1	To the mediated infilling response analysis target college College and Additional
[	1		1	I I I I I I I I I I I I I I I I I I I
1835	2555	NINA 040007		Indication Action in all its Surface Molecules. T Cytotoxic Call Confe
1033	2005	NM_012967	a, y, z, kk	INICICULOS. I DEIDELLEI SIITACA MOIOCULOS
1				Addresion Molecules on Lymphocyte, Cells and Molecules involved in Land
- 1	[		1	The state of the s
1	l		1	Tooling in Comeal Epithelia, Frk1/Frk2 Mank Signaling and
- 1				Through Digitality Falliway, Monnocyte and its Surface Malacular party
40				dependent cell cycle arrest and apoptosis, Ras-Independent pathway in NK
1356	14989	AI177366	f, g, l, m, kk	100" INCOIDED CYLUIUXICIIV
	1		1	Adhesion Molecules on Lymphocyte, Monocyte and its Surface Molecules,
1826	1625	NM_012924	gg	Neutrophil and Its Surface Molecules
Ţ				ATT Signaling Pathway, ATM Signaling Pathway, Acomprise and
]	1		1	Deadelylation of RelA in The Nucleus Activation of DVC through Co.
[			1	coupled receptor, CD40L Signaling Pathway, Double Stranded RNA Induced
	1		1	Gene Expression Fruthropoietin modicine de la company de l
1			{	Gene Expression, Erythropoietin mediated neuroprotection through NF-kB,
- 1			1	HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through
i	1		1	151 to and DIATO Deadli Receptors, infllience of Recent Bho marks in a con-
1	1		1	In a management ML-KD Standard Dathway Matropostides MD - 10404-
1	1			principle the apoptosis of activated 1 cells. Signal transduction the control of the
l	- 1	İ		100" Receptor Digitaling Fallway. INF/Strace Palatod Cianalina Turno
2670	25090 X	62504		Joint in a live of the distriction of the state of the st
2010	23030 X	05094	j, k	incooptoi rattiway. Illieracib_1
	-			AKT Signaling Pathway, ChREBP regulation by carbohydroton and a Miles
}	1			LIN VLINZ Wapk Signaling Dathway. Inactivation of Ceva by AVT access
i		ļ		decontribution of p-catenin in Alveniar Macrophages. Decolotion of the party of
1010	222			My Tro I giuldillate recepiors Skeletal mucclo hunodrant
1918	3203 N	M_017039	C	""" O' Paulway, WINT Signaling Pathway mTOD Clanaling Date
	}			AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of
815	17524 A	010568	jj, kk	elF4e and p70 S6 Kinase
				AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of
1936	10886 N	M_017094	ji l	elF4e and p70 S6 Kinase
				AKT Signaling Pathway Growth Users St. 15
1936	10887 N	M_017094	j, kk	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase
			<del>,, , , , , , , , , , , , , , , , , , ,</del>	on to and pro 30 Milase
1936	10888 NI	V_017094	e, r, hh	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of
2082	23424 N		-1 . 1 . 1 . 1	en te and pro 36 Kinase
		021000		Alanine and aspartate metabolism, Aminoacyl-tRNA biosynthesis
	1478 NI	/_012744 r	i.	The target as a spartate metabolism. Citrate cycle (TCA cycle) Pygnyste
1785		1_V12144	· · · · · · · · · · · · · · · · · · ·	110(0)0(0)11
1785				Alpha-synuclein and Parkin mediated annual in the
	7486 NIA	4 010100		akar-mediated proteolysis in Parkinson's dicases Data
2028	7486 NN	/_019169 r	<del></del>	Alpha-synuclein and Parkin-mediated proteolysis in Parkinson's disease, Rote of Parkin in Ubiquitin-Proteasomal Pathway
1785 2028 1/121	7486 NN 15756 AA 12031 AA	818089 II		of Parkin in Ubiquitin-Proteasomal Pathway  Aminoacyl-tRNA biosynthesis, Glycine, serine and threonine metabolism  Aminoacyl-tRNA biosynthesis, Glycine, serine and threonine metabolism

		GenBank Acc	2.1	Atty. Ref. 44921-5090-01-WO/21054
SEQ ID	GLĢC II	No.	Model Code	Pathways
1376		2 AI178283	r	Aminoacyl-tRNA biosynthesis, Phenylalanine, tyrosine and tryptophan biosynthesis
2426	792	NM_053765	d ;	Aminosugars metabolism
				Aminosugars metabolism Endhromusis bis
				Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannos
1748	619	NM_012565	l, m, n, o	metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch a sucrose metabolism
			1,,	
				Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannos
2093	17100	NM_022179	h, l, w, x, dd	metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch a sucrose metabolism
1771	21087	NM_012661	cc, dd	_   Jacob Coc McCabolisiii
2195	25070	NM_024392	r, ii	Androgen and estrogen metabolism
		1111_024002	1, 11	Androgen and estrogen metabolism
ł			1	Androgen and estrogen metabolism, Pentose and glucuronate
2477	15125	NM_057105	: 1.1. II	Interconversions, Porphyrin and chlorophyll metabolism. Stareh and a
	10120	MINI_007 100	jj, kk, ll	
				Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent
				logically Alterial IOMII Mechanism of Action Rigartico Dontido Indicardo
				10-9-14-19 1 dutway, EIK I/EIKZ WADK Signaling nathway Intogrin Cianali
.			j	I dulway, Lillo Delween PVKY and Man Kinggoo MADIZinggoo "
2540	47504			I aurway, Phosphorylation of MEK1 by cdk5/n35 down regulates the MAD
2510	1/564	NM_133283	hh	randoc paulyady
			}	Apoptotic Signaling in Response to DNA Damage, Hypoxia and p53 in the
			l	Cardiovascular system, Regulation of BAD phosphorylation, Role of
1924	910	NM_017059	d	Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
- 1				Apoptotic Signaling in Response to DNA Damage, Hypoxia and p53 in the
1				Cardiovascular system. Regulation of DAD already Hypoxia and p53 in the
1924	911	NM_017059	d	Cardiovascular system, Regulation of BAD phosphorylation, Role of
				Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
		\ .	,	Apoptotic Signaling in Response to DNA Damage, Hypoxia and p53 in the
1924	912	NM_017059	d, l, m	Cardiovascular system, Regulation of BAD phosphorylation, Role of
602	22283	110151	е	Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
2214	15682	10.4 00.4044	n, o	Arginine and proline metabolism
2214	15683		cc, dd, gg	Arginine and proline metabolism
-			oo, aa, gg	Arginine and proline metabolism
				Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile
		Į		design biosynthesis, butanoate metabolism. Faffy acid metabolism. Chronelinia
		1		Interesponding Glycolysis / GillConeogenosis Historia materialisms
	1			Juegrauduon, Propanoate metabolism, Pyrnyate metabolism, Tambantan
119	11901	A801058	d	motabolism, valine, leucine and Isoleucine degradation, beta-Alapine
		0.001000	· ·	melabonan.
	1			Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile
		j	- 1	and prosyntresis, butanoate metabolism. Fathy acid metabolism. Change it is
İ			1	metabolism, Glycolysis / Gluconeogenesis. Histidine metabolism. Lucina
	1	1	1	degradation, Proparioate metabolism Pyruvate metabolism Tarabases
1988	20012	M 047070		metabolism, valine, leucine and isoleucine degradation, beta-Alanine
1300	20913 N	M_017272 r	,, -	inclapolisiii
		1	$ \frac{1}{2}$	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile
			l'	acid biosynthesis, butanoate metabolism. Fatty acid metabolism. Channelland
			l,	"Total billion of the control of the
	l		l	degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan
			1	metabolism, Valine, leucine and isoleucine degradation, beta-Alanine
118	20915IN	M_022407 k	ι l.	netabolism

ABLE		GenBank Acc.		Atty. Ref. 44921-5090-01-WO/2105
EQ ID	GLGC ID	No.	Model Code	Pathways
				Arginine and proline metabolism. Ascorbate and alderste metabolism. Blie
- 1				acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glyceroli
				metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine
]			1	degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan
1			1	metabolism, Valine, leucine and isoleucine degradation, beta-Alanine
2353	12299	NM_032416	c	metabolism
				Arginine and proline metabolism, Glycine, serine and threonine metabolism
1296	19118	Al175281	hh	Turea cycle and metabolism of amino groups
				Arginine and proline metabolism, Glycine, serine and threonine metabolism
1798	16947	NM_012793	b, u, v, jj, kk	Urea cycle and metabolism of amino groups
				Arginine and proline metabolism, Hypoxia-Inducible Factor in the
1842	19393	NM_012998	h, I	Cardiovascular System
1739	4467	NM_012529	f, g	Arginine and proline metabolism, Urea cycle and metabolism of amino grou
				ground the tabolish of all more abolish of all more grounds
1739	4468	NM_012529	g	Arginine and proline metabolism, Urea cycle and metabolism of amino grou
				your and motabolism of animo grou
1862	13283	NM_013078	b	Arginine and proline metabolism, Urea cycle and metabolism of amino grou
2422				
2128	4242	NM_022521	b, l, m	Arginine and proline metabolism, Urea cycle and metabolism of amino ground of an annual region of an annua
l	1	ļ		ATIVI Signaling Faurway, Angiotensin il mediated activation of sivin Faurway
		į		via Pyk2 dependent signaling, BCR Signaling Pathway, D4-GDI Signaling
				I Fairway, EGF Signaling Pathway. EPO Signaling Pathway EAS signaling
				pairway ( CD95 ), FC Epsilon Receptor I Signaling in Mast Calle Dimovia
- 1				Inducible Factor in the Cardiovascular System, IGF-1 Signaling Pathway, II
	1			Isignating pathway, it is signaling pathway. Inhibition of Cellular Proliferation
	1	1		by Gleevec, Insulin Signaling Pathway, Integrin Signaling Pathway, Links
	1	1		Detween Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Nepre
1	į			growth factor pathway (NGF), PDGF Signaling Pathway, Pertussis toxin-
- 1		1		Insensitive CCR5 Signaling in Macrophage, Repression of Pain Sensation by
-		ì		The Transcriptional Regulator DREAM. Signal transduction through ILIP
				Signaling Pathway from G-Protein Families. T Cell Recentor Signaling
		]		Pathway, TNF/Stress Related Signaling, TNFR1 Signaling Pathway, TDO
2089	222541	IM 034035		Signaling Pathway, ISP-1 Induced Apontosis in Microvescular Endotholial
2003	2230111	IM_021835	e, ff	Cell, The 4168-dependent immune response. Tall like Pocenter Bethum.
2173	2521	IM 004407		A IW Signaling Fairway, Cell Cycle: G2/M Checkpoint Hypoxia and p53 in
2173	302	IM_024127 r	), q	me Cardiovascular system, p53 Signaling Pathway
2173	353 1	IM 024127	i	ATM Signaling Pathway, Cell Cycle: G2/M Checknoint, Hypoxia and p53 in
-173	3031	IM_024127 c	, ee, 11, gg	tne Cardiovascular system, p53 Signaling Pathway
2173	35/ N	IM_024127 p		ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in
205			, q, ee, II	the Cardiovascular system, p53 Signaling Pathway
209				ATP Synthesis, Oxidative phosphorylation
2000				ATP Synthesis, Oxidative phosphorylation
2327		M_031785 f		ATP Synthesis, Oxidative phosphorylation
448		14 050004	g	ATP Synthesis, Oxidative phosphorylation
2566			y , hh	ATP Synthesis, Oxidative phosphorylation ATP Synthesis, Oxidative phosphorylation
566		M_139099 g	1 - 10 - 1	TIT Symulesis, Uxidative phosphorylation

7 ;	1	GenBank Ac	×	AUV. Ref. 44921-5000 01 WOY04054
SEQ ID	GLGC II	DINo.	Model Code	
	1 - 1 - 1	110.	Model	
	1	İ		BUK Signaling Pathway, EGF Signaling Pathway, EPO Signaling Pathway,
	1	1		- Perior Receptor Folymaning in Wast Cells, Rife-1 Signaling Deth
	1			Joighanny Paulway, IL 3 Signaling nathway II 6 cignaling nethers II a
	l			Interestion of College Design Pathway Inhibition of College Design Desig
	Ì	İ	İ	Polocyco, mount oldismit Pathway Nerve growth footage and
		ļ		1 DOI DIGITALITY FALLIWAY, Perfficely toyin-inconditive CODE of the contract o
	1	j		Macrophage, Repression of Pain Sensation by the Transcriptional Regulator
				DREAM, Signaling Pathway from G-Protein Families, T Cell Receptor
				Signaling Pathway TDO Signaling Pathway TDO
		Ĭ	1	Signaling Pathway, TPO Signaling Pathway, TSP-1 Induced Apoptosis in
1319	1018	2 AI176185	p, q, gg	Imiorovasoulai Eliuulielisi Cell Toillika Dacontor Dathiini C
		-	P, 4, 99	il2, il3, il6, insulin, ngf, pdgf, tpo  BUR Signaling Pathway, EGF Signaling Pathway, EPO Signaling Pathway, EGF Signaling Pathway, EGF Signaling Pathway, EPO Signaling Pathway, EDF S
		ĺ	1	Epsilon Recentor I Signaling in Most Cally 105 4 8
		1		
			l	signaling pathway, IL 3 signaling pathway, IL 6 signaling pathway, IL-2
				I Cooptor D Trotell litteraction Pathway Inhibition of Collular D. 114
l		1		10.00 too, mount olymania Painway Nerve growth footor neth (10.5)
ļ			1	I' DO O'GITAING FALIWAY, PERUSSIS TOYIN-inconcitive CODE Commun.
l l		1		Industry in the Property of Pain Sensation by the Transaction of the Property in the Property
}			1	Diversity Olymania Falliway from Gerotein Familias, T.Cali Dana (
			1	Joighaing Falliway, IPO Signaling Pathway, TCD 1 Induced Appet 1
2044	10101		İ	Iniciovasculai Eliuolifeliai Celi , (Ol-Like Recentor Pathway oct and i-t.4
2641	10181	X06769	p, q	1"2, "0, "0, "15u(ii), I(d), (l(d) Th)
				Benzoate degradation, Bile acid biosynthesis, Butancato metabolicas, Fatt
				doid biosylidiesis (ball) XI. Fatty acid metabolism I
4000	40000			i ropanoale metabolism. Pyruvate metabolism. Synthosis and desired in
1930	18956	NM_017075	aa	harana padica, mybibilidii mpianniem
- 1				Benzoate degradation, Bile acid biosynthesis, Butanoate match all and the
1				Table blookillies (Dall) / Fatty and metabolism I wain a line in the
			ļ	Propanoate metabolism, Propanoate metabolism, Synthesis and degradation of ketone bodies. Toptoplan metabolism, Synthesis and degradation of
1930	18957	NM_017075	г, s, t, II	Ingrano podica, i i Apropriari (iletabulism
				Benzoate degradation, Fatty acid metabolism, Lysine degradation,
1150	23596	AI105435	bb	Triyblophan melabolism
				Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism,
1732	23698	NM_012489	1	Valine, leucine and isoleucine degradation
				Bile acid biosynthesis, Fatty acid metabolism, Glycerolipid metabolism,
				Glycolysis / Gluconeogenesis, Methane metabolism, Pyruvate metabolism,
280		AA874874	p, q	Tyrosine metabolism
1781	25563	NM_012732	f, g	Bile acid biosynthesis, Glycerolipid metabolism
1781	16613	VM_012732	g	Bile acid biosynthesis, Glycerolipid metabolism
1970	13938	VM_017212	jj, kk	Bioactive Peptide Induced Signaling Pathway
1970	13940	NM_017212	a	Bloactive Pentide Induced Signaling Deltures
T				Bioactive Peptide Induced Signaling Pathway, Enthropoletic mediated assumption of the Pathway, EPO Signaling Pathway,
	1			Erythropoietin mediated neuroprotection through the last
	1			Erythropoietin mediated neuroprotection through NF-kB, Growth Hormone
				Signaling Pathway, IFN gamma signaling pathway, IL 3 signaling pathway, IL
				17 Tightening Paulyray, ICZZ Ollillia Recentor Cignolina Dall
2276	12580	IM_031514	a.h.likv =	
$\neg$			-, ., , , , , N, Y, Z	
	-	j		Diocotto i opide iliduced Signaling Pathway EDO Cignalina Data
				I - Juliopole III Medialed Relifontotection through NE LD O
		1		orginality of autway, if it udiffing signaling nathway. If a signality and it is
	1		i	1
276	12581 N	M_031514		TOMERANDI DY GREEVER STATS Signaling Dathumy TDO CL
	1200111	W_U31314	/, z, hh	' worrd), opo, iii udiliiid. iid lib interacte 1 ndaf taa
133	23020	A817823 i		Blood group glycolipid biosynthesis - neolact series, Galactose metabolism, Keratan sulfate biosynthesis, N-Glycans biosynthesis
	7.30/NIA	MATI/X/X li		TO THE PROPERTY OF THE PROPERT

	i.	GenBank Ac	c.   :	Atty. Ref. 44921-5090-01-WO/21054
SEQ ID	ĠLGC ID	No.	Model Code	Pathways
412	11007	AA892828		Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism
712	11997	AA092020	f, h, I	I valine, leucine dilu ispielicine niceynthecie
1313	5076	AI176117		Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism
2541		NM_134387	hh	valine, leucine ditu ispieticina hinevnihaeje
2071	0032	134367	hh	Butanoate metabolism, Pentose and glucuronate interconversions
1987	20600	NM_017268	ļ	Dutailodle illetabolism, SKEBP and controls linid synthosis. Combanies
1007		14141_017200		judgraudium of kelone bodies. Valine leucine and icolousine describer
1987	20601	NM_017268		Buttandate including of EDP and controls linid cynthesis Cynthesis and
2465		NM_053995	r	Judgiaudion of kelone bodies, Valine, leticine and isolaticing dogradation
	11700	14141_0000000	g	Dutanuale Heldbuilsin, Synthesis and degradation of traters be at
2193	2811	NM_024386	00 dd	butanoate metabolism, Synthesis and degradation of ketone bodies. Voline
	2011	1410_024300	cc, dd	henome and isoleficite dedisusion
2193	2812	NM_024386	,,, ,, ,,, ,,,,,,,,,,,,,,,,,,,,,,,,,,,	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine,
	2012	NW_024366	w, x, cc, dd	lieddine and isoleucine degradation
2193	2813	NM_024386	h	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine,
1587		Al237212	f, g, hh	reductie and isoleucine degradation
		711207212	1, 9, 1111	Calcium Signaling by HBx of Hepatitis B virus
	ļ			Corpon funding City I
2126	162	NM_022516	e, u, v	Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate
2365	1311	NM_053291	e, u, v	metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation
		1111_000251		Clycolycia Dethucus
				Caspase Cascade in Apoptosis, FAS signaling pathway ( CD95 ), HIV-I Nef:
873	20086	AI013260	·z	inegative effector of Fas and TNE Induction of anontoois through DDs I
		110 10200		DINAGO DESIGNACIONES E INFRA Signaling Dathway
- 1	-			Calabolic Pathways for Arginine . Histidine Glutamate Glutamine and
544	5206	AA925755	II	Fromite, D-Glutamine and D-glutamate metabolism. Glutamate metabolism
1850		VM_013022	r	Introgen metabolism
	-1000	11/1_010022		CCR3 signaling in Eosinophils
1952	15354	NM_017147	ii	CCR3 signaling in Eosinophils, Rac 1 cell motility signaling pathway, Rho cell
		017147	11	inounty signaing pathway
1952	15365 N	NM_017147	aa, bb, II	CCR3 signaling in Eosinophils, Rac 1 cell motility signaling pathway, Rho cell
	10000	111/2017 147	aa, DD, II	mounty signature dathway
2427	15996 N	NM_053769	cc, dd	CD40L Signaling Pathway, Phosphatidylinositol signaling system, TNFR2
	100001	****_000700	cc, du	Journalium Painway
	-		<u> </u>	Cell Cycle: G1/S Check Point , Cyclin E Destruction Pathway, Cyclins and
	1		1 1	Our Oyole (regulation), EZF   Destruction Pathway FAS signaling nathway
. !			j i	CD95), HIV-I Nef: negative effector of Fas and TNF, Influence of Ras and
İ	ľ		[	Rho proteins on G1 to S Transition, Overview of telomerase RNA component
	1		ĺ	gene hTerc Transcriptional Regulation, RB Tumor Suppressor/Checkpoint
			[	Signaling in response to DNA damage, Regulation of p27 Phosphorylation
1658	17264 D	25233		during Cell Cycle Progression, TNFR1 Signaling Pathway, p53 Signaling Pathway
			la l	rauiway
			[ [	Cell Cycle: G1/S Check Point , Cyclins and Cell Cycle Regulation, Inactivation
	.			of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages,
1657	25041 D	14014	1.	Influence of Ras and Rho proteins on G1 to S Transition, WNT Signaling Pathway, p53 Signaling Pathway
	-  -		, 11	CANIMAY, USS SIBBAIRD PATRICAY
1	İ	l		Cell Cycle: G1/S Check Point , Cyclins and Cell Cycle Regulation, Inactivation
			ľ	one by ANI causes accumulation of hecatanin in Alycelar Magraphages
2677	24232 X	75207	יו	nfluence of Ras and Rho proteins on G1 to S Transition, WNT Signaling Pathway, p53 Signating Pathway
			ממן טט	autway, poo oknaling Parkway
; 	I 	1		Cell Cycle: G1/S Check Point , Cytokines and Inflammatory Response,
		ŀ	l,	Erythrocyte Differentiation Pathway, Function of SLRP in Bone: An Integrated
1	ł		1.3	Now, delective expression of chemokine recentors during T coll relestant
الا الا	18729 N	M_021578	, ,	Signal transduction through IL1R, TGF beta signaling pathway, p38 MAPK Signaling Pathway, tgf-beta
				NULUUU FAIIWAV TOLDATA

:		GenBank Acc	• 1	Atty. Ref. 44921-5090-01-WO/2105
SÉQ ID	GĽGÇ ID	No.	. Model Code	Pathways
73	42000			Cell Cycle: G2/M Checkpoint, Cyclin E Destruction Pathway, E2F1
/3	13683	AA799788	e	Destruction Falliway
4700	40000			Cell Cycle: G2/M Checkpoint, Cyclin E Destruction Pathway, E2F1
1702		L38482	e	Destruction Pathway
2212	21166	NM_031005	a, n, o	Cell to Cell Adhesion Signaling Integrity City
				Total did Molecules involved in local actife inflormation.
ŀ			ł	1. The street of the street of
l			1	I domain Della II Olyllalliu Falliway II 5 Signaling Delland. II 6
				pathway, Regulation of hematopoiesis by cytokines, Signal transduction
1755	24716	NM_012589	j, k, p, q	through IL1R, il6, interact6-1
875	6758	Al013394	d, jj, kk	Chondroitin / Heparan sulfate biosynthesis
				Citrate cycle (TCA cycle), Glutathione metabolism, Reductive carboxylate
2275	17427	NM_031510	b, u, v	cycle (CO2 fixation)
2425	18175	NM_053752	aa, bb	Citrate cycle (TCA cycle), Propanoate metabolism
	T			Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent
	j			kinase (CaMK), Erk1/Erk2 Mapk Signaling pathway, IGF-1 Signaling
- 1	j		į	Pathway, Multiple antiapontotic pathways for the
	ſ		I	Pathway, Multiple antiapoptotic pathways from IGF-1R signaling lead to BAI phosphorylation. Regulation of RAD shows the control of RAD shows the c
2363	25072	NM_052807	j, k	phosphphorylation, Regulation of BAD phosphorylation, Skeletal muscle
			<u> </u>	hypertrophy is regulated via AKT/mTOR pathway, igf-1
				Cysteine metabolism Charakette / Ch
1915	17807	NM_017025	h, i	Cysteine metabolism, Glycolysis / Gluconeogenesis, Hypoxia-Inducible Facting the Cardinyascular System Bronze et al. 18 June 19 June 1
1757	7125	VM_012595	aa, bb	Cysteine metabolism, Glycolysis / Gluconeogenesis, Propanoate metabolism Pyruvate metabolism
			44, 55	i yiwate metanoism
- 1	ľ			Cytokine Network, Cytokines and Inflammatory Response, Dendritic cells in
2017	20318	VM_019127	n, o	regulating TH1 and TH2 Development, IFN alpha signaling pathway, Signal transduction through IL1R
872	1332 A	1013222	e	ון מוויסמטטנטון עון טעטון די ראַ
				Cytokines and Inflammatory Response, PDGF Signaling Pathway, pdgf
1910	8417N	IM_017008	aa	- "3" "I dita D'ottituille lifetabolism. (Tivenives / Giuconogonosio
1583	22939 A		y, z, jj, kk	Glycolysis Fainway
1951	24106 N		s, t, bb	DNA polymerase, Purine metabolism, Pyrimidine metabolism
1951	24107 N		<u>, , , , , , , , , , , , , , , , , , , </u>	DIVA polymerase, Purine metabolism Dyrimiding metabolism
470	24329 A	4.000000	aa, bb	DNA polymerase, Pune metabolism, Pyrimiding metabolism
1784	25650 N	14 04000	d d	Lifects of Calcifulin in Kerainocyte Differentiation
		0.2700	<u> </u>	Electron - I ransfer Reaction in Mitochandria Olympia
1	-	ļ		The state of the s
	}			1. The second of the second of
- 1		1		Tand I non minimize application of activated T colle. Our devented
1759	2628 N	M_012603	. n a u =	Protein component gene in Left Transcriptional Regulation Will Ciangling
		012003	a, p, q, y, z	i animal pooliner Signaling Pathway
1	l	ļ		Erk I/Erk2 Mapk Signaling pathway II -2 Recentor B Protein Internal
				i durway, illibution of Cellular Proliferation by Gleeves, Nouropostides yill
ļ	}	Į,		I AND I MINIMILLIE ADDITIONS OF ACTIVATED T COME OF A CONTRACT OF THE CONTRACT
1759	2620 11		a, j, k, p, q, y,	protein component gene nien transcriptional Regulation WAT Com-19
	2023 141	VI_U 12003   2	,,,	i warmay, poo wark oldilaling Pathway
	l			Erk1/Erk2 Mapk Signaling pathway Nerve growth factor nothing (NOE)
1761	1209 11	/_012610		Thospholylaudii of MEK1 by cdk5/p35 down regulator the MAD kings
	1230 141	<u>/_012610</u>   c		Pagistay, IIII
İ		į		Erk1/Erk2 Mapk Signaling pathway, Nerve growth factor pathway (NGF),
1761	1200	1 040045		. Modernor history of MED/1 DA CORD/D35 GOMB reciplator the WVD Process
1761	1299 NA		-,	patiway, ngi
1911	246/6 NA	1_017010 a	a, bb	Erythropoletin mediated neuroprotection through NE I/O
			i	cryan opoleun mediated neuroprotection through NE kR. Hypovia and area
3400	44.4			are deletionascular system. Hypoxia-inducible Eactor in the Conditional I
2188	1146 NM	1_024359 y	z	System

			GenBank A	CCI	Atty, Ref. 44921-5090-01-WO/210
SEQ ID	GLGC	ы	No.	Model Cod	
2004			NM_017332		Pathways
431		05	AA893242		ratty acid biosynthesis (nath 1)
431		00	AA893242		Fatty acid metabolism
431	209	00	AA893242	]]	Fatty acid metabolism
070	000				
972		83/	A1044900	a, h, I, ee, fi	, kk Fatty acid metabolism
1652		86	D00729	g, hh	Fatty acid metabolism
1668		84 1	D90109	11	Fatty acid metabolism
1999		87 1	VM_017306	hh	Fatty acid metabolism
2410		05 1	VM_053623	j, k, y, z	Fatty acid metabolism
1896	208	55 N	VM_013200	a, w, x, hh	Fatty acid metabolism
		Т		a, w, x, aa, l	Fatty acid metabolism, Glycerolipid metabolism
1896	208	56 N	NM_013200	]]	
		+			Fatty acid metabolism, Glycerolipid metabolism
1827	197	7 N	IM_012930	2 W Y 20 d	ratty acid metabolism. Glycerolipid metabolism. Mitochandi I Communication and the communication of the communicat
1708	2071	41	114972	a, w, x, cc, d s, t	"   Switter   Call   Switch
1743	2070	41	IM_012541		Fatty acid metabolism, Tryptophan metabolism
1831	10	ON	M_012940	aa, bb	Fauly acid metabolism. Tryptophan metabolism
1832	2092	8 N	M_012940	j, k	Fatty acid metabolism. Tryptophan metabolism
1909	2002	1 1	M_012941 M_016999	l, m	ratty acid metabolism. Tryptophan metabolism
2030	117	112	M_019184	s, t	I duy dolo metabolism. Tryptophan metabolism
2281	404	7 17	M_019184	С	Traily acid metabolism. Tryptophan metabolism
2281	401	UIN	M_031543	u, v	Ir duy dold metabolism. Trynfonhan motobolism
2201	401	III.	M_031543	V	If ally acid metabolism. Involophan motoballand
		1			To Epsilon Receptor I Standing in Mast Calla Chiange line in the
0500				a, j, k, y, z, ee	Phospholipid degradation, Prostaglandin and leukotriene metabolism, p38
2528	244	IN	M_133551	ff, kk	MAPK Signaling Pathway
2000					Flavonoids, stillene and lignin biography is the in-
2398	19252	N	M_053576	а	Flavonoids, stilbene and lignin biosynthesis, Methane metabolism, Phenylalanine metabolism
1718	21400	M:	36410	ee, ff, gg	Folate biosynthesis
2109	13480	NN	M_022390	1	Folate biosynthesis
2187	15349	NN	A_024356	a, y, z	Folate biosynthesis
2187	15353	ΝN	1_024356	j, k, y, z, ii	Folate biosynthesis
1858	14997	NN	/_013059	e, ee, ff	Folate biosynthesis
		$\Box$		0,00,11	Folate biosynthesis, Glycerolipid metabolism
1971	1527	NN	1_017220	ee, ff	orace biosynthesis. Nicotinate and nicotinamide match allow D
1922	20875	NN	1_017050	hh	Time reportation to Attituding Welshubilding
1922	20876	NM	1_017050	r	Free Radical Induced Apoptosis
2202	1852	ΝM	_030826	<u> </u>	Free Radical Induced Apoptosis
	.502		00020	aa, gg	Free Radical Induced Apoptosis, Glutathione metabolism
1956	21975	NIN.	_017154	d, e, j, k, n, o,	
1923	1876	VIV		y, z, kk	Free Radical Induced Apoptosis, Purine metabolism
2060	1220	NIA	_017052	W, X	1 ructose and mannose metabolism
-500	1230	IAIAI	_019333	99	Fructose and mannose metabolism
- 1	- 1				
733	15544		040455		Fructose and mannose metabolism, Galactose metabolism, Glycerolipid
100	10011	NIN.	_012498	<u>ii</u>	I TO THE PARTY OF THE PROPERTY OF THE PARTY
704	4005-	۵		· <del>-</del>	Fructose and mannose metabolism, Galactose metabolism, Glycolysis /
701	12058	25	387	W	Gluconeogenesis, Pentose phosphate pathway
704					Fructose and mannose metabolism College
701	25377 L	.25	387	hh	Fructose and mannose metabolism, Glactose metabolism, Glycolysis /
					restricted to the contract of
320	<u> 1340 N</u>	IM_	031715	j, kk	Fructose and mannose metabolism, Galactose metabolism, Glycolysis /
693	19694 2	<u> 48</u> 4	144	c, dd	Larrage Logic Legitosa Dunenhata pathunu
398 <sub>1</sub>	14004 N	iΜ		a, bb	Generation of amyloid b-peptide by PS1
929;	11152 N	M.			Glutamate metabolism, Glutatnione metabolism
2201	111531	M			Glutalitäte metabolism, Nitrogen metabolism
- Jōj	7867 A			, ///	Glutamate metabolism, Nitrogen metabolism Glutamate metabolism, Purine metabolism
			<u>-</u> [[		Call Tall Tall Tall Tall Tall Tall Tall

	2 0 :	GenBank Ad	c. I	Atty. Ref. 44921-5090-01-WO/2105
	GLGC ID	No.	Model Code	
658		AA957007	g	Glutathione metabolism
1799		NM_012796	9	Glutathione metabolism
1912	21013	NM_017014	b	Glutathione metabolism
1958	17686	NM_017165	hh	Glutathione metabolism
2131	4615	NM_022525	cc, dd	Glutathione metabolism Glutathione metabolism
2265	20862	NM_031154	w, x	Glutathione metabolism  Glutathione metabolism
2274	25525	NM_031509	b, r	Glutathione metabolism
2274	634	NM_031509	d, r	Glutathione metabolism
2274		NM_031509	d, r	Glutathione metabolism
2639		X02904	ii	Glutathione metabolism
2669		X62660	_ 1"	Glutathione metabolism
1885		NM_013161	c, f, g	Glutathlone metabolism
1989		NM_017274	b, I, m	Glycerolipid metabolism
2380		NM_053437	99	Glycerolipid metabolism
2260		NM_031143	e, hh	Glycerolipid metabolism
	1000	14141_031143	d, e, ii, kk	Glycerolipid metabolism, Phosphatidylinositol signaling system
1962	0270	NIA 047474		Glycerolipid metabolism, Phospholipid degradation, Prostaglandin and
1758	10200	NM_017174	jj, kk	_lieukoliterie metapolism
1758		NM_012598	w, x	Glycerolipid metabolism, Visceral Fat Deposits and the Metabolic Syndrome
1844	1838/	NM_012598	W, X	Officeron pid Thetabolistii, Visceral Fat Denosits and the Motabolia Condesses
	24/18	NM_013003	ii	Crycline, settine and urreonine metabolism
1894	16448	NM_013197	b, c, v	Glycine, serine and threonine metabolism
2003	24533	NM_017328	n, o	Glycolysis / Gluconeogenesis
				Glycolysis / Gluconeogenesis, Histidine metabolism, Phenylalanine
2343	24644	NM_031972	cc, dd	metabolism, Tyrosine metabolism
				Glycosaminoglycan degradation, Porphyrin and chlorophyll metabolism,
1913	17815	VM_017015	w, x	Starch and sucrose metabolism
Ì			a, h, I, z, aa,	The street of the capolisti
2073	574	NM_019905	kk, li	Glyoxylate and dicarboxylate metabolism
1726	5733 N	//81855	d	Hypoxia and p53 in the Cardiovascular system
1754	15098 N	NM_012588	bb	Hypoxia and p53 in the Cardiovascular system
2309	18403 N	M_031677	d, jj, kk	Hypoxia and p53 in the Cardiovascular system
2409	20243 N	IM_053615	aa, bb	Hypoxia and p53 in the Cardiovascular system
			144,00	Hypoxia and p53 in the Cardiovascular system, WNT Signaling Pathway
2516	657 N	IM_133380	j, k, y, z	The digitality partially. Selective expression of chemokine recentors during
1914	6598 N	IM_017020	j, k, y, z	ceii polarization, Th1/Th2 Ditterentiation il/
2172	21238 N	IM_024125	p, q	IL 6 signaling pathway, il6, interact6-1
		024120	p, q, r, bb, ee,	IL 6 signaling pathway, il6, interact6-1
2172	21239 N	IM_024125		W A
1939	4391 N	M_017101	ff, kk	IL 6 signaling pathway, il6, interact6-1
	- 1001	017 101	s, t	IL-2 Receptor B Protein Interaction Pathway
1749	482 N	M_012567		Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar
778	3278 4	1008988	s, t	iwacropnages
2092	2/3 N	M_021989	y, z	Inhibition of Cellular Proliferation by Gleevec, Integrin Signaling Pathway
229	17236 4	A858903	h, l, n, o, li	This blot of Matrix Metalloproteinases
512	17231 4	A924107	s, t, gg	Inhibition of Matrix Metalloproteinases, p53 Signaling Pathway
697	17231 A	A965161	ii	IIIIIDITION Of Matrix Metalloproteinases, p.53 Signaling Dethuses
1891	1744 N	M 042407	11	initibility of Matrix Metalloprofeinases, n53 Signaling Dathway
2186	20022	M_013187	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	mostor prospriate metapolism. Phosphatidylinosital signaling system
	4474 N	M_024353		mostor prospriate metapolism. Phosphatidylinositol signaling and an
2352	17/1 N	M_032071	71-	moster phospitate metapolism. Phosphatidylinosital signaling system
200	00000		i	wissian pricepitate assistancism. Phosphatidylinosital signaling system
260	23336 AA	A859981	00, 11, JJ, KK	Streptomycin biosynthesis
2024	20863 NI	V_019152		integrin Signaling radiway
2620	25593 U2		99	Integrin Signaling Pathway
1983 1738	1496 NA	V_017255	aa, bb	lon Channel and Phorbal Esters Signaling Pathway
	4 4 4 4 4 4	M_012520		· · · · · · · · · · · · · · · · · · ·

		GenBank A	CC. E	Atty. Ref. 44921-5090-01-WO/210
SEQ ID	GLGC ID	No.	Model Cod	
1967		NM_017201		
1007	20110	14W_017201	b, I, m	Methionine metabolism, Selenoamino acid metabolism
2277	20448	NM_031530	ja, o, z, ee, t	i, II, Washing Receptor Signaling Pathway Pertussis toxin income!!
2211	20440	MINI_031230	kk	
2277	20440	NINA 004500		Msp/Ron Receptor Signaling Pathway, Pertussis toxin inconsists, const
1318		NM_031530	a, z, ee, ff, k	19-3-19-19 IT MICHODIANE
		Al176170	е	mTOR Signaling Pathway
1945		NM_017130	u, v	N-Glycan degradation, Sphingoglycolipid metabolism
2314		NM_031698	w, x	N-Glycans biosynthesis
1874		NM_013127	e, bb	Nicotinate and nicotinamide metabolism
2056	15056	NM_019291	b, c	Nitrogen metabolism
				Nucleotide sugars metabolism. Pontoco cod del
2267	18596	NM_031325	u, v	Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism
			a, j, k, p, q, y	To take of and oddloge filefallfillstri
2267	18597	NM_031325	z, ee, ff	
			-, 50, 11	Total of and Sucrose merannism
299	4339	AA875121	jj, kk	Overview of telomerase RNA component gene hTerc Transcriptional
			IJI KK	i regulation
1810	4338	NM_012866	lu v	Overview of telomerase RNA component gene hTerc Transcriptional
1138	23574	Al104520	u, v hh	_   Cgulatoff
1712	15049	M24542		Oxidative phosphorylation
1795		NM_012786	aa, bb	Oxidative phosphorylation
1795	450	NA 040700	hh	Oxidative phosphorylation
1968	146041	NM_012786	f, hh	Oxidative phosphorylation
2383	240001	VM_017202	aa	Oxidative phosphorylation
2041	210001	VM_053472	u, v	Oxidative phosphorylation
2041	20938	VM_019223	hh	Oxidative phosphorylation, Ubiquinone biosynthesis
0407	444			
2107	11454	VM_022381	d, I, m, n, o, s	, t p53 Signaling Pathway
2107	11455 N	IM_022381	S	p53 Signaling Pathway
				Pantothenate and CoA biosynthesis, Valine, leucine and isoleucine
495	23038 A	A900881	a, j, k, y, z	biosynthesis Valino Joueine and isoleucine
			1,7,7,7	biosynthesis, Valine, leucine and isoleucine degradation
2117	24643 N	IM_022400	b, u, v	Pantothenate and CoA biosynthesis, Valine, leucine and isoleucine
269	17742 A	A866302	c	production valide, lettine and isoleticine degradation
1468	14430 A	1230798	ir	Phenylalanine metabolism, Tyrosine metabolism
1767		M_012637	d, jj, kk	Fnosphatidylinositol signaling system
1767	1844 N	M_012637		Phosphatidylinositol signaling system
2021	14973 N	M_019140	p, q, y, z	Phosphatidylinositol signaling system
1906	64 N	M_016991	aa ii kk	Phosphatidylinositol signaling system
	3714	010981	jj, kk	Phospholipase C d1 in phospholipid associated and all all all all all all all all all al
1746	23868 N	M_012551	a, h, i, p, q, y,	in hospitorylation of IVIEK1 by cdk5/p35 down regulates the MAD kinese
., 10	2000 N	W_U 12001	z, ee, ff	1 Pauling
1746	22060	M 04055:		Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase
1740	20009 NI	M_012551	a, h, I, p, q, y, z	
1740	00074			Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase
1746	238/1 N	M_012551	p, q, y, z, ii	pautway
1740	0000			Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase
746	23872 NI	V_012551	p, q, y, z	pathway
			a, p, q, r, y, z,	
402	16081 AI	179610	gg, kk	Porphyrin and chlorophyll metabolism
741	16520 NA	/_012532	C	Porphyrin and chlorophyli metabolism  Porphyrin and chlorophyli metabolism
751	16080 NA	1 01000	p, q, y, z, kk	Pornhyrin and chlorophyll metabolism
			1 . 7, 1, 2, tot	Porphyrin and chlorophyll metabolism
688	19279 YO	0350	a aa hh II LL	Possibly and all all and all al
	20193 NN		a, aa, bb, jj, kk P, q	Porphyrin and chlorophyfl metabolism
	17063 NN			Prostaglandin and leukotriene metabolism
	17064 NN	040455	i, <u>g</u>	Prostaglandin and leukotriene metabolism
		-0191/0	f, g	Prostaglandin and leukotriene metabolism

TABLE 2	2	N.		Atty. Ref. 44921-5090-01-WO/2105485
Jose 15	Oi oò io	GenBank Acc		7.1071.017 0000-01-VVO/Z100400
	GLGC ID		Model Code	Pathways
2029		NM_019170	g	Prostaglandin and leukotriene metabolism
2213	25517	NM_031010	c, v	Prostaglandin and leukotriene metabolism
2213		NM_031010	c, v	Prostaglandin and leukotriene metabolism
2285	692	NM_031557	s, t, li	Prostaglandin and leukotriene metabolism
190		AA849028	t	Proteasome
1662		D30804	hh	Proteasome
1777	4003	NM_012708	е	Proteasome
1991		NM_017278	l, m	Proteasome
1992	15538	NM_017283	r	Proteasome
1				PTEN dependent cell cycle arrest and apoptosis, Phosphatidylinositol
			Ì	signaling system, Regulation of elF4e and p70 S6 Kinase, mTOR Signaling
2297		NM_031606	f	Pathway
63		AA799729	j, k	Purine metabolism
1450		Al230130	s, t, ii	Purine metabolism
1762	638	NM_012613	aa, bb	Purine metabolism
1816	16708	NM_012895	u, v	Purine metabolism
1916	14247	NM_017031	h, I	Purine metabolism
2053	8200	NM_019285	11	Purine metabolism
2229	79	NM_031079	y, z, ee, ff	Purine metabolism
2325	14184	NM_031776	kk	Purine metabolism
2325	14185	NM_031776	kk	Purine metabolism
2299	24234	NM_031614	r, y, z, jj, kk	Pyrimidine metabolism
2299	24235	NM_031614	y, z, kk	Pyrimidine metabolism
2404	20896	NM_053592	h, I	Pyrimidine metabolism
2351	21807	NM_032067	99	Rac 1 cell motility signaling pathway, Ras Signaling Pathway
2351	21809	NM_032067	11	Rac 1 cell motility signaling pathway, Ras Signaling Pathway
				Ras Signaling Pathway, Role of PI3K subunit p85 in regulation of Actin
1423		Al227887	e, aa, bb	Organization and Cell Migration, p38 MAPK Signaling Pathway
630	22771	AA946432	b, I, m	Regulation of ck1/cdk5 by type 1 glutamate receptors
2075		NM_020075	p, q, s, t	Regulation of eIF2
2075	18715	NM_020075	ee, ff	Regulation of eIF2
2208	1928	NM_030872	s, t	Regulation of eIF4e and p70 S6 Kinase
2208	1929	NM_030872	hh	Regulation of elF4e and p70 S6 Kinase
1206	23152	Al169170	r	Regulation of elF4e and p70 S6 Kinase, mTOR Signaling Pathway
				Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR
1957	17104	NM_017160	h, i	Signaling Pathway
				Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR
1957	17105	NM_017160	h, I	Signaling Pathway
				Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR
1957	17106	NM_017160	n, o	Signaling Pathway
1933	22552	NM_017087	n, o	Small Leucine-rich Proteoglycan (SLRP) molecules
2691	18352	Z12298	aa, bb	Small Leucine-rich Proteoglycan (SLRP) molecules  Small Leucine-rich Proteoglycan (SLRP) molecules
1236		AI170663	cc, dd	SREBP and controls lipid synthesis
92		AA800190	a, e, ii, kk	Starch and sucrose metabolism
1232		Al170502	r	Starch and sucrose metabolism
2595		NM_153821	h, 1	Starch and sucrose metabolism
1948	16681	NM_017136	ii	Sterol biosynthesis, Terpenoid biosynthesis
2251	14970	NM_031127	a, h, l, n, o	Sulfur metabolism
2336	4748	NM_031834	s, t, aa, bb	Sulfur metabolism
2336		NM_031834	t, bb	Sulfur metabolism
1806		NM_012844	c, d	Tetrachloroethene degradation
2162	2006	NM_022936	aa	Tetrachloroethene degradation
2162		NM_022936	w, x, aa, bb	Tetrachloroethene degradation
2033	15244	NM_019191		TGF beta signaling pathway, tgf-beta
2286	183151		e, u	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
			<u> </u>	- maded Apoptosis in Microvascular Endothelial Cell

TABLE		GenBank Acc.	<del> ` ` ` -</del>	Atty, Ref. 44921-5090-01-WO/21054
SEQ ID	GFCC ID	No.	Model Code	Pathways
2286	18316	NM_031561	е	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
2286	18317	NM_031561	r, aa, bb, ii	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
2286	18319	NM_031561	w, x	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
1740	11115	NM_012531	f, g	Tyrosine metabolism
1740		NM_012531	f, g	Tyrosine metabolism
889		AI013861	a, h, l	Valine, leucine and isoleucine degradation
1688		J02827	С	Valine, leucine and isoleucine degradation
1756			С	Valine, leucine and isoleucine degradation
2577	13712	NM_144744	ii	Visceral Fat Deposits and the Metabolic Syndrome
2035	18572	NM_019201	n, o	WNT Signaling Pathway
2035	18573	NM_019201	f, g	WNT Signaling Pathway

TABLE 3	က			The state of the s	
SEQ		GenBank Acc.		A STATE OF THE STA	Atty. Ref. 44921-5090-01-WO/2105485
<u>.</u>	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Himan Homolooniis Somenoo Olinkor Tillo
2486		15408 NM_057197	f, g, l, m	2,4-dienovl CoA reductase 1 milrochondrial	D
2486		15409 NM_057197	f, a	2.4-dienovl CoA reductase 1 mitochondrial	2,4-uleiloyi coA reductase 1, mitochondriai
			2	2-bydrowy 2 methyleteral Oceania	4,4-dlenoyi CoA reductase 1, mitochondrial
				o-riyuloxy-o-liletilyigititaryi-coenzyme A synthase 1, 3-	
1987		20600 NIM 047269		hydroxy-3-methylglutaryl-Coenzyme A synthase 1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble), 3-hydroxy-3-
		VIIVI_017200	=	(soluble)	Imethylglutaryl-Coenzyme A synthase 2, pre R-sell leukemia franscription factor 1
				3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1, 3-	י פיין יכויים בין דיכי בין בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין דיכי בין בין דיכי בין בין דיכי בין בין בין דיכי בין בין דיכי בין בין בין בין בין בין בין בין בין בי
1007		07000		hydroxy-3-methylglutaryl-Coenzyme A synthase 1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble), 3-hydroxy-3-
200	1	2001 NM 01/268	_	(soluble)	methyldiutaryl-Coenzyme A synthase 2 are B sell touleaning transmissions.
0				4-hydroxyphenylpyruvate dioxygenase, 4-	The property of the property o
69. 79.	- 1	17742 AA866302	ပ	hydroxyphenylpyruvic acid dioxygenase	4-hvdroxynhenvlnvnyste dioxynapac / hvdroxynchenvlnvnhynnes
1/53	- 1	203 3 NM 012585	b, u, v	5-hydroxytryptamine (serotonin) receptor 1A	5-hydroxytruntamine (septonin) popular 1/4
1878	2	IM_013148	n, o	5-hydroxytryptamine (serotonin) receptor 5A	Al longood (minoroo) or minoroo
2189	767 N	767 NM_024365	p'c	5-hydroxytryptamine (serotonin) recentur 6	A hudroughmine Land
	<del> </del> -			חומססו (יייייים (סיייים) מיייים להיל	o-nyuroxyuypiamine (serotonin) receptor 6
					6-pyruvoyl-tetrahydropterin synthase, 6-pyruvoyltetrahydropterin synthase, ESTs,
				-	Weakly similar to JC1405 6-pyruvoy/tetrahydropterin synthase [H.sapiens]. ESTs.
1071	45 17 N			o-pyruvoyi-tetranydroptenn synthase, 6-	Weakly similar to PTPS RAT 6-PYRUVOYL TETRAHYDROBIOPTERIN
		13:11 MINI 01/220	ee, π	pyruvoyitetrahydropterin synthase	SYNTHASE PRECURSOR [R.norvegicus]
1207				6-pyruvoyl-tetrahydropterin synthase/dimerization	
1/5/1	218K2 M83740	83740	E	cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	
					ESTs, Moderately similar to PC4265 disintegrin and metalloproteinase 10
		-			[H.sapiens], Homo sapiens cDNA FLJ13398 fis, clone PLACE1001377, highly
					similar to Homo sapiens ADAM10 (ADAM10) mRNA, RIKEN cDNA 1700031C13
2693	19694 748444		<u>-</u>	a disintegrin and metalloprotease domain 10, a	gene, a disinfegrin and metalloprotease domain 10, a disintegrin and
	110001			uisiiriegi iii arid metalioproteinase domain 10	metalloproteinase domain 10

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ķ					Ath. Ref 44091,5000,04,000,040,000
g <u>C</u>	3' GC ED No.	Genbank Acc.	Model Cod	Model Code Human Horlologous Known Gene Name	Sequence Clister Tile
					For its in the control of the cont
					AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8 (ADAMTS.
					8) (ADAM-TS8) (METH-2) [M.musculus], ESTs, Weakly similar to ATS1 MOUSE
					ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH
				-	THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1) [M.musculus]. ESTs.
		·			Weakly similar to T47158 hypothetical protein DKFZp762C1110.1 [H.sapiens], Mus
					musculus, Similar to a disintegrin and metalloproteinase with thrombospondin motifs
					1 (ADAMTS-1), clone IMAGE:3491991, mRNA, partial cds, Mus musculus, Similar
					to a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type
					1 motif, 4, clone MGC:38401 IMAGE:5345809, mRNA, complete cds, a disintegrin-
					like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1, a
2108		NIM COAACO	120	ase (reprolysin type)	disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1
7 130		22020 NINI_U24400	¥	with thrombospondin type 1 motif, 1	motif, 8
2475		19658 NM_057103	55	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein (gravin) 12, ESTs, Highly similar to gravin
					4 kinase (PRKA) anchor motein (gravin) 42 ECT. Uicht.
2630	2153	2153 U75404	n, v	A kinase (PRKA) anchor protein (gravin) 12	(H.sapiens)
					Homo sapiens, Similar to acetyl-Coenzyme A acetyltransferase 1 (acetoacety)
					Coenzyme A thiolase), clone MGC:13582 IMAGE:4278329, mRNA, complete cds,
		-			Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, ctone
				/me A acetyltransferase 1, acetyl-	MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A
1020	18056	18056 NIM 047075		A acetyltransferase 1 (acetoacetyl Coenzyme	acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), acetyl-Coenzyme A
3	10000	C/0/10 MINI	99	A molase)	acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
	_				tomo sapiens, Similar to acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl
					Coenzyme A thiolase), done MGC:13582 IMAGE:4278329, mRNA, complete cds,
					Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone
					MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A
1930	18957 N	18957 NM 017075	-	zyme	acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), acetyl-Coenzyme A
	10001	T		A unotable)	acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
	_				Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone
					MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A
1732	2360R	23698 NM 012480		lerase i (peroxisomal 3-oxoacyi-Coenzyme A	acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase), acetyl-Coenzyme A
	Topon T	1012102 M		uiloidase)	acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)

TABIE	2				
- VDCC	2				Attv. Ref. 44921-5090-01-WO/2105485
<u> </u>		GenBank Acc.		から またい かいかい かいかい 一大学 のできる できる かいかい かいかい かいかい かいかい かいかい かいかい かいかい かい	11 人名其人人名 如此人名 多次的
۵	GLGC ID No.	No.	Model Code	logous Known Gene Name	Human Homologous Sequence Cluster Title
2037		18569 NM_019212	f, w, x, hh	actin, alpha 1, skeletal muscle	BRG1/brm-associated factor 53A, Rat messenger RNA for alpha-actin, actin, alpha 1, skeletal muscle, actin-like 6, expressed sequence AA959943
275		16001 AA866452	bb, cc, dd	actin, alpha, cardiac, actin, alpha, cardiac muscle	ESTs, Weakly similar to ACTA_HUMAN Actin, aortic smooth muscle (Alpha-actin 2) [R.norvegicus], Homo sapiens, clone MGC:33407 IMAGE:4824606, mRNA, complete cds, actin, alpha 2, smooth muscle, aorta, smooth muscle, and
2212		21166 NM_031005	a, n, o	actinin, alpha 1	ESTs, Weakly similar to alpha actinin 4 [Mus musculus] [M.musculus], RIKEN cDNA 3110023F10 gene, actinin alpha 2, actinin alpha 3, actinin, alpha 3, alpha actinin 4
2307	53 38	53 38 NIM_031675	٠	actinin, alpha 4, alpha actinin 4	ESTs, Weakly similar to alpha actinin 4 [Mus musculus] [M.musculus], RIKEN CDNA 3110023F10 gene, actinin, alpha 4, alpha actinin 4
1821	244 11	244 11 NM_012912	a, p, q, y, z, ee, ff	activating transcription factor 3	ESTs, Weakly similar to A39382 liver regeneration factor LRF1 - rat [R.norvegicus], ESTs, Weakly similar to A54025 transcription factor ATF3 [H.sapiens], activating transcription factor 3
1864	202:12	202 12 NM_013084	99	acyl-Coenzyme A dehydrogenase, short/branched chain	acyl-Coenzyme A dehydrogenase, short/branched chain
903	179:37	179:i7 Ali)28975	s, t	adaptor prutein complex AP-1, beta 1 subunit, adaptor- related protein complex 1, beta 1 subunit	
1990	17939	17959 NIM 017277	s, t	adaptor protein complex AP-1, beta 1 subunit, adaptor- related protein complex 1, beta 1 subunit	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 1, beta 1 subunit
2495	17958	17958 NIM_080583	66	adaptor-related protein complex 2, beta 1 subunit	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 2, beta 1 subunit
2495	17960	17960 NM_080583	<b>L</b>	adaptor-related protein complex 2, beta 1 subunit	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 2, beta 1 subunit
2366	15961	1596 NM_053294	-	adenosine A2a receptor	adenosine A2a receptor, adenosine A3 receptor
1816	16708	16708 NM_012895	u, v	adenosine kinase	adenosine kinase, expressed sequence Al987814
2053	8200	8200 NM_019285	-	adenylate cyclase 4	ESTs, Moderately similar to A41542 adenylate cyclase (EC 4.6.1.1) IV - rat [R.norvegicus], adenylate cyclase 2 (brain), adenylate cyclase 4
				adenylate cyclase activating polypeptide 1 (pituitary)	ESTs, Weakly similar to PACR MOUSE PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE I RECEPTOR PRECURSOR IM.musculus)
2521	24775 N	24775 NM_133511	0	receptor type I, adenylate cyclase activating polypeptide 1 receptor 1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I, adenylate cyclase activating polypeptide 1 receptor 1
1905	17972N	17972 NM_016989	m'l	adenylate cyclase activating polypeptide 1, adenylate cyclase activating polypeptide 1 (pituitary)	adenylate cyclase activating polypeptide 1, adenylate cyclase activating polypeptide 1 (pituitary)

TABLE 3	<u>س</u>			The second secon	
SEQ		GenBank Acc.	**************************************	The second secon	Atty. Ref. 44921-5090-01-WO/2105485
<u>_</u>	GLGC 1D No.	No.	Model Code	Model Code Human Homologious Known Gene Name	Human Homologous Sequence Cluster Title
					ESTS, Highly similar to 1917150A collagen: SUBUNIT = alpha1: SOTYPE = VIII   Raffins
					norvegicus] [R.norvegicus], ESTs, Moderately similar to CA18 MOUSE COLLAGEN
					ALPHA 1(VIII) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to ACR3
					MOUSE 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR
					[M.musculus], Mus musculus, Similar to DKFZP586B0621 protein, clone
					MGC:38635 IMAGE:5355789, mRNA, complete cds, RIKEN cDNA 5530401N20
2577	13719	13712 NM 144744			gene, adipose most abundant gene transcript 1, collagen, type VIII, alpha 1.
	31 101	14.1 - IAIN	=	adipose most abundant gene transcript 1	procollagen, type VIII, alpha 1
1728		3762 M86341	s, t	ADP-ribosylarginine hydrolase	ADP-ribosylarginine hydrolase, ESTs, Weakly similar to ADP-RIBOSYLARGININE
					ADP-ribosylation factor 4-like, ADP-ribosylation factor-like 7 ADP-ribosylation-like 7
					ESTs, Weakly similar to ADP-ribosylation-like 4 [Mus musculus] IM musculus] Mus
					musculus, Similar to ADP-ribosylation-like 4, clone MGC:5774 IMAGE:3599701
2032	24019	24019 NM 019186		ADB-ribosylation factor like A ADB stranger and	mRNA, complete cds, RIKEN cDNA 1110036H21 gene, epithelial protein lost in
				incopiation factor line 4, ADF-1100sylation-like 4	neoplasm beta
i i				adrenergic receptor kinase, beta 1, adrenergic, beta,	ESTs, Weakly similar to GRK6 MOUSE G PROTEIN-COUPLED RECEPTOR KINASE GRK6 IM musculust 3 protein-counted recentor times 6 oderson:
3	3505/	3505 AA998430	w, x	receptor kinase 1	recentor kinase heta 1 adranamio hata manata titana d
1006			:	adrenergic receptor, alpha 1b, adrenergic, alpha-1B-,	cooper misse, beta 1, autorayle, beta, leceptor Kinase 7
	5		J, KK	receptor	
1778	3221	322 NM_012715	d, gg	adrenomedullin	adrenomedullin
					ECT. World, ci
					ESTS, Weakly similar to Assues penecan precursor [H.sapiens], ESTS, Weakly
					Similar to AGR1 agrin - rat (R.norvegicus), ESTs, Weakly similar to BASEMENT MFMBRANE-SPECIFIC HEDADAN SILI EATE BECTTOSI YOUR COLLECTION
					PRECURSOR IM misculius ESTE Weakly similar to DOBY 111111111
					MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOCI YCAN COBE DEOTEIN
			-		PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:3494258, mRNA, partial
			_		ods, heparan sulfate proteoglycan 2 (perlecan), perlecan (heparan sulfate
1725	10743 M64780				proteoglycan 2), serine protease inhibitor, Kazal type, 5, sialoadhesin,
					transmembrane protein with EGF-like and two follistatin-like domains 1

TABLE 3	щ Э			Company of the second of the s	
SHO D	GLGC ID No.	GenBank Acc. No.	Model Code		Atty, Ket. 44921-5090-01-WO/2105485
					inuman riomologous Seguence Cluster Title
					ESTs, Weakly similar to A38096 perlecan precursor [H.sapiens], ESTs, Weakly
					Similar to AGK I agrin - rat (R.norvegicus), ESTs, Weakly similar to BASEMENT MEMBRANE-SPECIFIC HEPARAN SI II FATE PROTEORI YCAN CODE BEOTEIN
					PRECURSOR [M.musculus], ESTs, Weakly similar to PGBM HUMAN BASEMENT
					MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
					PRECURSOR [H.sapiens], Mus musculus, done IMAGE:3494258, mRNA, partial
					cds, heparan sulfate proteoglycan 2 (pertecan), pertecan (heparan sulfate
1725		10744 M64780	4-	i.i.i.	proteoglycan 2), serine protease inhibitor, Kazal type, 5, sialoadhesin,
2082		23424 NM 021680	يد	alanvi-tRNA svnthetase	uansmernorane protein with EGF-like and two follistatin-like domains 1
					alanyi-trivA synthetase
5			:	aldehyde dehydrogenase 1 family, member A1, aldehyde	Mus musculus, Similar to aldehyde dehydrogenase 8 family, member A1, clone aldehyde dehydrogenase 8 family, member A1, clone lMAGE:4234742, mRNA, partial cds, aldehydrogenase 1 family, member A1, and lMAGE:4234742, mRNA, partial cds, aldehyde dehydrogenase 1 family, member
0117		ZUST 5 NIM 02240/	ž	dehydrogenase family 1, subfamily A1	A1, aldehyde dehydrogenase family 1, subfamily A1
					ESTs, Moderately similar to DHAM_RAT ALDEHYDE DEHYDROGENASE.
_					MITOCHONDRIAL PRECURSOR (ALDH CLASS 2) (ALDH1) (ALDH-E2)
- 1					[R.norvegicus], RIKEN cDNA 2410004H02 gene, aldehyde dehydrogenase 1 family,
2353	122001	12200 NIM 032416		ondrial),	member B1, aldehyde dehydrogenase 2 family (mitochondrial), aldehyde
200	122031	T	3	aldenyde denydrogenase 2, mitochondral	dehydrogenase 2, mitochondrial
					Mus musculus, Similar to aldehyde dehydrogenase 4 family, member A1, clone
		-			IMAGE:5102023, mRNA, partial cds, RIKEN cDNA 1110038i05 gene, aldehyde
119	11901	11901 44801058		dobirdroonsoo onterning, member A1, aldehyde id	alderlyde derlydiogenase 9 family, member A1, aldehyde dehydrogenase 4 family, member A1, aldehyde dehydrogenase 9 family, member
2	8			uenyurogenase s, subramily A1	A1, aldehyde dehydrogenase 9, subfamily A1
		-		<u> </u>	ES1, Weakly similar to A39/63 aldehyde reductase [H.sapiens], ESTs, Moderately
				<i>3</i>	similar to ALDR_RAT Aldose reductase (AR) (Aldehyde reductase) [R.norvegicus],
					ESTs, Weakly similar to ALDR_RAT Aldose reductase (AR) (Aldehyde reductase)
			<u>-</u>		[R.norvegicus], Rattus norvegicus mRNA for aldose reductase-like protein, aldo-
1733	15511 NI	15511 NIM 012400		sto reductase tamily 1, member B3	keto reductase family 1, member B1 (aldose reductase), aldo-keto reductase family
3	2	10 12430 III		(aldose reductase)	1, member B3 (aldose reductase)
1802	15032 N		K	a a support And material and a support And And And And And And And And And And	alpha-methylacyl-CoA racemase, cDNA sequence AF397014, chromosome 7 open
2039	2070 NI	2079 NM 019220			reading frame 10
		7		animo-terminal ennancer of split	amino-ferminal enhancer of split

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ا الار		Prop Bank Acc		Control of the Contro	Atty. Ref. 44921-5090-01-WO/2105485
, <u></u>	31.GC   3 No.	No.	194	Model Code Human Hornologous Known Gene Name	Human Homologous Sequence Chister Title
2663		25711/X60468	<u> </u>	amyloid beta (A4) precursor protein-binding, family B, member 1, amyloid beta (A4) precursor protein-binding, family B. member 1 (Fe65)	Mus musculus, Similar to amyloid beta (A4) precursor protein-binding, family B, member 3, clone MGC:38710 IMAGE:5357681, mRNA, complete cds, amyloid beta (A4) precursor protein-binding, family B, member 1, amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65), amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65), amyloid beta (A4) precursor protein-
1745		225 NM_012544	aa, bb	zyme (peptidyl-dipeptidase A)	Estra, Highly similar to A31759 peptidyl-dipeptidase A [H.sapiens], RIKEN cDNA 2010305L05 gene, angiotensin I converting enzyme (peptidyl-dipeptidase A) 1,
1366		7196 NM_012904	a, II		annexin A1
3			1 (1)		annexin A2, annexin A9
					EST, Moderately similar to 0806162C protein COI [M.musculus], EST, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C protein COI [M.musculus], ESTs, Highly similar to hydroxyacid oxidase 3 (medium-chain) [Rathus nonvenious] [R. nonvenious]
			1 1 2 2		0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], ESTs, Weakly similar to 0806162C protein COI
2073	574	574 NM_019905	a, II, I, 2, da, kk,	4, II, I, 4, 44, all lievin AZ, nydroxyacid oxidase (glycolate oxidase) 3,   kk,   hydroxyacid oxidase 3 (medium-chain)	[M.musculus], annexin A2, annexin A9, hydroxyacid oxidase (glycolate oxidase) 3, hydroxyacid oxidase 1, liver
					ESTs, Moderately similar to ANX4 MOUSE ANNEXIN IV [M.musculus], ESTs,
1559	8440 A	N235611	ڡ	annexin A4	weakly similar to ZAP 36/annexin IV [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to annexin A8, clone MGC:13875 IMAGE:4013266, mRNA,
2181	561 N	561 NM_024156	jj, KK		Complete Cus, annexin A13, annexin A4, annexin A8
2181	562 N	VM_024156		annexin A6	annexin A6
					ESTs, Moderately similar to AOP2 MOUSE ANTIOXIDANT PROTEIN 2 [M.musculus], ESTs, Moderately similar to AOP2 HUMAN ANTIOXIDANT
2398	19252 N	19252 NM_053576	a A A		PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phoenholings As)
1819	1834 <u>N</u>	1834 NM 012905	<u> </u>	aortic preferentially expressed gene 1, nuclear protein, marker for differentiated aortic smooth muscle and down-remated with vascular intury.	aortic preferentially expressed gene 1, nuclear protein, marker for differentiated
4	1 70000			A repair enzyme),	au its smooth musicle and down-regulated with vascular injury APEX nuclease (multifunctional DNA repair enzyme). Mus musculus ane? mRNA
//12	NILLIBUZ	Z0801 NM_024148	d, s, t		for AP endonuclease 2, complete cds, apurinic/apyrimidinic endonuclease

TABLE 3	33		7.		
CHS		ConRant Acc		1850	## Attv. Ref. 44971-5090-01-WO/10548F
<u>.</u>	D GLGC ID No.	No.	٠٠.	Model Code Human Homologous Known Gene Name	ofor Title
2552		16400 NM_138828	c, dd		anolinamenta Capacita Cultura
1793		5758 NM 012778	4	quaporin 1 (channel-forming integral	application of the state of the
1794		104 NM 012779	٠ ١٠ ١٠ ١٠ ١٠	Adianorin 5	aquaporin 1, aquaporin 1 (channel-forming integral protein, 28kD)
			:	5-lipoxygenase activating protein.	aquaporin 5, aquaporin 6 arachidonata 5, linoximenase antimiting modeling acceptators of F. II.
1986	-	7593 NM_017260	w, x		activating protein
1986		7594 NM_017260	w, x, ii		arachidonate 5-lipoxygenase activating protein, arachidonate 5-lipoxygenase-
				ırophysin	activating protein
1907		248 18 NM 016992	C		arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone,
	ı		2	- January Constitution of the Constitution of	diabetes insipidus, neurohypophyseal)
				Il antiditretic hormone dishotos incipile.	
1907	24819	248#9 NM_016992	n, o		arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diahetes instinitus neurophysool)
				7	ARP3 actin-related protein 3 homolog (veast). EST. Weakly similar to
				A .	ARP3_HUMAN ACTIN-LIKE PROTEIN 3 [H.sapiens], EST, Weakly similar to ATRT
-				æ	actin, skeletal muscle - rat [R.norvegious], ESTs, Moderately similar to
				<b>4</b>	ARP3_HUMAN ACTIN-LIKE PROTEIN 3 [H.sapiens], ESTs, Weakly similar to
					ATHU actin alpha 1, skeletal muscle [H.sapiens], Homo sapiens cDNA FLJ14201
1464	230437	23013 AI230743	hh	related protein 3 homolog (yeast), actin-	its, clone NT2RP3002955, actin-related protein 3-beta, hypothetical protein FLJ12785, mitochondrial rihosomal protein i 47
				A	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9)
					isoform 1, ESTs, Highly similar to AT91_HUMAN ATP SYNTHASE LIPID-BINDING
2000	16844 N	16844 NM_017311	0 6	ATE Sytutiase, H+ transporting, mitochondrial F0 Pl Complex, subunit c (subunit 9) isoform 1	PROTEIN P1 PRECURSOR [H.sapiens], Homo sapiens cDNA: FLJ23586 fis, clone
				+ transporting, mitochondrial F1	ATP synthase H+ transporting mitochondrial E1 complex graphs arrived Parices
7266	172031v	17203 NM_139099	g, hh		CDNA 2410043G19 gene, expressed segmence AV000645
2566	17204 N	17204 NM_139099	_ 6	ATP synthase, H+ transporting, mitochondrial F1  Complex, epsilon subunit	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit, RIKEN
1994	123¢7 N	12347 NM 017290	7	ansporting cardiac mucha cloud thinks	State of Select appreased sequelice Avounded
_	<del> </del>			With Z	
1994	12349N	12349 NM_017290	aa	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	

IABLI	8				
SEO	'	GenBank Acc.			Ally Ref A4031 5000 04 World Season
₽	SCC D No.	CN C		Model Code Human Homologous Known Gene Name	
					ATPase, Ca++ transporting, plasma membrane 2, ATPase, Class V, type 10C, ATPase, class V, type 10A, ESTs, Highly similar to A34308 Ca2+-transporting
1731		17931 M96626	cc, dd, gg	ATPase, Ca++ fransporting plasma momentage, 2	ATPase [R.norvegicus], ESTs, Weakly similar to 149143 gastric H(+)-K(+)-ATPase alpha subunit - mouse [M.musculus], RIKEN cDNA 1110019114 gene, RIKEN cDNA
1822		24783 NM_012914	조	ATPase, Ca++ transporting, ubiquitous	ATPase Catt transnorting ukimitkans
					ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide, ATPase, Na+/K+ transporting, alpha 2 polypeptide, ATPase, Na+/K+ transporting, alpha 2 polypeptide, ATPase, Na+/K+ transporting, alpha 2 polypeptide, ATPase, Na+/K+ transporting, alpha 4
1734	583	583 NM_012505	h, I	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide, ATPase, Na+/K+ transporting alpha 2 polymortide	polypeptide, ESTs, Highly similar to A1A4_HUMAN Sodium/potassium-transporting ATPase alpha-4 chain (Sodium pump 4) (Na+/K+ ATPase 4) [H.sapiens], expressed
		-			Sequence AW000554  ATP-binding cassette, sub-family B (MDR/TAP), member 1, ATP-binding cassette, sub-family B (MDR/TAP), member 14. ATP-hinding cassette, sub-family B (MDR/TAP).
					(MDRTAP), member 18, EST, Highly similar to MDR3 MOUSE MULTIDRUG
1726	5733	5733 M81855		ATP-binding cassette, sub-family B (MDR/TAP), member 1, ATP-binding cassette, sub-family B (MDR/TAP),	RESISTANCE PROTEIN 3 [M.musculus], EST, Weakly similar to MULTIDRUG MULTIDRUG RESISTANCE PROTEIN 1 [M.musculus]
-				Cassette sub-family B (MOBITAD)	IMAGE:358242, mRNA, partial cds
2656	1037 >	1037 X57523	g	2, transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	ATP-binding cassette, sub-family B (MDR/TAP), member 2, ESTs, Highly similar to S13426 multidrug resistance protein homolog - rat [R.norvegicus], transporter 1,
					ATP-binding cassette, sub-family B (MDR/LAP)  ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Weakly similar to T42751 sulfonylurea receptor 2 - rat [R.norvegicus], Homo sapiens cDNA FLJ31957 fis, clone NT2RP7007381 binhly similar to C. Konton
1853	733 N	733 NM_013040	j, k	ATP-binding cassette, sub-family C (CFTR/MRP), c	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14:ATP-binding cassette, sub-family C (CFTR/MRP), member 9, full insert sequence.
				- B .5	BAI1-associated protein 2, ESTs, Weakly similar to brain-specific angiogenesis
728	3511/4	3511/AA998152	B B	BAI1-associated protein 2, brain-specific angiogenesis Rinhibitor 1-associated protein 2	Similar to KIAA0429 gene product, clone IMAGE:2811240, mRNA, partial cds, RIKEN cDNA 1300006M19 gene, brain-specific angiogenesis inhibitor 1-associated protein 2, hypothetical protein FLJ22582, insulin recentor tunesing stranges.
					September 1 in company of the september 1 in company of the september 2 in company of the septem

TABLE 3	٠ ا		·	See The Chief	
SEO		GenBank Acc		The state of the s	Attv. Ref. 44921-5090-01-WO19105485
Q	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Himan Lowolyania Commence of the commence of t
					Pasis bally loca balls down in the constant of
9370		OCCUSO FAIN		basic helix-loop-helix domain containing, class B, 2, basic	basic helix-loop-helix domain containing, class B, 2, basic containing, class B, 3, basic helix domain containing, class B, 2, basic helix-loop-helix domain containing class B, 2, basic helix-loop-helix domain containing class B, 2, basic helix-loop-helix domain containing class B, 2, basic helix-loop-helix domain containing class B, 2, basic helix-loop-helix domain containing class B, 2, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain containing class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 3, basic helix-loop-helix domain class B, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4,
200		TUDS INIM UD3328	Ф	helix-loop-helix domain containing, class B2	loop-helix domain containing, class B3
2514		1064 NIM 133303	4	basic helix-loop-helix domain containing, class B, 3, basic	basic helix-loop-helix domain containing, class B, 3, basic basic helix-loop-helix domain containing, class B, 2, basic helix-loop-helix domain
		COCCO TIME	D, 4, IIII	nelix-loop-nelix domain containing, class B3	containing, class B2, basic helix-loop-helix domain containing, class B3
					B-cell translocation gene 1, anti-proliferative, Homo sapiens cDNA FLJ30547 fts.
1984		19 NM_017258	p, q	B-cell translocation gene 1, anti-proliferative	clone BRAWH2001439, transducer of ERBB2, 1, transducer of ERBB2, 2,
					uansoucel of Einb-z. I B-cell transfocation gene 2, anti-proliferative B-cell transfocation con 4 btc
1985		15: 00 NM 017259	D. G. KK	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN
		'			PRECURSOR [H.sapiens]
			j, k, p, q, y,	B-cell translocation gene 2, anti-proliferative BTG family	B-cell translocation gene 2, anti-proliferative. BTG family. family. family. family. Serv. Lichtofile 1, pt. of 100 member 2, etc. Lichtofile 1, pt. of 100 member 3, anti-proliferative.
88		15: 01 NM_017259	$\neg \neg$	member 2	namy, member 2, E31s, ruginy similar to B1 G2_HUMAN B1G2 PROTEIN PRECURSOR IH saniens
					B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG
1985		15: 99 NM 017259	V. Z	D-ceil if affisiocation gene 2, anti-proliterative, BTG family, imember 2	ברכנו עמוז:וסכמנסה gene 2, anti-proliterative, BTG family, family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN
1924	2.00			iciated X protein Bol2-associated V protein	PRECURSOR (H.sapiens)
1924	S			PCI 2 associated V protein, Data associated A protein	ا انگ د
1924	155		ε	PCI 2 accounted V protein, bdz-associated X protein	
十				DOLL-associated A protein, Bci2-associated X protein	
1913	17815N	17815 NM_017015	w, x		ESTs, Highly similar to A26581 beta-glucuronidase [H.sapiens], SMA3, beta- glucuronidase structural, glucuronidase, beta
	_				ESTs, Highly similar to asporin (LRR class 1); periodontal ligament associated
_					protein 1 [Homo sapiens] [H.sapiens], ESTs, Weakly similar to PGS1_RAT
1933	22552 N	22552 NM 017087			Bone/cartilage proteoglycan I precursor (Biglycan) (PG-S1) [R.norvegicus], asportin.
+	Zewe II	Т	0 1		biglycan
1735	1745N	1745 NM_012513 p	D, Q, II	brain derived neurotrophic factor, brain-derived  brain-derived	brain derived neurotrophic factor, brain-derived neurotrophic factor, expressed
495	23038 AA900881		, y, z	inotransferase 1 cytosolic	Sequelice Al402039
	-		Т		Diameter chall affilinotranslerase 1, cytosolic
				<u>.</u>	normo sapiens culva FLJ1384/ its, ctone THYRO1000852, highly similar to Human highly shair amino coid coming from the control of the control
2117	24643 N	24643 NM 022400 b	b, u, v	branched chain aminotransferase 2 mitochondrial	aminotransforms 2 miles actualistic actualistic actualistic (ECA40) mKNA, branched chain
					aminou ansierase 2, mitochongnal

TABLE 3	:			で発生 一般など、	
SEO		GenBank Acc.			**Aty. Ref. 44921-5090-01-WO/2105485
	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Himan Homologonic Sequence Objects, Title
1688		17285 J02827		branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease), branched chain ketoacid dehydrogenase E1, alpha polypentide	A CONTRACT OF THE CONTRACT OF
					ESTs, Highly similar to breakpoint cluster region, isoform 1 [Homo sapiens] [H.sapiens], ESTs, Highly similar to chimerin (chimaerin) 1 [Rattus norvegicus]
					[R.norvegicus], ESTs, Weakly similar to SH3-BINDING PROTEIN 3BP-1 [M.muscufus], RIKEN cDNA 1700112L09 gene, RIKEN cDNA 2310069104 gene,
778		3278 AI008988	y, z	breakpoint cluster region	Nincay culva 3133400C09 gene, RIKEN cDNA 5730403H17 gene, SH3-domain binding protein 1, breakpoint cluster region, chimerin (chimaerin) 1
2347		18499 NM_031984	aa, bb	calbindin 1, (28kD), calbindin-28K	Mus musculus, Similar to secretagogin, clone MGC:27615 IMAGE:4504330, mRNA, complete cds, calbindin 1, (28kD), calbindin-28k
2347			qq	calbindin 1, (28kD), calbindin-28K	Mus musculus, Similar to secretagogin, clone MGC:27615 IMAGE:4504330, mRNA,
128		1632 NM_012717	u, v		calcitonin recentar-like
					ESTS, HIGHIY SIMILAT TO CICZ RAT DIHYDROPYRIDINE-SENSITIVE L-1YPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR [R.norvegicus],
					CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR (R.norvegicus).
				elta	Rattus norvegicus L-type calcium channel alpha2/delta subunit mRNA, complete ods, calcium channel, voltage-dependent, alpha 2/delta subunit 1 calcium channel
1824	1765	1765 NM_012919	u, v	Subunit 1, calcium channel, voltage-dependent, alpha2/delta subunit 1	voltage-dependent, alpha 2/delta subunit 2, calcium channel, voltage-dependent, alpha2/delta subunit 1
2442	1011	1011 NM_053851 e		E calcium channel, voltage-dependent, heta 2 suhunit	ESTs, Weakly similar to 2111412A Ca channel:SUBUNIT=beta [M.musculus], calcium channel, voltage-dependent, beta 2 subunit, expressed sequence
					RIKEN cDNA 2310068022 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin
2340	19190 N	19190 NM_031969 h	h, i	calmodulin 1, calmodulin 1 (phosphorylase kinase, delta) Al	<ol> <li>calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence Al327027, expressed sequence AL024000, troponin C, fast skeletal</li> </ol>
				¥	Kinen CDNA 2310068022 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin 1, calmodulin 2, calmodulin 3, calmodulin 3, calmodulin 3, calmodulin 2, calmodulin 3, calmodulin 2, calmodulin 3, calmodulin 3, calmodulin 4, calmodulin 4, calmodulin 4, calmodulin 5, calmodulin 5, calmodulin 6
2340	19191N	19191 NM_031969 h, I		calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)   Al	Al327027, expressed sequence AL024000, troponin C, fast skeletal

TABLE 3	E3	>	4.2	一年 一年 一種で	77
SEQ.		GenBank Acc.		・	Atty, Ref. 44921-5090-01-WO/210548F
으	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologies Serinance Cliester Titls
	<del></del>				1, calmoduli
2340		19195 NM_031969	l),	calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)	
2340		25802 NM_031969	h, I, aa, bb, II	calmodulin 1, calmodulin 1 (phosphorylase kinase, delf.	
587		15476 AA944426	h, f	calmodulin 3, calmodulin 3 (phosphorylase kinase, delta)	RIKEN CDNA 2310068022 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 1, centrin, EF-hand protein, 1, expressed sequence
1736		20518 NM 012518	. o. r	calmodulin 3. valmodulin 2. Johannakas 1.	RIKEN cDNA 2310068022 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence
1698	6963	6963 L18889		- (	Januarium 3 (priospriorylase Kinase, delta) Al327027, expressed sequence AL024000, troponin C, fast skeletal
					ESTs, Weakly similar to CAN1_MOUSE CALPAIN 1, LARGE [CATALYTIC]
2024	208631	20863 NM_019152	bb, cc, dd	calpain 1, calpain 1, (mu/l) large subunit	M.musculus), calpain 1, calpain 11, small optic lobes homolog (Drosophila)
296	1190	1190 AA875089	hh	calpastatin	ESIS, Moderately similar to ICAL_HUMAN CALPAIN INHIBITOR [H.sapiens], calpastatin
2064	23491 N	23491 NM_019359	2	calponin 3, acidic	ESTs, Moderately similar to CALPONIN H1, SMOOTH MUSCLE [M.musculus], calbonin 2, calponin 3, aridic
			<del></del>		ESTS, Highly similar to CAQS MOUSE CALSEQUESTRIN, SKELETAL MUSCLE ISOFORM PRECURSOR [M.musculus]. ESTS. Moderately similar to CAOC BAT
530	168A	168 AA924985	<u> </u>	calsequestrin 2 calsemnestrin 2 (condisco musulo)	CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM PRECURSOR [R.norvegicus], calsequestrin 1, calsequestrin 1 (fast-twitch, skeletal muscle), calsequestrin 2,
					Calsequestrin 2 (cardiac muscle)

TABIE	  -  -		<b>単語のはいってい</b>	の機能はある。 ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・	
بن	•	Bank Acc	Γ.		- Alty Ret. 44921-5090-01-WO/2105485
e l	GLGC ID No.	No.		Model Code Human Hr mologous Known Gene Name	Human Homologous Sequence Cluster Title
· · · · · · · · · · · · · · · · · · ·	· •				ESTs, Highly similar to CAQS MOUSE CALSEQUESTRIN, SKELETAL MUSCLE ISOFORM PRECURSOR [M.musculus], ESTs, Moderately similar to CAQC_RAT CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM PRECURSOR [R.norvegicus],
1946		167 NM_017131	b, e, u, v, II	calsequestrin 2, calsequestrin 2 (cardiac muscle)	calsequestrin 1, calsequestrin 1 (fast-twitch, skeletal muscle), calsequestrin 2, calsequestrin 2 (cardiac muscle)
					EST, Weakly similar to CRMS2 carbonate dehydratase [M.musculus], ESTs, Weakly similar to CAH2_RAT Carbonic anhydrase II (Carbonate dehydratase II)
2056		15056 NM_019291	b, c	carbonic anhydrase 2, carbonic anhydrase II	(CA-II) [R.norvegicus], carbonic anhydrase 2, carbonic anhydrase I, carbonic anhydrase II, carbonic anhydrase VIII, carbonic anhydrase III, carbonic anhydrase VIIII, carbonic anhydrase VIII, carbo
2029		17063 NM_019170	<del>ب</del> و	carbonyl reductase 1	ESTs, Weakly similar to S52349 carbonyl reductase (NADPH) (EC 1.1.1.184) - rat [R.norvegicus], RIKEN cDNA 1110001J05 gene, RIKEN cDNA A930033N07 gene,
					ESTs, Weakly similar to S52349 carbonyl reductase (NADPH) (EC 1.1.1.184) - rat
2029	17064	17064 NM_019170	f, g	carbonyl reductase 1	Ir. norvegicusi, RIKEN cDNA 1110001J05 gene, RIKEN cDNA A930033N07 gene, carbonyl reductase 1, carbonyl reductase 3
				-	ESTs, Weakly similar to S52349 carbonyl reductase (NADPH) (EC 1.1.1.184) - rat
2029	170661	17066 NM_019170	6	carbonyl reductase 1	carbonyl reductase 1, carbonyl reductase 3
					ESTs, Weakly similar to A41010 carboxylesterase [H.sapiens], Mus musculus, Similar to carboxylesterase 2 (intestine, liver), clone MGC-18908 MAGE-1994029
					mRNA, complete cds, Mus musculus, clone MGC:18894 IMAGE:4239756, mRNA, complete cds. RIKEN chan 2310030034 2000 T COLLEGE COLL
					carboxylesterase 1, carboxylesterase 1 (monocyte/macrophage serine esterase 1).
2512	20879 N	20879 NM_133295	hh	carboxylesterase 3, carboxylesterase 3 (brain)	carboxylesterase 3, carboxylesterase 3 (brain), carboxylesterase-related protein, esterase 22
					EST, Weakly similar to MAST CELL CARBOXYPEPTIDASE A PRECURSOR
1908	24354 N	24354 NM 016998		1.11	carboxypeptidase A1 (pancreatic), carboxypeptidase A3, mast cell,
1875	21840 N		=	carboxypeptidase E	carboxypeptidase B1 (tissue)
2350	20554 NI		b, l, m, aa, cc. dd	camiline O-octanovltransferase	
! I	205555 NI	20555 NM 031987		carnitine O-octanoyltransferase	carnitine O-octanovitransferase
					valiilii Cookaliyili alisiclase

TABLE 3	E3		9	(日本)・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	
C V		Tonbank Age			TANKS TO SEE TO SEE TO SEE THE TANKS THE PROPERTY OF THE PROPE
<u>.</u>	GLGC ID No.	No.			MIN. K. H. 1987 1987 1987 1987 1987 1987 1987 1987
1896		20855 NM_013200	a, w. x. hh	camitine palmitoyltransferase 1, muscle, camitine palmitoyltransferase 1 muscle	i unidatignogous Sequence Cluster Title
1896		20856 NM 013200	a, w, x, aa, hh II		camitine palmitoyltransferase 1, muscle, camitine palmitoyltransferase I, muscle
			a, W, X, CC,	Camiline palmitoytransferase 2 camiline	camitine palmitoyltransferase 1, muscle, camitine palmitoyltransferase I, muscle
1827		1977 NM_012930	pp	- 1	camitine palmitoyltransferase 2 camiting malmitographics.
2409		20243 NM_053615	aa, bb	casein kinase 1, alpha 1	ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA 2610208K14 gene, RIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, casein kinase 1, delta
					ESTs, Moderately similar to KC1D_HUMAN CASEIN KINASE I, DELTA ISOFORM [H.sapiens], ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA
630	-	22. 71 AA946432	b, I, m	casein kinase 1, delta	ZO 10208K14 gene, KIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, casein kinase 1, delta
2 5	- 1	070710 MINI		catalase, catalase 1	Catalase, catalase 1
1740	- 1	MM_012531	f, g	catechol-O-methyltransferase	RIKEN cDNA 6330414C15 gene, catechol-O-methyltransferase
1937	1 1	2: 50 NM_017097		cathebsin C	RIKEN cDNA 6330414C15 gene, catechol-O-methyltransferase
					RIKEN CLINA 492153717 gene, cathepsin C
1882	34.30 N	3430 NM_013156	c, I, m, t, kk o	cathepsin L	ESTs, Weakly similar to CATL MOUSE CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 4930486L24 gene, cathepsin L, expressed sequence AA40R230
1882	3431N	3431 NM_013156	c, kk	cathepsin L	ESTs, Weakly similar to CATL MOUSE CATHEPSIN L PRECURSOR [M.musculus],
2284	25795 N	25795 NM 031556	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	caveolin 1, caveolae protein, 22kD, caveolin, caveolae	Trincing 4530400L24 gene, camepsin L, expressed sequence AA408230
2172	21238 NI			CCAAT/enhancer binding protein (C/EBP), beta	caveolin 1, caveolae protein, 22kD, caveolin, caveolae protein, 22 kDa
2172	21239 NI	21239 NM_024125	p, q, r, bb, ee, ff, kk C	CCAAT/enhancer binding protein (C/FRP) heta	COAAT/chance billioning protein (C/EBP), beta
1880	21682 NI	21682 NM_013154	-	CCAAT/enhancer binding profein (C/EBP), delta	CCAAT/change binding protein (C/EBP), beta
1880	21683 MA	21683 NM 013164	5		CCAA Definiancer binding protein (C/EBP), defta
200	WINDOIN		), z, KK	CCAAT/enhancer binding protein (C/EBP), delta	CCAAT/enhancer binding protein (C/EBP), delta

TABI F.3	ļ		di dinist !	はなると、一般を続け、一般を行	
ပ္သ	·   ·   ·	GenBank Acc.		10000	Atty-Ref. 44921-5090-01-WO/2105485
₽	GI GC ID No.	O No.		Model Code Human Hr mologous Known Gene Name	Human Homologouis Seguience Chietar Title
2280		16049 NM 031541	C	_	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1, scar
2286	l	18315 NM 031561	n e	CD36 antigen, CD36 antigen (collagen type I receptor, thromhospondin resented)	receptor class B1
2286		18316 NM_031561	a)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombosoondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)
2286		18317 NM_031561	r, aa, bb, ii	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin recentor)	CU35 angen, CU36 antgen (collagen type I receptor, thrombospondin receptor)
2286		18319 NM_031561		CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CL39 anugen, CL36 anugen (collagen type I receptor, thrombospondin receptor)
1874	2002	NM_013127	e, bb	CD38 antigen, CD38 antigen (p45)	CD38 antigen, CD38 antigen (collagen type I receptor, thrombospondin receptor)
1826	1625	1625 NM_012924	) 30	CD44 antigen, CD44 antigen (homing function and Indian blood group system)	ordo anagen, ordo anagen (p45)
386	2832	2832 AA892388	b, u, v	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen	
1943	1435	1435 NM_017125	<u> </u>	CD63 antigen (malanoma 4 antigon). CARS, continued	CD63 antigen (melanoma 1 antigen), Cd63 antigen, EST, Weakly similar to CD63 MOUSE CD63 ANTIGEN [M.musculus], ESTs, Weakly similar to CD63_RAT CD63 antigen (AD1 antigen) [R.norvegicus], Mus musculus, clone MGC:36554 [MAGE:4954874, mRNA, complete cds, RIKEN cDNA 1300010A20 gene, expressed sequence C75951, expressed sequence CR0071, transmembrane 4
2424	10510	10510 NM_053743	u, v	CDC37 cell division cycle 37 homolog (S. cerevisiae), cell division cycle 37 homolog (S. cerevisiae), cell (	CDC37 cell division cycle 37 homolog (S. cerevisiae), cell CDC37 cell division cycle 37 homolog (S. cerevisiae), cell division cycle 37 homolog (S. cerevisiae) (S. cerevisiae)
					ESTs, Highly similar to A41222 ubiquitin-protein ligase [H.sapiens], ESTs, Weakly similar to A41222 ubiquitin-protein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed
2	13683 A	13683 AA799788	8	cell division cycle 34	sequence Al327276, ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae) Inhiguitin-conjugating enzyme E2B.
					מיסיימים, מחקשישו כחון ששמוון פוובאווום בבכ

(IABLE 3	را در		,	さんき 一 一 一 一 一 一 一 一 一 一 一 一 一 一 一 一 一 一 一	(Sets.)
SEO	,	GenBank Acc.			Atti/Ref. 44921-5090-01-WO/2105485
ੂ	GLGC ID No.	No	Model Coc	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					ESTs, Highly similar to A41222 ubiquitin-protein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD
					[M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed
1702		13682 L38482	Ð	cell division cycle 34	Sequence At3Z/Z/5, ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae). Inhinitiin-conjugating enzyme E2C.
				المرافعة الم	RIKEN cDNA 4930544G11 gene, RIKEN cDNA 5830400A04 gene, cell division
1423		22845 AI227887	e, aa, bb	ceil division cycle 42 (GTP binding protein, 25kD), cell division cycle 42 homolog (S. cerevisiae)	cycle 42 (GTP binding protein, 25kD), plysia ras-related homolog A2, ras homolog 9
				(2000)	DNA segment, Chr 3, ERATO Doi 555, expressed EST Highly similar to
					FA8_HUMAN COAGULATION FACTOR VIII PRECURSOR IH saniens1 ESTs
					Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus].
			<del>-</del> 1		ESTs, Weakly similar to CERU_RAT CERULOPLASMIN PRECURSOR
	-				(FERROXIDASE) [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase
1741	165.201	NM_012532	_ ပ	(certifox)lastnin centholasmin (farrovidae)	[H.Sapiens], ceruloplasmin, ceruloplasmin (ferroxidase), coagulation factor VIII,
2321	190-181	19048 NM 031719	jj, kk	chloride channel, nucleotide-sensitive, 1A	procequiant component (hemophilia A)
					יומספסיים ביומומים ביומים ביומים ביומומים ביומומים ביומומים ביומים ביומומים ביומומים ביומומים ביומומים ביומומים ביומומים
			,		EST, Highly similar to CTRO_HUMAN CITRON PROTEIN [H.sapiens]. ESTs. Highly
2329	1132 N	1132 NM 031790	E 	_	
	-	001100	2, 1, 111	Gruon, Gruon (mo-interacting, senne/threonine kinase 21)	_
2344	17075N	17075 NM_031974		clathrin, light polypeptide (1.ca)	H.sapiens dathrin light chain a gene, clathrin, light polypeptide (Lca), clathrin, light
2					EVIDENTIA (LCD), expressed sequence AV020306 ESTs. Weakly similar to CLD7 RAT CLAIDIN-718 promoning Museum.
917	1362/ A	1362/ AA851493	aa, bb	claudin 7	claudin 19 mRNA, complete cds. claudin 10. claudin 15. claudin 7
1952	15384N	15384 NM 047447		, V IJ	cofilin 1 (non-muscle), cofilin 1, non-muscle, cofilin 2 (muscle), cofilin 2, muscle.
	1	141 J 10 IAI		conin 1 (non-muscie), conin 1, non-muscle	expressed sequence AW987265
1952	15365 N	15365 NM 017147	44 44	Fig. (Louise mon) Fillipso	cofilin 1 (non-muscle), cofilin 1, non-muscle, cofilin 2 (muscle), cofilin 2, muscle,
		T		Commit i (non-muscle), comm 1, non-muscle	expressed sequence AW987265
					Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched
1659	16610 D28557		ر د ا	Cold chock domain and in A	library, clone:2610205119:Y box protein 1, full insert sequence, Mus musculus Y-box
			1		binding protein (oxyR) mRNA, partial cds, cold shock domain protein A

TABLE3	3			5.453	- 1
SEO		GenBank Acc.	\$ 1.5	Design to the design of the second se	700-01-WO/2105485
۵	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Seguence Chreter Title
					EST, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN
					CHAIN PRECIED IN THE
					COLLAGEN AI PHA 1(1) CHAIN DEFLIDED IN COLLAGEN AI TOTAL MAIN TO THE WAY
					PROCOLLAGEN AT PHA 11/11 CHAIN PRECIIES OF Manufactures of Man
					protein 29, Mus musculus. Similar to RIKEN CONA 170005110 2000
					MGC:28741 IMAGE:4481590 mRNA complete cds colleges than 17 of the 2
					(Goodbasture antiden), expressed segmence AM742721 procedure to a price of the continuous antident.
1405					1, procollagen, type IV, alpha 1, procollagen, type IV, alpha
5		133/2 AIZ314/2	1, 9	collagen, type I, alpha 1, procollagen, type I, alpha 1	alpha 5. procollagen five V/ alpha 1. mitative emit
					EST, Weakly Similar to CATT HUMAN COLLAGEN ALPHA TITL HAIN
		-			PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLI AGEN AI PHA 1/11
					CHAIN PRECURSOR IM misculus ESTE Westly similar to 044 (1) 180
	<del></del>				COLLAGEN ALPHA 1(1) CHAIN PRECIIES IN Equipment CETA WASHINGTON
					PROCOLLAGEN AT PHA 1/11 CHAIN DRECTIDE OF IN TRIBUTION OF THE PROCOLLAGEN AT PHA 1/11 CHAIN DRECTIDE OF IN TRIBUTION OF THE PROCOLLAGEN OF THE PROCESS OF TH
					protein 20 Miss misseules Giant Charles and Theory of Maria Control of the Contro
		•			Protein 23, Mus musculus, Similar to KiKEN cDNA 1700051112 gene, clone
					McC. 28741 IMAGE: 4481590, mRNA, complete cds, collagen, type IV, alpha 3
					(Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha
1713	15571 M27207			long the form the for	1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV.
				collegen, type I, alpina I, procollegen, type I, alpha 1	alpha 5, procollagen, type VI, alpha 1, putative emu1
					E.S.I., WEARIN SIMILIAR TO CALLAGEN ALPHA 7(1) CHAIN
					PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(t)
	_	_			CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CA11_HUMAN
	-				COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs. Weakly similar to
					PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus]. F-box only
					protein 29, Mus musculus, Similar to RIKEN cDNA 1700051112 gene. clone
					MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV. alpha 3
			-		(Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha
2696	15569 778279				1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV
	2000		C, 9, 00	collagen, type I, apna 1, procollagen, type I, alpha 1	alpha 5, procollagen, type VI, alpha 1, putative emu1

TABLE 3	က		Parket State of the State of th	1000	で記事が出		
SEO		GenBank Acc.	L	r.			Atty. Ref. 44921-5090-01-WO/2105485
Ω.	GLGC ID No.	No.		Model Code Human Hom	omologous Known Gene Name	ne Name	Hüman Homologous Sequence Cluster Title
2696		15570 Z78279	c, f, g, j, k	collagen, ty	collagen, type I, alpha 1, procollagen, type I, alpha 1	gen, type I, alpha 1	ES1, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein 29, Mus musculus, Similar to RIKEN cDNA 1700051112 gene, clone MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV, alpha 5, procollagen, type VI, alpha 1, putative emu1
2	6153,	6153 AA875531	,	collagen, typ	collagen, type I, alpha 2, procollagen. type I, alpha 2	en. fvoe I. aloha 2	EST, Moderately similar to 0806162B cytochrome b [M.musculus], EST, Moderately similar to 810024B cytochrome b [H.sapiens], EST, Weakly similar to 810024B cytochrome b [H.sapiens], EST, Weakly similar to 0812187A cytochrome b [Rattus norvegicus] [R.norvegicus], EST, Weakly similar to 810024M URF 6 [H.sapiens], F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor
233	6158	6158 AA859284	f, g	collagen, typ	collagen, type I, alpha 2, procollagen, type I, alpha 2	en, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinobastoma binding protein 4.
2376	6154	6154 NM_053356	j.,	collagen, typ	collagen, type I, alpha 2, procollagen, type I, alpha 2	en, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1
2376	6155	6155 NM_053356	D	collagen, typi	collagen, type I, alpha 2, procollagen, type I, alpha 2	en, type I, alpha 2	P-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1
2376	6156 N	6156 NM_053356	6	collagen, type	e I, alpha 2, procollagen, type I, alpha 2	อก, type I, alpha 2	collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1
2376	6157N	6157 NM_053356	<del>ار</del> ع	collagen, type	e I, alpha 2, procollagen, type I, alpha 2	ม, type l, alpha 2	r-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1

an Hi mologous Known Gene Name  Jen, type III, alpha 1 (Ehlers-Danlos syndrome type en type III, alpha 1 sent type III, alpha 1 (Ehlers-Danlos syndrome type of type III, alpha 1 sent type III, alpha 1 sent type V, alpha 1, procollagen, type III, alpha 1 sent iii iii iii iii iii iii iii iii iii i	The second secon	
GC ID No.  Model Code Human H. mologous Known Gene Name  collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1 s  Research (Code Human H. mologous Known Gene Name IV, autosomal dominant), procollagen, type III, alpha 1 s  collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1 s  collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1 s  collagen, type V, alpha 1, procollagen, type V, alpha 1 h  men		12105485
collagen, type III, aipha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, aipha 1   F F F F F	Human Homologous Sequence Cluster Title	4
16426 X70369 c, g, bb IV, autosomal dominant), procollagen, type III, alpha 1 short syndrome type 6 IV, autosomal dominant), procollagen, type III, alpha 1 short syndrome type 6 IV, autosomal dominant), procollagen, type III, alpha 1 short syndrome type V, alpha 1, h h coollagen, type V, alpha 1, h h	ndrome type III, alpha 1	AGEN 13 T., SOR (SOR ein ein flad Danlos)
2262 AA859757 hh collagen, type V, alpha 1, procollagen, type V, albha 1	90	AGEN SOR in in factor anlos
1	EST, Weakly similar to CGHUTV collagen alpha 1(V) chain precursor [H.sapiens], Homo sapiens cDNA FLJ30442 fs, clone BRACE2009212, Homo sapiens proline-nich acidic protein mRNA, complete cds, Mus musculus, clone IMAGE:3490511, mRNA, partial cds, collagen, type V, alpha 1, collagen, type X1, alpha 1, MGC2705, procollagen, type V, alpha 1, procollagen, type V, alpha 1, procollagen, type V, alpha 1, procollagen, type V, alpha 3, procollagen,	ins], 1, 1, gen,

WO 2004/063334 PCT/US2004/000240

TABLE 3	E3	10000000000000000000000000000000000000	1、1の連門はあるなかっ	The state of the s	
SEO		GenBank Acc.	9	The state of the s	Attv. Ref. 4492/15090-01-WOJ2/05485
≘	GLGC ID No.	D Ñō.		Model Code Human Homologous Known Gene Name	, j
2544		25237 NM_134452		collagen, type V, alpha 1, procollagen, type V, alpha 1	EST, Weakly similar to CGHU1V collagen alpha 1(V) chain precursor [H.sapiens], Homo sapiens cDNA FLJ30442 fis, done BRACE2009212, Homo sapiens prolinerich acidic protein mRNA, complete cds, Mus musculus, clone IMAGE:3490511, mRNA, partial cds, collagen, type V, alpha 1, collagen, type XI, alpha 1, endoplasmic reticulum chaperone SIL1, homolog of yeast, hypothetical protein MGC2705, procollagen, type V, alpha 1, procollagen, type V, alpha 3, procollagen, type XI, alpha 1
1300		00007			EST, Weakly similar to CGHU2V collagen alpha 2(V) chain precursor [H.sapiens], EST, Weakly similar to 149607 procollagen type V alpha 2 - mouse [M.musculus], ESTs, Weakly similar to 149607 procollagen type V alpha 2 - mouse [M.musculus], ESTs, Weakly similar to S41067 collagen alpha 1(III) chain - rat [R.norvegicus], Musmusculus, Similar to putative protein phosphatase 1 nuclear targeting subunit, clone IMAGE:3157989, mRNA, partial cds, RIKEN, ADNA, 2000000000
2050		21443 NM_019262	<u>ير</u> رو	collagen, type V, alpha 2, procollagen, type V, alpha 2 complement component 1, q subcomponent, beta bolynentide	type V, alpha 2, procollagen, type III, alpha 1, procollagen, type V, alpha 2
2050	21444	21444 NM_019262	jj, kk	complement component 1, q subcomponent, beta polypeptide	
2304	1727h	1727 NM_031642	jj, KK	ar element binding protein	DNA segment, Chr 12, ERATO Doi 427, expressed, EST, Moderately similar to core promoter element binding protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to core promoter element binding protein [Rattus norvegicus] [R.norvegicus], Kruppel-like factor 7 (ubiquitous), core promoter element binding protein
2040	15347 N	15347 NM_019222 4467 NM_012520	= 4	protein 1B, coronin, actin-binding	ESTs, Moderately similar to CO1B_RAT Coronin 1B (Coronin 2) [R.norvegicus], coronin 6, coronin, actin binding protein 1B, coronin, actin binding protein 1C, hypothetical protein DKFZnZ62146
1739	4468	4468 NM 012529	o . o	Greatine Kinase, brain Greatine kinase, brain	
1/42	2035711	20357 NM_012534	pp'30	crystallin, alpha A	Crystallin, alpha A expressed semions Al322427
					יין מלאומי יי בעלו בפפרת פפלחם וכם אוסרסילים

TABI 5	~			1000年の日本の日本の日本の日本の日本の日本の日本の日本の日本の日本の日本の日本の日本の	
SEO		GenBank Arr	F		Atty. Ref. 44921-5090-01-WO/2105485
<u>C</u>	0.5	No.		Model Code Human Ho nologous Known Gene Name	Human Homologous Sequence Cluster Title
					ESTs, Moderately similar to T46637 transcription factor 1, neural - rat [R.norvegicus], ESTs, Weakly similar to A35804 nucleolin [H.sapiens], ESTs, Weakly similar to alpha-crystallin chain R IM muscribus]. Homo explans mDNA:
					CDNA DKFZp434E0922 (from clone DKFZp434E0922), Mus musculus 10, 11 days
			<u>.</u>		embryo whole body cDNA, RIKEN full-length enriched library,
1829		13723 NM_012935	aa, bb	crystallin, alpha B	done.28 rocust i 8:myelin transcription factor 1-like, full insert sequence, crystallin, alpha B, myelin transcription factor 1-like, nucleolin
					EST, Highly similar to CRB2_MOUSE BETA CRYSTALLIN B2 (BP) [R.norvegicus],
					EST, Weakly similar to A Chain A, The N-Terminal Domain Of Beta-B2-Crystallin
1830	487	487 NM 012937	_ =	crystallin. beta 82	Resembles The Putative Ancestral Homodimer [M.musculus], Homo sapiens, done
2312	8844	8844 NM_031690	q	aystallin, beta B3	absent in melanoma 1, absent in melanoma 1-like, crystallin heta R3
2035		18572 NM_019201	n, o	C-terminal binding protein 1	C-terminal binding protein 1, Homo sapiens mRNA; cDNA DKFZp434B0914 (from clone DKFZp434B0914); partial cds
2035	18573	18573 NM_019201	<u></u>	C-terminal binding protein 1	C-terminal binding protein 1, Homo sapiens mRNA; cDNA DKFZp434B0914 (from
1657	25041	250411014014	,	cyclin D1, cyclin D1 (PRAD1: parathyroid adenomatosis	EST, Moderately similar to JC2342 cyclin D1 - rat [R.norvegicus], cyclin D1, cyclin
				cyclin D1, cyclin D1 (PRAD1: parathyroid adenomatosis	POLICIAND I. parattiyloto adenomatosis 1) FST Moderately similar to 102342 wells D4 and 12 materials and and 12 materials and
2677	24232 X75207	X75207	aa, bb	1)	DO , model acety strings to 502342 cyclin D1 - rat [K.norvegicus], cyclin D1, cyclin D1, cyclin D1 (PRAD1: parathyroid adenomatosis 1)
1825	20757	20757 NM_012923	c, dd	cyclin G, cyclin G1	ESTs, Weakly similar to CGG1_RAT Cyclin G1 (Cyclin G) [R.norvegicus], cyclin G, cyclin G2. cyclin I
9,				cyclin-dependent kinase inhibitor 3 (CDK2-associated	
1468	14430,	14430 AIZ30798	_	dual specificity phosphatase)	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
1804	7823	2853 NM_012838	0'u	cystatin B, cystatin B (stefin B)	cystatin B, cystatin B (stefin B)
		-			ESTs, Moderately similar to CYTC MOUSE CYSTATIN C PRECURSOR [M.musculus], ESTs, Weakly similar to CYTC MOUSE CYSTATIN C PRECURSOR
				cystafin C cystafin C famyloid annionathy and corretain	[M.musculus], RIKEN cDNA 1110017E11 gene, RIKEN cDNA 9230101F08 gene,
1482	24327 A	24327 AI231292	gg	hemorrhage)	cystatin C, cystatin SA, cystatin SN cystatin SN
2483	1892 N	1892 NM_057144	a, o, x, ee, ff, kk	cysteine and glycine-rich protein 3 (cardiac LIM protein), cysteine-rich protein 3	RIKEN cDNA 1200007021 gene, cysteine and glycine-rich protein 3 (cardiac LIM protein), cysteine-rich protein 3

TABLE 3	3	· · · · · · · · · · · · · · · · · · ·			Total Control Control Foot Foot Action Act
SEQ	Ger Grand No	GenBank Acc.	Model Code		MILY. LEE, 4482 1-5030-0 1-W
2	פרפי וה	NO.	Intodel code	wodel code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					C OXIDASE derately similar to
				Cytichiome c oxidese subunit IV icoform 4 autorismo	COX4_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSO
1968		14694 NM_017202	gg	oxidase, subunit IVa	Systems of oxidase subuling the solution of the control of the control oxidase subunit IV isoform 1, cytochrome c oxidase, oxidase, subunit IVa
				cytochrome c oxidase subunit IV isoform 2, cytochrome c	+
2383		21866 NM_053472	u, v	oxidase, subunit IVb	Cytochrome c oxidase subunit IV isoform 2. cytochrome c oxidase subunit IVh
				cytochrome c oxidase subunit VIa polypeptide 1,	
138		23574 AI104520	표	cytochrome c oxidase, subunit VI a, polypeptide 1	
-				cytochrome P450, 1a2, aromatic compound inducible,	
				cytochrome P450, subfamily I (aromatic compound-	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily t
1743	<u>8</u>	20; 04 NM_012541	aa, bb	inducible), polypeptide 2	(aromatic compound-inducible), polypeptide 2
				cytochrome P450, 1b1, benz[a]anthracene inducible,	
,			_	cytochrome P450, subfamily I (dioxin-inducible),	cytochrome P450, 1b1, benz/alanthracene inducible, cytochrome P450, suhfamily I
1831	<u>s</u> t	190 NM 012940	j. K	polypeptide 1 (glaucoma 3, primary infantile)	(dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)
2000	- 40	07.770		cytochroms P450, 2e1, ethanol inducible, cytochrome	
1077	<u>₹</u>	41 IUINM_U31543	۵, ۷	P450, subtamily IIE (ethanol-inducible)	
2004	77.44	47.44 NIM 004540		cytochrome P450, 2e1, ethanol inducible, cytochrome	
1077	=  	WI_US 1343	>	P450, subramily IIE (ethanol-inducible)	
				cytochrome P450, 51, cytochrome P450, 51 (lanosterol	
1832	205281	20528 NM_012941	E,	14-alpha-demethylase)	cytochrome P450, 51, cytochrome P450, 51 (lanosterol 14-alpha-demethylase)
					EST, Moderately similar to 165981 fatty acid omega-hydroxylase [H.sapiens], Mus
					musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837,
					mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone
					MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22
7	77200			cytochrome P450, subfamily IV B, polypeptide 1,	gene, cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11.
2	20/14 M149/2	1149/2	s, t	cytochrome P450, subfamily IVB, polypeptide 1	expressed sequence Al314743
					ES1, Moderately similar to 165981 fatty acid omega-hydroxylase [H.sapiens], Mus
					musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837,
					MKC 25072 MAD TANABED Similar to cytochrome P450, 4a10, clone
				cytochrome P450, subfamily IV B, polypeptide 1,	moc.c.5312 impoc4240303, inicity, complete cas, Riken cund A230105L22 gene, cytochrome P450. 4a10. cytochrome P450. subfamily IVA polyneptide 11
1303	20921 N	20921 NM_016999	s, t	cytochrome P450, subfamily IVB, polypeptide 1	expressed sequence Al314743

TABL	E3		100	(活跃) (経済がた)	
SEQ ID GL	GLGC ID No.	GenBank Acc. D No.		Pana Nama	View of the second of the seco
1744		1762 NM_012543		D site albumin promoter binding protein, D site of albumin promoter (albumin D-box) binding protein	D site albumin promoter binding protein, D site of albumin D site albumin promoter binding protein, D site of albumin D-box) bromoter (albumin D-box) binding protein, protein, D site of albumin D-box)
1744		1763 NM_012543	hh	D site albumin promoter binding protein, D site of albumin promoter (albumin D-box) binding protein	D site albumin promoter binding protein, D site of albumin D site albumin promoter binding protein, D site of albumin D-box) promoter (albumin D-box) binding protein
2174	- 1	17226 NM_024131	b, c, u, v	D-dopachrome tautomerase	D-dopachrome tautomerase, EST, Moderately similar to DOPD_HUMAN D-DOPACHROME TALITOMERASE IN serions
2174		17227 NM_024131	ပ	D-dopachrome tautomerase	D-dopachrome tautomerase, EST, Moderately similar to DOPD_HUMAN D.
2691		18352 Z12298	aa, bb		RIKEN CDNA 5530600M07 gene, decorin, expressed sequence C85409, extracellular matrix protein 2 family consists of decorins.
					EST, Weakly similar to diacylglycerol Kinase zeta [Raftus norvegicus] [R.norvegicus], ESTs, Highly similar to KDGA MOUSE DIACYLGLYCEROL
					NIVASE, ALPHA [M.musculus], ES1s, Weakly similar to diacylglycerol kinase [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to KDGA MOUSE DIACYLG! YCFROL KINASE ALPHA M.musculus], diaculus diaculus
2260		1638 NM_031143	d, e, ii, kk	diacylglycerol kinase zeta, diacylglycerol kinase, zeta ((104kD)	(80 kDa), diacylglycerol kinase, gamma 3, diacylglycerol kinase, iota, diacylglycerol kinase, zeta (104kD)
					ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to
-	19424,	19424 AA850922	h, i	dimethylarginine dimethylaminohydrolase 1	dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrologo 1 dimethylaminohydrologo 1 dimethylaminohydrologo 1 dimethylaminohydrologo 1
					ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.saniens] ESTs, Weakly similar to
က	19421	19421 AA945152	qq	dinethylarginine dimethylaminohydrolaso 1	dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine
					uintertyläminohydrolase 1, dimethylarginine dimethylaminohydrolase 2 ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYI AMINOHYDROI ASE 1 IL SONIOGI SETT. MACHALLER II.
				i i i i i i i i i i i i i i i i i i i	dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine
2104	19423	19423 NM_022297	u, v	dimethylarginine dimethylaminohydrolase 1	dimethylaminohydrolase I vatus not vegicus] [K. norvegicus], dimethylaminohydrolase 1, dimethylaminohydrolase 2

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SEQ ID	GLGC ID No.	GenBank Acc. No.		Gene Name	Amy. Ker. 44921-5090-01-WO/2/105485 Human-Homologous Sequence-Cluster Title
774		7785,41008758	¥	dipeptidy/peptidase 4, dipeptidy/peptidase IV (CD26, adenosine deaminase complexion protein 2)	ESTs, Weakly similar to DPP4 MOUSE DIPEPTIDYL PEPTIDASE IV [M.musculus], ESTs, Weakly similar to DPP4_RAT Dipeptidyl peptidase IV (DPP IV) (GP110 glycoprotein) (Bile canaliculus domain-specific membrane glycoprotein) [R.norvegicus], dipeptidylpeptidase 4, dipeptidylpeptidase 8, fibroblast activation
153		6054 AA818658	p, q, ee, ff	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding epidermal growth factor-like growth factor	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth
1833	223	223 NM_012945	a, p, q, ee, f	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding a, p, q, ee, ff epidermal growth factor-like growth factor	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding epidermal growth factor-like growth
1796	1952	1952 NM_012788	<u>66</u>	discs, large (Drosophila) homolog 1, discs, large homolog 1 (Drosophila)	Mus musculus mRNA for mDLG6B, complete cds, discs, large (Drosophila)  discs, large (Drosophila) homolog 1, discs, large homolog 1, discs, large (Drosophila) homolog 5, discs, large homolog 1  (Drosophila) (Drosophila) quanylate kinase 1
1951	241061	24106 NM_017141	s, t, bb	DNA polymerase beta, polymerase (DNA directed), beta	Mus musculus, Similar to DNA polymerase beta, clone MGC:6386 IMAGE:3581916, mRNA, complete cds, polymerase (DNA directed), beta
1951	24107	24107 NM_017141	-	DNA polymerase beta, polymerase (DNA directed), beta	Mus musculus, Similar to DNA polymerase beta, clone MGC:6386 IMAGE:3581916, mRNA, complete cds, polymerase (DNA directed), beta
1652	18686 D00729	00729	g, hh	dodecenoyl-Coenzyme A delta isomerase (3,2 trans- enoyl-Coenyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase), dodecenoyl-Coenzyme A dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
1999 1950 2218	18687 N 492 N 1719 N	18687 NM_017306 492 NM_017140 1719 NM_031024	hh J. m, n, aa ii. xk	dodecenoyl-Coenzyme A delta isomerase (3,2 trans- enoyl-Coenyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) dopamine receptor 3, dopamine receptor D3	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase), delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) dodecenoyl-Coenzyme A isomerase) dodecenoyl-Coenzyme A isomerase) dopamine receptor 3, dopamine receptor 3, dopamine receptor 3, dopamine receptor 1, dopamine receptor 3, dopamine receptor 3, dopamine receptor 1, dopamine receptor 3
2427	15996 N		9	cificity phosphatase 1, protein tyrosine stase, non-receptor type 16	Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity phosphatase 1, expressed sequence BB104621, protein tyrosine phosphatase, non-receptor type 16

4B)	2		9°	3.0	AHP DAMA NO CONTRACTOR OF A PROPERTY A HP DAMA FOR A MANAGEMENT AND A PROPERTY
O		GenBank Acc.		Model Code Human Ho nologous Known Gene Name	Inmolonojis Sean
1797		24113 NM_012791		dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	ESTs, Moderately similar to DYRA_RAT Dual-specificity tyrosine-phosphorylation regulated kinase 1A (Protein kinase minibrain homolog) (MNBH) (RP86) (Dual specificity YAK1-related kinase) [R.norvegicus], ESTs, Weakly similar to DYRK MOUSE DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE [M.musculus], Mus musculus, clone MGC:6699 IMAGE:3584001, mRNA, complete cds, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a
1797		18135 NM_012791	e, gg, II	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	ESTs, Moderately similar to DYRA_RAT Dual-specificity tyrosine-phosphorylation regulated kinase 14 (Protein kinase minibrain homolog) (MNBH) (RP86) (Dual specificity YAK1-related kinase) [R.norvegicus], ESTs, Weakly similar to DYRK MOUSE DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE [M.musculus], Mus musculus, clone MGC:6699 IMAGE:3584001, mRNA, complete cds, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A.
2415		11 18 NM_053655	٦	dynamin 1-like	ESTs, Moderately similar to dynamin 2 [Mus musculus] [M.musculus], Mus musculus, Similar to KIAA0820 protein, clone MGC:37713 IMAGE:5066120, mRNA, complete cds, Mus musculus, Similar to dynamin 1-like, clone MGC:41233 IMAGE:1395338, mRNA, complete cds, dynamin 1-like, dynamin 2
1895		1693 NM_013199		dynamin 2	ESTs, Highly similar to A53165 dynamin II isoform aa - rat [R.norvegicus], ESTs, Moderately similar to dynamin 2 [Mus musculus] [M.musculus], Mus musculus, Similar to KIAA0820 protein, clone MGC:37713 IMAGE:5066120, mRNA, complete cds, Mus musculus, Similar to dynamin 1-like, clone MGC:41233 IMAGE:1395338, mRNA, complete cds, RIKEN cDNA 1200011N24 gene. dynamin 2
1775	425 N	425 NM_012698		dystrophin (muscular dystrophy, Duchenne and Becker types), dystrophin, muscular dystrophy	dystrobrevin alpha, dystrobrevin, beta, utrophin
1746	23868 N	23868 NM_012551	a, h, l, p, q, y, z, ee, ff	early growth response 1	early growth response 1, expressed sequence AI835008
1746	23869 N	23869 NM_012551		early growth response 1	early growth response 1, expressed sequence AI835008
7	2007 I IIV	100710-141	b, q, y, c,	early growin response 1	early growth response 1, expressed sequence AI835008

TABLE 3	33		1.37	在 一種一	(40)
SEQ	i i	GenBank Acc.			
Ω.	GC ID	0.	Model Code	Model: Code Human Homologous Known Gene Name	Human-Homologous-Sequence-Cluster Title
1746		23872 NM_012551	p, q, y, z	early growth response 1	early growth response 1, expressed sequence A1835008
2020	ı	M_019137	l, m	early growth response 4	RIKEN CDNA 4930563M09 gene, early growth response 4
					ESTs, Weakly similar to CD39 MOUSE VASCULAR ATP-
					DIPHOSPHOHYDROLASE [M.musculus], RIKEN cDNA 2010320H07 gene, ecto-
1450	23042 AI230130	230130	:=	o social statement of the section of	apyrase, ectonucleoside triphosphate diphosphohydrolase 1, ectonucleoside
	1	2012	2, 6	octonicocolde aipinospirate aipinospirate 2	urpnospnare dipnospnonydrolase 3, lysosomal apyrase-like 1
			_		
2476		9528 NM 057104		ectonucleotide pyrophosphatase/phosphodiesterase 2	ectonucleotide pyrophosphatase/phosphodiesterase 2, ectonucleotide
		100 100		(autotaxiii)	pyrophosphatase/phosphodiesterase 2 (autotaxin)
					EGL nine homolog 3 (C. elegans), ESTs, Moderately similar to A53770 growth
					factor-responsive protein, vascular smooth muscle - rat [R.norvegicus], ESTs,
					Weakly similar to A53770 growth factor-responsive protein, vascular smooth muscle
					- rat [R.norvegicus], Mus musculus, Similar to EGL nine homolog 3 (C. elegans).
-				EGL nine homolog 3 (C. elegans), egl nine homolog 3 (C.	EGL nine homolog 3 (C. elegans), egi nine homolog 3 (C. clone MGC:36685 IMAGE:5371854, mRNA, complete cds, egi nine homolog 1 (C.
7067	13.23INI	13.23 NM 019371	c, aa, bb, ii	elegans)	elegans), egl nine homolog 3 (C. elegans)
					EGL nine homolog 3 (C. elegans), ESTs, Moderately similar to A53770 growth
					factor-responsive protein, vascular smooth muscle - rat [R.norvegicus], ESTs,
					Weakly similar to A53770 growth factor-responsive protein, vascular smooth muscle
			;		<ul> <li>rat [R.norvegicus], Mus musculus, Similar to EGL nine homolog 3 (C. elegans),</li> </ul>
1000			, aa, bb,	EGL nine homolog 3 (C. elegans), egl nine homolog 3 (C.	EGL nine homolog 3 (C. elegans), egl nine homolog 3 (C. clone MGC:36685 IMAGE:5371854, mRNA, complete cds, egl nine homolog 1 (C.
7007	13524 NIV	1%24 NM_019371	촟	elegans)	elegans), egl nine homolog 3 (C. elegans)
4-					EST, Moderately similar to Peroxisomal enoyl hydratase-like protein; enoyl
				`	hydratase-like protein, peroxisomal [Rattus norvegicus] [R.norvegicus], enoyl
:				enoyl Coenzyme A hydratase 1, peroxisomal, enoyl	Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1.
2143	20925 NM_022594	022594	g, hh	coenzyme A hydratase 1, peroxisomal	peroxisomal
					EST, Highly similar to putative protein-fyrosine kinase [Homo sapiens] [H.sapiens],
3					Eph receptor B1, Eph receptor B2, Eph receptor B3, EphB1, expressed sequence
7044	2464 X13411		u, v		AW456895, expressed sequence AW488255
1805	338 NM	_012843	_		epithelial membrane protein 1
0	77.42.7			epoxide hydrolase 1, microsomal, epoxide hydrolase 1,	
1806	17:41 NM_012844		C, d	microsomal (xenobiotic)	epoxide hydrolase 1, microsomal, epoxide hydrolase 1, microsomal (xenobiotic)

TABI E	ers Lái		7. Ch	The second secon	
250	·    -	GenBank And		Size Williams	L
≘	0 0976	No.	Model Code	Model Code Human Ho nologous Known Gene Name	Human Homologous Sequence Cluster Title
					EST, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat
				·	[R.norvegicus], ESTs, Highly similar to EFHU1 translation elongation factor eEF-1
					alpha-1 chain [H.sapiens], ESTs, Weakly similar to S21055 translation elongation
		_			factor eEF-1 alpha chain - rat [R.norvegicus], G1 to S phase transition 1, G1 to
0360		NIM ODDEDO	- :		phase transition 1, G1 to phase transition 2, eukaryotic translation elongation factor
7007		2442U INIM 033339	J, KK, II	eukaryotic translation elongation factor 1 alpha 2	1 alpha 1
					ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs,
					Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs,
					Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation
					factor, Mus musculus, Similar to elongation factor G2, clone MGC:28160
					IMAGE:3984129, mRNA, complete cds, U5 small nuclear ribonucleonnotein 116
					kDa, U5 snRNP-specific protein. 116 kD. eukarvotic translation elongation factor 2
1980		17561 NM_017245	E',	eukaryotic translation elongation factor 2	expressed segmence AI451340
					ESIS, Highly similar to EF2 RAT Elongation factor 2 / FE-2/1R normanicus 1 ESTs
					Weakly similar to EF2 MOUSE Flondation factor 2 (FE-2) IM musculus LECTS
					Weakly similar to EF2 RAT Floroation factor 2 /EE-3 /R ponyenious C. elements
					factor, Mus misculus, Similar to elongation factor G2, elong MCC-28460
	_				IMAGE:2084170 mPMA complete and The configuration of the configuration o
					The life and the limited confined cost of single fluctual modification and the life
1080	175.52 N	176.52 NIM 01704E	-		KDa, US SIIKNP-Specific protein, 116 kD, eukaryotic translation elongation factor 2,
200	3	C47/10   MIN	(1, 1	eukaryouc translation elongation factor 2	expressed sequence Al451340
1206	03450	1460470	-		ESTs, Weakly similar to EUKARYOTIC INITIATION FACTOR 4A-II [M.musculus],
1200	770107	23132/AI109170		eukaryotic translation initiation factor 4A, isoform 2	eukaryotic translation initiation factor 4A, isoform 2
					DNA segment, Chr 1, ERATO Doi 692, expressed, ESTs, Highly similar to
					EUKARYOTIC TRANSLATION INITIATION FACTOR 5 [R.norvegicus], KIAA1856
C/07	18/13	18/13 NM_020075	p, q, s, t	eukaryotic translation initiation factor 5	protein, eukaryotic translation initiation factor 5
					DNA segment, Chr 1, ERATO Doi 692, expressed, ESTs, Highly similar to
1					EUKARYOTIC TRANSLATION INITIATION FACTOR 5 IR. norvegicus], KIAA1856
20/07	161/81	C/0070_MN CL/8L	ee' #	eukaryotic translation initiation factor 5	protein, eukaryotic translation initiation factor 5
	-			latty acid binding protein 3, muscle and heart, fatty acid	EST, Moderately similar to FABH MOUSE FATTY ACID-BINDING PROTEIN,
2407	101701		·	binding protein 3, muscle and heart (mammary-derived	HEART [M.musculus], fatty acid binding protein 3, muscle and heart, fatty acid
4017	10/601	10470 NINI 024102	aa	growth inhibitor)	binding protein 3, muscle and heart (mammary-derived growth inhibitor)

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	GLGC ID No.	No.		me	mologous Seguence Clucter IIIIa	015
					ES1s, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyr-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus	
					musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, ctone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty,	
431	20985	20985 AA893242		fatty acid Coenzyme A ligase, long chain 2, fatty-acid- Coenzyme A ligase, long-chain 2	acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-	
				ליינים לי	COA SYRUREISSE, IIDIDOSIS-related protein lipidosin ESTS, Weakly similar to Tatty acid Coenzyme A ligase, long chain 2; acetvi-	
					Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus]. Mus	
					musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds. Musculus, Similar to hundthetical	
			,		protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty	
5	Š			fatty acid Coenzyme A ligase, long chain 2, fatty-acid-	acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 1, gonadotronin-regulated long chain 2, and	
	TOSKO Z	Z0xx80 A4893242		Coenzyme A ligase, tong-chain 2	CoA synthetase, lipidosis-related protein lipidosin ESTS, Weakly Similar to Tatty acid Coenzyme A ligase Tong chain 2: acata	
					Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1	•
	_				(ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus	
_					musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744	
					IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical	
					protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty	
	,		a, h, l, ee, ff, f	a, h, l, ee, ff, fatty acid Coenzyme A ligase. long chain 2 fatty-acid-	deta Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long chain 5,	
972	20983 AI044900	N044900	꿏	Coenzyme A ligase, long-chain 2	rany-actur-coertzynie A ilgase, long-chain 1, gonadotropin-regulated long chain acyl- CoA synthetase, linidosis-ralated protein linidosis	
					יונים ביים וליונים ביים וכומים ליונים	

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SEO		GenBank Acc.	L	The second secon	Atty, Ref. 44921-5090-01-WO/2105485
Ω	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					ES1s, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744
					IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty
1668	1	20984 D90109		fatty acid Coenzyme A ligase, long chain 2, fatty-acid- Coenzyme A ligase, long-chain 2	acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase. Ilindosis-related protein lindosis.
2410		13005 NM_053623	j, k, y, z	fatty acid-Coenzyme A ligase, long chain 4, fatty-acid- Coenzyme A ligase, long-chain 4	and of the secon
1319	10182,	10182 Al176185	p, q, 9g	FBJ osteosarcoma oncogene, v-fos FBJ murine osteosarcoma viral oncogene homolog	FBJ murine osteosarcoma viral oncogene homolog B, FBJ osteosarcoma oncogene, FBJ osteosarcoma viral oncogene homolog
2641	10181	10181 X06769	b'd	FBJ osteosarcoma oncogene, v-fos FBJ murine osteosarcoma viral oncogene homolog	FBJ murine osteosarcoma viral oncogene homolog B, FBJ osteosarcoma oncogene, FBJ osteosarcoma oncogene B, v-fos FBJ murine osteosarcoma viral oncogene homolog
2440	208681	20868 NM_053843	kk	Fc fragment of IgG, low affinity Illa, receptor for (CD16), Fc receptor, IgG, low affinity III	
2440	20869	20869 NM_053843	w, x, kk	Fc fragment of IgG, low affinity IIIa, receptor for (CD16), Fc receptor, IgG, low affinity III	
2359	12364 N	12364 NM_033351	e, y, z, ee, ff r	Fc fragment of IgG, receptor, transporter, alpha, Fc e, y, z, ee, ff receptor, IgG, alpha chain transporter	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter
2359	12365 N	12365 NM_033351	9	ter, alpha, Fc	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter
1944	21662 N	21662 NM_017126			ferredoxin 1. similar to RIKEN CONA R230118C17 gene
1944	21663 N	21663 NM_017126	5 ₩	ferredoxin 1	ferredoxin 1, similar to RIKEN cDNA B230118G17 gene
					ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2
2119	8211N	8211 NM_022500	jj, kk	[ ferritin light chain 1, ferritin, light polypeptide	[M.musculus], RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide

TABLE 3	E3	6 7 5 7 7	The state of the s	2、任事の様です。 (1)2、 (1)過ぎとしてく	
SEO		Gen Rank Acc	ŀ	5	Atty. Ref. 44921-5090-01-WO/2105485
	GLGC ID	No.		Model Code Human Homologous Known Gene Name	noe Cluster Title
2119		8212 NM_022500	h, I, kk, II	ferritin light chain 1, ferritin, light polypeptide	1 [Rattus RRITIN L e, ferritin
					ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 4933416E14 nene ferritin linht chain 1 ferritin linht
307		8210 S61960	<u>흥</u>	ferritin light chain 1, ferritin, light polypeptide	dhain 2, ferritin, light polypeptide
1/4/		6477 NM_012559	Z	fibrinogen, gamma polypeptide	
1747	ľ	6478 NM_012559	y, z	fibrinogen, gamma polypeptide	
1607	_	20177 NM_021867	d, jj, &	fibroblast growth factor 16	fibroblast growth factor 16
1/29		13489 M91599	α, dd	fibroblast growth factor receptor 4	
2022		5618 NM_019143	s, t	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1
2022	5622	5622 NM_019143	n, o	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1
2025	6451	6451 NM_019153	f, g	fibulin 5	
1318	6782	6782 AI176170	Ð	FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa)	PK506 binding protein 10 (65 kDa), FK506 binding protein 14 (12kD), FK506 binding protein 1A (12kD), FK506 binding protein 7 (23 kDa), FK506 binding protein 8 (38 kDa)
2155	24346	24346 NM_022701	99		flotilin 1
188	25359 L13202	13202		1 box D3	
2309	18403N		d, ii, KK	four and a half LIM domains 2	EST, Weakly similar to four and a half LIM domains 2 [Rattus norvegicus] [R.norvegicus], activator of CREM in testis, four and a half LIM domains 2, four and
2411	1228 N	1228 NM_053625		ctor, mitochondrial elongation factor G	dual Lin dollalis 3, Vasculal Kab-CAP/I BC-containing
2358	23715N	23715 NM_033237	j, k, y, z, jj, kk	galanin	
2496	206N	506 NM_080586	:=	gamma-aminobutyric acid (GABA) A receptor, gamma 1, gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	gamma-aminobutyric acid (GABA) A receptor, gamma 2, gamma-aminobutyric acid (GABA-A) receptor. subunit aamma 1

TABL		, r., r.			
	j	- Conbont Ann	· · · · · · · · · · · · · · · · · · ·	TANK THE TAN	一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个
ج ا	erec i	D No.		Model Code Human Hr mologous Known Gene Name	Pulp Chief
1749		1 82 NM_012567	s, t	gap Juncticn membrane channel protein alpha 1, gap Junction protein, alpha 1, 43kD (connexin 43)	gap junction membrane channel protein alpha 1, gap junction protein, alpha 1, 43kD
2051		1143 NM_019280	w, x	gap junction membrane channel protein alpha 5, gap junction protein, alpha 5, 40kD (connexin 40)	gap junction membrane channel protein alpha 5, gap junction protein, alpha 5, 40kD
2831		23481 NM_019185	aa, bb	GATA binding protein 6	(GATA hinding motein 5, CATA hinding gratein 6
1934		1383 NM_017088		GDP dissociation inhibitor 1, guanosine diphosphate (GDP) dissociation inhibitor 1	DE Alicenta protein of Corto billianty protein o
2374	-	18949 NM_053345	i=	general transcription factor II A, 2 (12kD subunit), general transcription factor IIA, 2 (12kD subunit)	general transcription factor II A, 2 (12kD subunit), general general transcription factor II A, 2 (12kD subunit), general general transcription factor II A, 2 (12kD subunit), general transcription factor IIA, 2 (12kD subunit)
1748		619 NM_012565	l, m, n, o		
2293		5496 NM_031589	а, ее, ff	glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1	Mus musculus, Similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 1, clone MGC:28167 IMAGE:3985469, mRNA, complete cds, glucose-6-glucose-6-phosphatase, transport (glucose-6-phosphatase, transport protein 1, glucose-6-phosphatase, transport protein 1, glucose-6-phosphatase, transport protein 1 member 1
2293	5497	5497 NM_031589	:=	afe)	Mus musculus, Similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 1, clone MGC:28167 IMAGE:3985469, mRNA, complete cds, glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1, solute carrier family 37 (glycerol-3-phosphate transporter),
2597	15693	15693 S56679	aa, bb		glutamate receptor, ionotropic, AMPA 1, glutamate receptor, ionotropic, AMPA1 (albha 1)
1911	246761	24676 NM_017010	aa, bb	nyl D-aspartate 1, 1 (zeta 1)	
1929	11152N	11152 NM_017073	g c, s, t, kk	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	
1929	11153 N	11153 NM_017073	9 y, kk g	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	
1998	14004 N	14004 NM_017305	aa, bb	glutamate-cysteine ligase , modifier subunit, glutamate- g cysteine ligase, modifier subunit	glutamate-cysteine ligase, modifier subunit, glutamate-cysteine ligase, modifier subunit

TABLE 3	3			は、日本のでは、	
SEO		GenBank Acc		を行うでは、 100mmの 100mm	Atty. Ref. 44921-5090-01-WO/2105485
<u></u>	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name.	Hűman Homológóus Segueñce Cluster Title
					ESTs, Highly similar to GLSK RAT GLUTAMINASE, KIDNEY ISOFORM PRECURSOR [R. norvegicus], ESTs, Moderately similar to GLSK_HUMAN GLUTAMINASE, KIDNEY ISOFORM, MITOCHONDRIAL PRECURSOR (GLS) (L-GLUTAMINE AMIDOHYDROLASE) (K-GLUTAMINASE) II sanions
544		5206 AA925755	_=	glutaminase	glutaminase isoform M precursor, mRNA, complete cds, expressed sequence Al314027, clutaminase
1150		23596 AI105435	qq	glutaryl-Coenzyme A dehydrogenase	expressed sequence Al266902, expressed sequence D17825, glutaryi-Coenzyme A dehydrogenase
2202		1£ 52 NM_030826	aa, gg	glutathione peroxidase 1	ESTs, Weakly similar to GSHC_RAT Glutathione peroxidase (GSHPX-1) (Cellular glutathione peroxidase) [R.norvegicus], glutathione peroxidase 2, glutathione peroxidase 2 (nastrointestinal)
1958	176.861	176.86 NM 017165	<u> </u>	glutathione peroxidase 4, glutathione peroxidase 4	ESTs, Weakly similar to GSHH_RAT Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (PHGPx) (GPX-4) [R.norvegicus], RIKEN cDNA 2310016C16 gene, RIKEN cDNA 3110050F08 gene, glutathione peroxidase 4.
1912	21(13)	21( 13 NM_017014		(priospirolpha ilydroperoxidase) glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2	glutathione peroxidase 4 (phospholipid hydroperoxidase)
1799	261	961 NM_012796	6	glutathione S-transferase theta 2, glutathione S-transferase, theta 2	glutathione S-transferase theta 2 clutathione S-transferase thoto 3
1910	N 7178	8417 NM_017008	as	glyceraldehyde-3-phosphate dehydronenase	ESTs, Moderately similar to G3P MOUSE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE [M.musculus], Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3000002C10:glyceraldehyde-3-phosphate dehydrogenase, full insert sequence, RIKEN cDNA 4930448K20 gene,
1784	25650 N	M_012736		ondrial,	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610001M21:glycerol phosphate dehydrogenase 1, mitochondrial, full insert sequence, glycerol phosphate dehydrogenase 1, mitochondrial, glycerol-3-
2513	19456N	19456 NM_133298	7 7	T	glycoprotein (transmembrane) nmb
2513	4048 N	4048 NM_133298		glycoprotein (transmembrane) nmb	divcoprotein (transmembrane) nmb
2513	4(t49)NI	4(49 NM_133298	c, h, l, n, o, w, x		divcoprotein (transmembrane) nmb
			!		בי

TABLE 3	۲.		1012 - W 40 "		Albert
35		GenBank Acc.			Atty: Ref. 44921-5090-01-WO/2105485
Ō.	GLGC ID No.	No.		Model Code Human Hamologous Known Gene Name	Himan Homologous Continuo Cliestos Titis
133		16. 56 AA818089		glycyl-tRN 4 synthetase	Ahrand PMA curefication
2203	- 1	NM_030828	ပ	glypican 1	gryptrining synutetase olynican 1
					ESTs, Moderately similar to S34421 GTP-binding regulatory protein Gs alpha chain
2019		15975 NM_019132	:=	GIVAS (guanine nucleotide binding protein, alpha stimulating) complex locus, GNAS complex locus	[H.sapiens], GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus, GNAS complex locus, RIKEN CDNA 5530400H20 neme, Sang 31 as protein.
12		21152 X14848	<u>.</u>	ONAD is location of the second	Homo sapiens, Similar to golgi SNAP receptor complex member 1, clone MGC:13657 IMAGE:4250494, mRNA, complete cds, golgi SNAP receptor complex
1941	1 1	NM_017113		gogi siyar receptor complex member 1 granulin	member 1
1941	20746	20746 NM_017113	s, dd, gg	granulin	glanulin
2173	352	352 NM_024127	D d	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damane-inducible, states	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage
2173	353	353 NM_024127	3, ff, gg		growth arrest and DNA-damage-inducible, alpha growth arrest and DNA-damage inducible 45 lepha.
2173	354	354 NM_024127	_	and DNA-damage-inducible 45 alpha, and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage inducible 45 beta, growth arrest and DNA-damage.
1026	17506/	17506 AI070068	p, q	growth arrest and DNA-damage-inducible, beta	growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible alona growth arrest and DNA-damage-inducible.
2473	25290	25290 NM_057100	d, u, v		ESTs, Highly similar to growth arrest specific 6 [Rattus norvegicus] [R.norvegicus], growth arrest specific 6 growth arrest specific 6 arrest specific 6 growth arrest specific 6 growth arrest specific 6.
2301	15767 N	15767 NM_031623	aa, bb, jj, g kk, ll	5	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein, growth factor receptor bound protein 10, growth factor receptor bound protein 14, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 10, growth factor receptor bound protein 14, growth factor receptor bound protein 10, growth factor receptor bound growth factor receptor bound growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth factor growth fact
1902	1396 N	1396 NM_013222 17524 AI010568	p = 3	of liver regeneration (ERV1 growth factor, erv1 (S. er of liver regeneration)	growth factor, augmenter of liver regeneration (ERV1 homolog, S. cerevisiae), growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
1 1	10886 N			e receptor e receptor	growth hormone receptor growth hormone receptor
1936	10888N	4	ji, kk e, r, hh	e receptor	growth hormone receptor growth hormone receptor
DR77	12.ZN	942 NM_031577  u	u gr	hormone	

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אר ה		Genbank Acc.		さらない とない かんしょう しゅうしゅう かんしょう しゅうしゅう かんしょう しゅうしゅう しゅう	*** Ally. Relighted 1-5090-01-WO/2105485
≘	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologicie Sourie and Chiester Take
1807		1249 NM_012850	u, v	for	right some of the first training to the first training to the first training to the first training to the first training to the first training training to the first training tr
2199		862 NM_024487	Æ	GrpE-like 1, mitochondrial, GrpE-like protein cochaperone	grown no mone receptor
2407		0.000		GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa-	
7017		13349 NM_024356	a, y, z	responsive dystonia)	GTP cyclohydrofase 1. GTP cyclohydrolase 1 (dona-responsive dysfania)
2187		15353 NM_024356	j, k, y, z, ii	GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa- responsive dystonia)	TD moleting of the company of the co
1296	_	19118 AI175281		guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	guanidinoacetate N-methyltransferase, guanidinoacetate expressed sequence AA571402, guanidinoacetate N-methyltransferase, methyltransferase
1798		165 17 NM_012793	b, u, v, jj, kk	ا-methyltransferase, guanidinoacetate المالية	
					ESTs, Moderately similar to guanine nucleotide binding protein (G protein) alpha 12
2220		6-30 NM_031034	×, w	guanine nucleotide binding protein (G protein) alpha 12, guanine nucleotide binding protein, alpha 12	Irkatus norvegicus IR.norvegicus), guanine nucleotide binding protein (G protein), alpha 13, guanine nucleotide binding protein, alpha 12, guanine nucleotide binding protein, alpha 13
1870		19549 NM_013106	, m	guanine n.cleotide binding protein (G protein), alpha inhibiting activity polypeptide 3, guanine nucleotide binding protein, alpha inhibiting 3	guanine nucleotide binding protein (6 protein), alpha inhibiting activity polypeptide
139	2143	2143 AA817892	<u> </u>	ide binding protein (G protein), beta	ESTS, Weakly similar to Chain C, Apaf-1 Card in Complex With Prodomain Of Procaspase-9 (SUB 1-95 [H.sapiens], Homo sapiens mRNA expressed only in placental villi, clone SMAP5, PWP2 periodic tryptophan protein homolog (yeast), Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds, guanine nucleotide binding protein), beta polypeptide 2, guanine
				granter transcours bittaining protein, Delaz.	Indiceotide binding protein, beta 2  EST, Weakly similar to B33928 GTP-binding protein beta chain homolog  [H.sapiens], EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE- BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [H.sapiens], Homo sapiens cDNA: FLJ21913 fis, clone HEP03888. Mus musculus. Similar to
2506	14959N	14959 NM_130734 w	go bo w, x	h guanine nucleotide binding protein (G protein), beta ((polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1	hypothetical protein FLJ10385, clone MGC:28622 IMAGE:4220923, mRNA, complete cds, expressed sequence AL033335, guanine nucleotide binding protein (G protein), beta polypeptide 1-like, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1

TABLE 3	رن د		i direction	Part State S	The state of the s
SEO		GenBank Acc.			Auy. Ker. 44821-5090-U1-WO/2105485
₽	GLGC ID No.	No.		Mödel Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					ES1, Weakly similar to 633928 GTP-binding protein beta chain homolog
					[H.sapiens], EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-
					BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [H.sapiens], Homo
					sapiens cDNA: FLJ21913 fis, clone HEP03888, Mus musculus, Similar to
				***************************************	hypothetical protein FLJ10385, clone MGC:28622 IMAGE:4220923, mRNA,
					complete cds, SWI/SNF related, matrix associated, actin dependent regulator of
					chromatin, subfamily b, member 1, expressed sequence AL033335, guanine
				guanine nucleotide binding protein (G protein), beta	nucleotide binding protein (G protein), beta polypeptide 1-like, quanine nucleotide
				polypeptide 2-like 1, guanine nucleotide binding protein,	binding protein (G protein), beta polypeptide 2-like 1, quanine nucleotide binding
007.	- 1	14960 AI171319	w, x	beta 2, related sequence 1	protein, beta 2, related sequence 1
				guanine nucleotide binding protein (G protein), gamma 7,	
				guanine nucleotide binding protein (G protein), gamma 7	guanine nucleotide binding protein (G protein) gamma 12 guanine purkeatide
2175		1879 NM_024138	l, m	subunit	binding protein (G protein), gamma 7
1750		16025 NM_012578	p, q	H1 histone family, member 0	H1 histone family member 0 H1 histone family member 0 (socute society)
			p, q, s, t, ee,		
1750		16026 NM_012578	#	H1 histone family, member 0	H1 histone family, member 0. H1 histone family member 0 (occude-snecific)
1964	1488	1488 NM_017182	h	H2A histone family, member Y	H2A histone family, member Y. RIKEN cDNA 4933437H23 nene
		<u> </u>			EST, Weakly similar to histone H2A.F/Z variant [Homo sapiens] [H.sapiens]. ESTs.
					Highly similar to S03644 histone H2A.Z - rat [R.norvegicus], ESTs, Weakly similar to
					H2AZ_HUMAN HISTONE H2A [H.sapiens], H2A histone family, member Z, Homo
24,41	71007	7.0000 7414			sapiens cDNA FLJ32241 fis, clone PLACE6005231, RIKEN cDNA C530002L11
7#17	1/00/1	1/001 NM_0226/4	d, 9g	H2A histone family, member Z	gene, histone H2A.F/Z variant
					ESTs, Weakly similar to S47532 chaperonin groES [H.sapiens], expressed
1007	000	000000		J KUa protein 1 (chaperonin 10), heat shock	sequence AW108200, heat shock 10 kDa protein 1 (chaperonin 10), heat shock
20	2003	DUSS INM UTSBOO	3,1	10kD protein 1 (chaperonin 10)	10kD protein 1 (chaperonin 10)
			-		ESTs, Weakly similar to S47532 chaperonin groES [H.sapiens], expressed
1824	E024	ED24 NIM 042066		- ·	KDa protein 1 (chaperonin 10), heat shock   sequence AW108200, heat shock 10 kDa protein 1 (chaperonin 10), heat shock
20	4000	NWI_U12900	ш 'ее' п	10KD protein 1 (chaperonin 10)	10kD protein 1 (chaperonin 10)
2505	117001	11709 NM 130431			EST, Moderately similar to heat shock 27kD protein 2 [Rattus norvegicus]
2002		100101	0	KD protein 2	(K.norvegicus), heat shock 27kD protein 2

TABLE 3	<i>:</i> ကျ		:	Consideration of the Constitution of the Const	
SEO		GenBank Acc.			Atty. Ref: 44921-5090-01-WO/2105485
₽	GLGC ID No.	O No.		Model Code Human Homologoüs Known Gene Name	Human Homologous Sequence Cluster Title
1707		1466 M14050	Φ	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	EST, Weakly similar to GR78_RAT 78 KD GLUCOSE-REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN) (BIP) (STEROIDOGENESIS-ACTIVATOR POLYPEPTIDE) [R.norvegicus], expressed sequence AL022860, heat shock 70kD protein 5 (glucose-regulated
					EST, Moderately similar to HS7C_HUMAN HEAT SHOCK COGNATE 71 KDA PROTEI [H.sapiens], EST, Weakly similar to A27077 dnaK-type molecular chaperone [H.sapiens], EST, Weakly similar to A45935 dnaK-type molecular
2185		17764 NM_024351	e, p, r, ee, ff	e, p, r, ee, ff heat shock 70kD protein 8	chaperone hsc70 - mouse [M.musculus], ESTs, Moderately similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], ESTs, Weakly similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], heat shock 70kD protein 8
					EST, Moderately similar to HS7C_HUMAN HEAT SHOCK COGNATE 71 KDA PROTEI [H.sapiens], EST, Weakly similar to A27077 dnak-type molecular chaperone [H.sapiens], EST, Weakly similar to A45935 dnak-type molecular chaperone hsc70 - mouse [M.musculus], ESTs, Moderately similar to HS7C MOUSE HEAT SHOCK COGNATE 71 kDA PROTEIN IN TOTAL TOTAL COGNATE 71 kDA PROTEIN IN TOTAL COGNATE 71 kDA PR
2185	17765	17765 NM_024351	e, p, q, r, ee, ff	heat shock 70kD protein 8	similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN  Miniscribis heat shock 70kD protein 8
1402	16081	16081 A1179610	a, p, q, r, y, z, gg, kk	9) 1	heme oxygenase (decycling) 1
1751	16080	16080 NM_012580	p, q, y, z, kk	p, q, y, z, kk heme oxygenase (decycling) 1	heme oxygenase (decycling) 1
1389	18907	18907 Al178971	۸ ئ	E C 1 1 H H hemoglobin alpha, adult chain 2, hemoglobin, albha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemöglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin alpha 1 hemoglobin alpha 2 hemoglobin alpha 2 hemoglobin alpha 1
					יייייטטטטיין, שניום ני יייייטטייין, פוניום ב, וופוווטטוטעון, וופום ו

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W = 1	alec D	GenBank Acc.	Model Code		Human Homologous Sequence Cluster Title
1406		1686 <u>/</u> Al179971	·	EST, Moderate CHAINS [R.nor 1 AND ALPHA-HEMOGLOBIN 2, hemoglobin, alpha 1 1, hemoglobin,	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1
1406		1687/AI179971	b, c, v	EST, Moderatel CHAINS [R.non 1 AND ALPHA; HEMOGLOBIN 2510042H12 ge hemoglobin alpha, adult chain 2, hemoglobin, alpha 1 1, hemoglobin, a	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1
1869	16841	1684 NM_013096	b, c, v h	EST, Moderately CHAINS [R.norv 1 AND ALPHA-2 HEMOGLOBIN / HEMOGLOBIN / 2510042H12 ger hemoglobin alpha, adult chain 2, hemoglobin, alpha 1 1, hemoglobin, a	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1
1869	1685 <sub>N</sub>	1685 NM_013096	b, c, v he	EST, Moderately CHAINS [R.norw 1 AND ALPHA-2 HEMOGLOBIN A PHA-2 HEMOGLOBIN A 2510042H12 gen 1 1, hemoglobin, alpha 1 1, hemoglobin, al	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, the 1

TABLE 3	E 3		·	1000年	
<u>)</u>		GenBank Acc.			(1) Attv. Ref. 44921-5090-04-1MC/240640E
<u>.</u>	GLGC ID No.	O No.		Model Code Human Homologous Known Gene Name	
					EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-2 1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS IR propositions 1 Diversions 1
1869		1688 NM_013096	0	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, theta 1
					EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT
1869		16-89 NM_013096	b, c, v	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, alpha 3, hemoglobin, alpha 4, hemoglobin, alpha 4, hemoglobin, alpha 6, hemoglobi
305	186.97	18t-97 AA875207		hemoglobin beta chain countlex hemonlokin heta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence Al036344, hemoglobin, beta
839	17830	17830 At011943	O	hemoglobin beta chain complex hemoglobin beta	EXT. Moderately similar to HBB1_RAT Hemoglobin, hemoglobin, delta EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence Al036344, hemoglobin, beta
2356	25468 N	25468 NM_033234	b, c, v		EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence Al036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta
2356	17829.N	17829 NM_033234	ن	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence Al036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta
2356	17832 N	17832 NM_033234	b, c, v he		EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence Al036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta
					della della della della della della della della

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SEO		GenBank Acc.		1	Atty. Ref. 44921-5090-01-WO/2105485
<u></u>	3. GC D	GN O	Model Code	Himan De pologonia Visiona O	
	2		anòn ianow	would could intering the mount of the Name	Human Homologous Sequence Cluster Title
					EST, Highly similar to HSS2 MOUSE HEPARIN SULFATE N-DEACETYLASE/N-
					HEPARIN SULFATE N-DEACETYLASEN-SULFOTRANSFERASE IM musculus
					ESTs, Weakly similar to HSS2_HUMAN HEPARIN SULFATE N-DEACETYLASE/N-
					SULFOTRANSFERASE [H.sapiens], N-deacetylase/N-sulfotransferase (heparan
					glucosaminyl) 2, N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3, N-
					deacetylase/N-sulfotransferase (heparin glucosaminyl) 4, N-deacetylase/N-
875		6758 AI013394	d. ii. kk	benaran sulfate (dimeasonino) 9 O sulfate	sulfotransferase 4, RIKEN cDNA 4930439H17 gene, heparan sulfate (glucosamine)
1587	-			henafitis R vine v interacting protein	3-O-sulfotransferase 3A, heparan sulfate (glucosamine) 3-O-sulfotransferase 4
			T	יילאמיינים בי אוימי א ווינפומרמיות לויטופוע	hepatitis B virus x interacting protein
			hafal		DAZ associated protein 1, Musashi homolog 1(Drosophila), Musashi homolog 2
2269	4235 N	4235 NM 031330			(Drosophila), RIKEN cDNA 4933434H11 gene, expressed sequence AA959857.
	+	Г		neterogeneous nuclear noonucleoprotein A/B	heterogeneous nuclear ribonucleoprotein A/B, musashi homolog 1 (Drosophila)
					ESIS, Highly similar to 152962 FBRNP [H.sapiens], ESIS, Highly similar to
			,		heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar
		-			to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar
					to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing
			-		protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP)
			-		[R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone HSI14320, Mus
					musculus, Similar to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437,
1981	17501 N	17501 NM 017248			mRNA, complete cds, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear
				neterogeneous nuclear noonucleoprotein A1	ribonucleoprotein A1
					ESTS, riginly similar to 152962 FBRNP IH. sapiens], ESTS, Highly similar to
		_			neterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar
					to neterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar
					to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing
					protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP)
					[R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone HS114320, Mus
					musculus, Similar to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437.
1981	17502 NA	17502 NM 017248	E .		mRNA, complete cds, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear
		1		nucleal fiboliucieoprotein A1	ribonucleoprotein A1

<b>TABLE 3</b>	E3	Today in to tou	i o fig.	1、1の間を1・1の122	· delayers · · · · · · · · · · · · · · · · · · ·
SEO		GenBank Acc.	L	A CANADA AND A CAN	Atty. Ref. 44921-5090-01-WO/2105485
≘	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2482		2413 NM_057141	b, g, n, o, u,	heterogeneous nuclear ribonucleoprotein K	r ribo ated i
2482		24 16 NM_057141	-	heterogeneous nuclear ribonucleoprotein K	ESTS, Highly similar to heterogeneous nuclear ribonucleoprotein K, isoform b; dC-stretch binding protein; transformation upregulated nuclear protein [Homo sapiens] [H.sapiens], ESTs, Weakly similar to heterogeneous nuclear ribonucleoprotein K [Rattus norvegicus] [R.norvegicus], heterogeneous nuclear ribonucleoprotein K, poly(rC) binding protein 3, poly(rC) binding protein 3, poly(rC) binding protein 4.
767		10108 A1007857	, ,	HGF-regulated tyrosine kinase substrate, hepatocyte growth facion-regulated tyrosine kinase substrate	ESTs, Weakly similar to HGF-regulated tyrosine kinase substrate [Mus musculus] [M.musculus], HGF-regulated tyrosine kinase substrate, RIKEN cDNA 1700013B03 gene, WD40- and FYVE-domain containing protein 2, hepatocyte growth factor-regulated tyrosine kinase substrate, myotubularin related protein 3, phosphoinositide-binding protein SR1, target of myb1 homolog (chicken), zinc finger
1942		1375/NM_017122		hippocalcin	Protein, Subranniy ZA (F 1 V E domain containing), 1 ESTs, Highly similar to HIPP_HUMAN Neuron specific calcium-binding protein hippocalcin (P23K) (Calcium-binding protein BDR-2) [R.norvegicus], ESTs, Weakly similar to HIPP RAT NEURON SPECIFIC CALCIUM-BINDING PROTEIN HIPPOCALCIN [M.musculus], hippocalcin
696	17345/	17345 AA892014	hh t	HIA-B associated transcript 1, HIA-B-associated transcript 1A	ESTs, Highly similar to S33681 translation initiation factor elF-4A.I [H.sapiens], ESTs, Weakly similar to A42811 nuclear RNA helicase (DEAD family) homolog - rat IR.norvegicus], RIKEN cDNA 2610307C23 gene, hypothetical protein MCC8664
1839	5711	571 NM_012982	cc, dd	2	homeo box, msh-like 2, msh homeo box homolog 2 (Drosophila)
2368	15748 h 22306 h	15748 NM_053309 22306 NM_013179	ii aa, bb	Homer, neuronal immediate early gene, 2, homer, neuronal immediate early gene, 2 hypocretin, hypocretin (orexin) neuropeptide precursor	Homer, neuronal immediate early gene, 2, homer, neuronal immediate early gene, 1
2188	1146 N	1146 NM_024359	h in y, z		Mus musculus inhibitory PAS domain protein (ipas) mRNA, complete cds, hypoxia inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor), neuronal PAS domain protein 1, single-minded 1, single-minded homolog 1 (Drosophila)

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SEQ		GenBank Acc.			
으	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2302		21772 NM_031624	z ',	immunoglobulin (CD79A) binding protein 1	expressed sequence C81413, immunoglobulin (CD79A) binding protein 1, immunoglobulin (CD79A) binding protein 1,
1927		1427 NM_017063	바	importin beta, karyopherin (importin) beta 1	importin beta, karyopherin (importin) beta 1. karyopherin (importin) beta 3
1800		10248 NM_012797	b, j, k, s, t, u, jj, kk	inhibitor of DNA binding 1, inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	
1857		15253 NM_013058	n, 0, s, t	inhibitor of DNA binding 3, inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	
					ESTs, Highly similar to IP3R MOUSE INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR [M.musculus], ESTs, Moderately similar to IP3R
					MOUSE INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1
					RECEPTOR [M.musculus], ESTs, Weakly similar to IP3R MOUSE INOSITOL 1,4,5-
					14.5-triphosphate receptor 1, inositol 1.4.5-triphosphate receptor 2, inositol 1.4.5-triphosphate receptor 2, inositol 1.4.5-triphosphate receptor 2, inositol 1.4.5-triphosphate receptor 2, inositol 1.4.5-triphosphate receptor 2, inositol 1.4.5-triphosphate receptor 2, inositol 1.4.5-triphosphate receptor 2, inositol 1.4.5-triphosphate receptor 2, inositol 1.4.5-triphosphate receptor 3, inositol 1.4.5-t
				inositol 1,4,5-triphosphate receptor 2, inositol 1,4,5-	triphosphate receptor 5, inositol 1,4,5-triphosphate receptor, type 2, ryanodine
2223		18188 NM_031046	66	triphosphate receptor, type 2	receptor 2 (cardiac), ryanodine receptor 2, cardiac, ryanodine receptor 3
					ESTs, Moderately similar to A Chain A, Inositol Monophosphatase [H.sapiens], RIKEN CDNA 2900059K10 nene inositol/much 1/or A) monophosphatase 4
260		23336 AA859981	ee, ff, jj, kk	inositol(myo)-1(or 4)-monophosphatase 2	inosito((myo)-1(or 4)-monophosphatase 2
					EST, Highly similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR I
					RECEPTOR PRECURSOR (M.musculus), EST, Moderately similar to IGAR MOLISE INSUITING IRECEPTOR PRECUIDEDE
					[M.musculus], ESTs, Highly similar to IG1R_MOUSE INSULIN-LIKE GROWTH
				th factor 1 receptor, insulin-like growth	FACTOR I RECEPTOR PRECURSOR [M.musculus], insulin receptor-related
2363	250721	25072 NM_052807	), K		receptor, insulin-like growth factor 1 receptor, insulin-like growth factor I receptor
1754	15098	15098 NM_012588	g	insulin-like growth factor binding protein 3	insulin-like growth factor binding protein 3
				intentin beta 1 (fibroneoffin recentor bets) intentin bets 1	integrin beta 1 (fibrane-din recentor beta 1 integrin beta 1 (fibrane-din receptor beta), integrin beta 7, integrin, integrin, beta 1 fibrane-din recentor beta 2 integrin beta 7, integrin, and a 1 fibrane-din recentor beta 1 fibrane-din recentor beta 1 fibrane-din recentor beta 2 integrin beta 7, integrin, beta 1 fibrane-din recentor beta 1 fibrane-din recentor beta 1 fibrane-din recentor beta 2 fibrane-din recentor beta 1 fibrane-din recentor be
				(fibronectin receptor, beta polypeptide, antiden CD29	bota 1 (instruction receptor), beta polypeptide, anagen OD29 interduces into 2, MSK12), interdrin heta 2 (antiden CD18 (ng5), lymphonide function associated
1356	14989	14989 AI177366	f, g, l, m, kk		antigen 1; macrophage antigen 1 (mac-1) beta subunit), intenin, beta 7

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유	GLGC ID No.	No.		Model Code Human Homologous หกังพุท Cene Nama	7. Kel. 44921-5
					Human Homologous Sequence Cluster Trile
					ESTs, Weakly similar to ICA1_HUMAN INTERCELLUI AR ADHESTON MOLECITIF
_				internellular adbasion molecularistics	1 PRECURSOR [H.sapiens], intercellular adhesion molecule intercellular adhesion
1835		2555 NM_012967	a, y, z, kk	molecule 1 (CD54) human tripodicine	molecule 1 (CD54), human rhinovirus receptor, intercellular adhesion malession
2017	20318	20318 NM_019127	n. 0		intercellular adhesion molecule 5, telencephalin
				merce and included, interferon, beta 1, fibroblast	interferon beta, fibroblast, interferon, beta 1 fibroblast
					ESTs, Weakly similar to IFR1_RAT INTERFERON-RFI ATED DEVEL OBMENTAY
			a. p. q. v. z	N.	REGULATOR 1 (NERVE GROWTH FACTOR-INDITICIBLE PROTEIN DOWN WERE
2044	17908	17908 NM_019242	bb, ee, ff	  interferon-rela	[R.norvegicus], interferon-related developmental regulator 1 interferon-related
,	į			de la or 2	
2516	657	657 NM_133380	j, k, y, z	interleukin 4 receptor, interleukin 4 receptor, alaka	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macronhane)
1914	6598	JM_017020	z.	interleukin 6 recentor interleukin 6 months	Interleukin 4 receptor, interleukin 4 receptor, alpha
1755	24716N	24716 NM_012589	i, k, p, a	interleukin & interleukin & first &	interleukin 6 receptor
				inn responsive clear (interferon, beta 2)	
2158	202 N	202 NM_022863		responsive element binding protein 2, iron-	
<b> </b>	-			Separate element billioning protein 2	
					ESTS, Highly similar to IDHC_RAT ISOCITRATE DEHYDROGENASE MADE
					CYTOPLASMIC (OXALOSUCCINATE DECARBOXYLASF) (INH) (MADE)
					SPECIFIC ICDH) (IDP) [R.norvegicus], expressed semience A1788052 income.
2275	17427 NI	17427 NM_031510	b, u, v		dehydrogenase 1 (NADP+), soluble, isocitrate dehydrogenase 2 (NADP+)
				TOTAL CONTROL OF THE LANGE IN (INAUT+1), SOUDIO	mitochondrial
17Ec				isovaleryl Coenzyme A dehydrogenase. isovaleryl	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE.
3	N DC	286210 MN 0044	O		dehydnonenase isovalond occasional dehydnonenase isovaletyl Coenzyme A
					ESTs. Weakly similar to 104197 profess to 104197
			-	:	[R.novegicus], Janus kinase 1. Janus kinase 1.0 motol: 4.000.
2276	12580 NM 031514		4 1, 1, 1, N,	Janus Kinase 2, Janus Kinase 2 (a protein tyrosine	kinase 2, Janus kinase 2 (a protein fymsine kinase), Janus
	-	Τ			Al504024, expressed sequence C81284, functional kinase 2
					ESTs, Weakly similar to JC4127 protein-tyrosine kinase (EC 2.7.1.112) - rat
				Ith Janus kinase 2, Janus kinase 2 (a protein tyrosine	IK.norvegicus], Janus kinase 1, Janus kinase 1 (a protein tyrosine kinase), Janus
9/77	12581JNM 031514		y, z, hh k		Alfiduna expressed sequence
					Approximents and the control of the

TAB' 3			*		The state of the s
2		GenBank Acc.		;   ·	- 25.k. ** * * * * * * * * * * * * * * * * *
لَـ	GLGC ID No.	No.	Model Code	Model Code Human Hr mologous Known Gene Name	Human Homologous Sequence Cluster. Title
					ESTs, Highly similar to jumping translocation breakpoint [Rattus norvegious]
2038		2F.32 NM_019213	∞, dd	jumping translocation breakpoint	[K.norvegicus], ESTs, Moderately similar to jumping translocation breakpoint [Raffus norvegicus] imming translocation breakpoint
-	_			Jun oncogene, v-jun sarcoma virus 17 oncogene	is accepted it and egical, juniping ualistication preakpoint
5083		22351 NM_021835	ee, ff	homolog (avian)	Jun oncogene, v-jun sarcoma virus 17 oncogene homolog (avian)
				kangai 1 (suppression of tumorigenicity 6, prostate),	(min) Scarce Company
				kangai 1 (suppression of tumorigenicity 6, prostate; CD82	kangai 1 (suppression of tumorigenicity 6, prostate; CD82 kangai 1 (suppression of tumorigenicity 6, prostate), kangai 1 (suppression of
2330		15864 NM 031797	· ·	antigen (R2 leukocyte antigen, antigen detected by	tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by
2390		14380 NM 053536	e v 7	Knippel-like factor 15	monocional and antibody IA4]), tetraspan 1
			21/12	יייין איייין איייין איייין איייין איייין	
6				Kruppel-like factor 9, basic transcription element binding	ESTs, Moderately similar to Kruppel-like factor 9 [Rattus norvegicus] [R.norvegicus], Kruppel-like factor 9, basic transcription element hinding protein 1
7463	8641	8641 NM_057211	pp	protein 1	Expressed segrence AI 022736
1915	17807	17807 NM_017025	 .e	lactate dehydrogenase 1, A chain, lactate dehydrogenase A	lactate dehydrogenase 1, A chain, lactate dehydrogenase lactate dehydrogenase 1, A chain, lactate dehydrogenase A, lactate dehydrogenase
				lactate dehydrogenase 2. B chain lactate dehydrogenase	יוויכן, ומעמום חבון/עווטקפוומאפ ט
1757	71251	92	aa, bb	B	laciate dehydrogenase 2 R chain Tartata dehydrogenase 2
873	20086/	20086 AI013260	7	lamin A, lamin A/C	and a second of the control of the c
					EST, Weakly similar to 1405340A protein 40kD [M.musculus], EST, Weakly similar
_					to RSP4 MOUSE 40S RIBOSOMAL PROTEIN SA [M.musculus], ESTs, Highly
					similar to A31233 ribosomal protein RS.40K, cytosolic [H.sapiens], ESTs,
1040	24585 N	24585 NM 017138			Moderately similar to laminin-binding protein [H.sapiens], expressed sequence
2	20017	T	I, ', W, X	ianilini receptor 1 (b/KD, ribosomal protein SA)	AL022858, laminin receptor 1 (67kD, ribosomal protein SA)
<del></del>					ES1, Weakly similar to 1405340A protein 40kD [M.musculus], EST, Weakly similar to RSP4 MOUSE 40S RIBOSOMAL PROTEIN SA IM misculus ESTs. Highly
					similar to A31233 ribosomal protein RS.40K, cytosolic IH.sapiens1, ESTs.
1070	240070				Moderately similar to laminin-binding protein [H.sapiens], expressed sequence
240	740001	24000 IVM 017138	n, I, W, X	laminin receptor 1 (67kD, ribosomal protein SA)	AL022858, laminin receptor 1 (67kD, ribosomal protein SA)
					ESTs, Weakly similar to LMB2_HUMAN LAMININ BETA-2 CHAIN PRECURSOR
					[H.sapiens], Rattus norvegicus laminin-5 alpha 3 chain mRNA, complete cds,
				~ 6	expressed sequence AW211941, expressed sequence C80098, hypothetical protein
1836	22434 N	22a34 NM_012974	E.	laminin. beta 2. laminin. beta 2. (laminin. S)	ال 13 المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية ا المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالي
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SEO	ŀ	GenBank Acc.		The state of the s	105485 Color
٥	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					HAIN PREC A, complete
1836		22435 NM_012974	ပ	laminin, beta 2. laminin. beta 2 (laminin S)	BC018697, laminin B1 subunit 1, laminin, beta 1, laminin, beta 2, laminin, beta 2
2335		22321 NM_031832	a, h, l, n, o, x, kk	lectin, galacto	EST, Weakly similar to A35820 galectin 3 [H.sapiens], galectin-related inter-fiber
602		22283 AA945172	o o	leucine aminopeptidase 3	Aminopentidase-like 1 Tercina aminopentidase 3
					LIM and senescent cell antigen-like domains 1, LIM and senescent cell antigen-like
				LIM protein (similar to rat protein kinase C-hinding	domains 1-like, LIM protein (similar to rat protein kinase C-binding enigma), RIKEN
2369		7: 07 NM_053326	윤	enigma), enigma homolog (R. norvegicus)	povecious), leupaxin
				lipase A. Ivsosomal acid. cholesterol esterase (Wolman	ESTs, Weakly similar to cholesterol esterase (pancreatic), see D3Wox12,
1781	25:-63	251-63 NM_012732	f, g	disease), lysosomal acid lipase 1	Doving I. Doving and Doving I.Z. [Kartus norvegicus] [K.norvegicus], lipase A,
				lipase A, lysosomal acid, cholesterol esterase (Wolman	ESTs, Weakly similar to cholesterol esterase (pancreatic), see D3Wox12, D3Wox13, D3Wox26 and D3Moh25 Rattus novenicus IR novenicus III Incomediate III Incomediate III III III III III III III III III I
2	16.13	16( 13 NM_012732	g	disease), lysosomal acid lipase 1	lysosomal acid, cholesterol esterase (Wolman disease). Incressmal acid, cholesterol
1758	18387 N	18387 NM_012598	W, X	lipoprotein lipase	ESTs, Highly similar to JH0790 lipoprotein lipase (EC 3.1.1.34) precursor - rat R.norvedicus). lipase, endothelial linoprotein lipase
1758	18386 N	18386 NM_012598	×' ×	lipoprotein lipase	ESTs, Highly similar to JH0790 lipoprotein lipase (EC 3.1.1.34) precursor - rat
2375	9352 N	9352 NM_053347	n, v	LIS1-interacting protein NUDE1, rat homolog, nuclear distribution gene E homolog (Aspergillus)	(who regions), upoprotein lipase, ilipase, endontellal, lipoprotein lipase
217	21713A		e, r	n included)	Lutheran blood group (Auberger b antigen included)
					CD68 antigen, ESTs, Weakly similar to LMP1_RAT LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 1 PRECURSOR (LAMP-1) (120 KD LYSOSOMAL MEMBRANE GLYCOPROTEIN) (LGP-120) (CD107A) IR norvegicus], chromosome
1808	18770 N	18770 NM_012857	th s	lysosomal membrane glycoprotein 1, lysosomal- associated membrane protein 1	20 open reading frame 103, lysosomal membrane glycoprotein 1, lysosomal- associated membrane protein 1, lysosomal-associated membrane protein 3

TABLE	TABLE?		•	The second secon	TANKS OF THE PROPERTY OF THE P
SEC		GenBank Acc.		Are an exploration of the second of the seco	443Z1-2030-01-400/Z105485
<u>⊖</u>	GLGC ID No.	No.		Model Gode Human Homologous Known Gene Name	Human-Homologous Sequence Cluster Title
1928		6653 NM_017068	<u></u> 0	lysosomal membrane glycoprotein 2, lysosomal- associated membrane protein 2	にぶ
1928		6654 NM_017068	b, v	lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	CD68 antigen, ESTs, Weakly similar to JC4317 lysosome-associated membrane protein 2 precursor, splice form B [H.sapiens], lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2
410		12/18 AA892775	, n, x	lysozyme, lysozyme (renal amyloidosis)	EST, Weakly similar to LYC1_RAT Lysozyme C, type 1 precursor (1,4-beta-N-acetylmuramidase C) [R.norvegicus], RIKEN cDNA 9530003J23 gene, Iysozyme, Iysozyme (renal amyloidosis), similar to Iysozyme C-1 (1,4-beta-N-acylmuramidase C, EC 3.2.1.17)
1926		1942 NM_017061	=	lysyl oxidase	ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE PRECURSOR [H.sapiens], ESTs, Moderately similar to LYOX_RAT Protein-lysine 6- oxidase precursor (Lysyl oxidase) [R.norvegicus], ESTs, Weakly similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus], lysyl oxidase, lysyl oxidase-like, lysyl oxidase-like?
					ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE PRECURSOR [H.sapiens], ESTs, Moderately similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus], ESTs, Weakly similar to
1926	1943 N	1943 NM_017061	s, t		LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus], lysyl oxidase, lysyl oxidase, live 3
2033	15244 N	15244 NM_019191	=	MAD homolog 2 (Drosophila), MAD, mothers against decapentaplegic homolog 2 (Drosophila)	MAD homolog 2 (Drosophila), MAD, mothers against decapentaplegic homolog 2 (Drosophila)
1809	13151N	13151 NM_012862	n, o, II	matrix Gla protein, matrix gamma-carboxyglutamate (gla)	EST, Weakly similar to MGP_HUMAN MATRIX GLA-PROTEIN PRECURSOR [H.sapiens], ESTs, Highly similar to MGP_HUMAN MATRIX GLA-PROTEIN matrix Gla protein, matrix gamma-carboxyglutamate (gla) PRECURSOR [H.sapiens], matrix Gla protein, matrix gamma-carboxyglutamate protein
					18:1 E C.C.

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있 고 고	GLGC ID No.	GenBank Acc.	Model Code	Model Code Human Homologous Known Gene Name	Human Definition Comment of the Comm
					initiation of the property of
					EST, Weakly similar to MCM5_HUMAN DNA REPLICATION LICENSING FACTOR
					MCM5 [H.sapiens], ESTs, Weakly similar to MCM6_HUMAN DNA REPLICATION
					LICENSING FACTOR MCM6 [H.sapiens], MCM2 minichromosome maintenance
					deficient 2, mitotin (S. cerevisiae), MCM6 minichromosome maintenance deficient 6
				ON	(MIS5 homolog, S. pombe) (S. cerevisiae), mini chromosome maintenance deficient
					2 (S. cerevisiae), mini chromosome maintenance deficient 5 (S. cerevisiae), mini
2615		16675 017565	:= <u>-</u>	ilontolog, s. pombe) (s. cerevisiae), mini chromosome maintenance deficient 6 (S. cerevisiae)	chromosome maintenance deficient 6 (S. cerevisiae), mini chromosome
2675		25, 37 X70667	l, m	melanocortin 3 receptor	manitaliative delicient ( o. cerevisiae)
					RIKEN cDNA 1700056A17 gene, RIKEN cDNA 1700080O16 gene, RIKEN cDNA
344	19: 21	19: 21 AA891666	g, dd	melanoma antigen. family D. 1	2410003J06 gene, RIKEN cDNA 3830417A13 gene, melanoma antigen, family D,
					RIKEN CDNA 2010107K23 gene. RIKEN CDNA 5730494G16 gene. general
2407	2, 44				transcription factor II H, polypeptide 1 (62kD subunit), melanoma antigen, family B,
1017	7	Z, +1 INWI U004/3	da, DD	melanoma anugen, tamily D, 2	3, melanoma antigen, family D, 2, melanoma antigen, family E, 1
1877	56371	5637 NM_013143	cc, dd	meprin 1 aipna, meprin A, aipha (PABA peptide hydrolase)	expressed sequence Al098089, meprin 1 alpha, meprin A, alpha (PABA peptide hydrolase)
					formers for
1054	175871v	17587 NIM 047440		mesenchyme homeo box 2 (growth arrest-specific homeo	homeo box 2 (growth arrest-specific homeo homeo box A11, mesenchyme homeo box 1, mesenchyme homeo box 2 (growth
3	3			box), mesencnyme nomeobox 2	arrest-specific homeo box), mesenchyme homeobox 1, mesenchyme homeobox 2
					EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately
			4 20	•	similar to SMHU1E metallothionein 1E [H.sapiens], ESTs, Moderately similar to
2550	15180	15480 NIM 420026	, 2, ee,		MT1_RAT METALLOTHIONEIN-I (MT-I) [R.norvegious], metallothionein 1,
2007	100101	Τ	II, NA	metallomionein 1, metallomionein 1A (functional)	metallothionein 4, metallothionein IV
					EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately
					similar to SMHU1E metallothionein 1E [H.sapiens], ESTs, Moderately similar to
2550	15100 N	15100 NIM 128026		: : : : : : : : : : : : : : : : : : : :	MT1_RAT METALLOTHIONEIN-I (MT-I) [R.norvegicus], metallothionein 1,
2000	NIOCIOI NIOCIOI	ļ	I), K, Y, C, II (II	metallothionein 1, metallothionein 1A (functional)	metallothionein 4, metallothionein IV

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	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					ESTs, Highly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus], KIAA1266 protein, KIAA1610 protein, metastasis associated 1,
2142		20762 NM_022588	r, s, t	metastasis associated 1	metastasis associated 1-like 1, metastasis associated 3, metastasis-associated 1-
90		13938 NM_017212	jj, kk	microtubule-associated protein tau	
1970	13940	13940 NM_017212	B	microtubule-associated protein tau	
2510	17564	17564 NM_133283	<del>L</del>	mitogen activated protein kinase kinase 2, mitogenactivated protein kinase kinase 2	
2300	14957	14957 NIM_031622	<u> </u>	mitogen-activated protein kinase 6	ESTs, Weakly similar to B40033 protein kinase (EC 2.7.1.37) ERK3 - rat [R.norvegicus], mitogen-activated protein kinase 4, mitogen-activated protein kinase 6
					ESTS, Highly similar to M3K3 MOUSE MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 3 [M.musculus], ESTS, Moderately similar to S12207 hypothetical protein [M.musculus], ESTS, Weakly similar to M3K3_HUMAN MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 3 [H.sapiens], hypothetical protein FLJ23074, mitogen activated protein kinase kinase 1, mitogen activated protein kinase kinase kinase kinase kinase kinase kinase
236	16499 A	16499 AA925300	p, ee, ff, gg	mitogen-activated protein kinase kinase kinase 3	kinase 3, mitogen-activated protein kinase kinase kinase 2, mitogen-activated
2156	28 28	58 NM_022715	u, v		Protein Milase Milase 3
2036	21508 N	21508 NM_019208	:=:	multiple endocrine neoplasia 1, multiple endocrine neoplasia I	milling and order of the second order of the second order of the second order of the second of the s
1152	15291 AI111401	1111401	H.	multiple inositol polyphosphate histidine phosphatase 1, multiple inositol polyphosphate histidine phosphatase, 1	manpre endodine neoplasia 1, multiple endocrine neoplasia I
					ESTs, Highly similar to multiple PDZ domain protein [Mus musculus] [M.musculus], ESTs, Weakly similar to T30259 multiple PDZ domain protein - mouse [M.musculus], ESTs, Weakly similar to T46612 multi PDZ domain protein 1 - rat [R.norvegicus], Homo sapiens cDNA FLJ25282 fis, clone STM06685, highly similar to Rattus norvegicus mRNA for multi PDZ domain protein, RIKEN cDNA 2810455810 gene, channel-interacting PDZ domain protein, RIKEN cDNA
2306	21421 NN 17448 NN	21421 NM_019196 17448 NM_031668	= 4	muttiple PDZ domain protein MYB binding protein (P160) 1a	protein
				5. (5)	

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SEO		GenBank Acc.			Atty, Ref. 44921-5090-01-WO/2105485
٥	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Tifle
1759		2628 NM_012603	a, p, q, y, z	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog
1759		2629 NM_012603	a, j, k, p, q, y, z, ee, ff, kk	tosis oncogene, v-myc myelocytomatosis e homolog (avian)	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)
1978		1498 NM_017239	o .	scle, adult, myosin, scle, alpha )	ÈST, Weakly similar to MYH6_RAT Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [H.sapiens], KIAA1000 protein, myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, heta
1979	20482 IN	20482 NM_017240	<u> </u>	cle, adult, myosin, licle, alpha , myosin, heavy	EST, Highly Similar to MYH7_KAT Myosin hear of the factor of the social of the factor
1979	20483 N	20483 NM_017240	B (0 ± 3	myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 6, cardiac muscle, alpha m (cardiomyopathy, hypertrophic 1), myosin, heavy mpolypeptide 7, cardiac muscle, beta	ESÍ, Highly similar to MYHZ, RAT Myosin heavy chain, cardiac muscle beta isotorm (MyHC-beta) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYHB_MOUSE MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) [M.musculus], ESTs, Weakly similar to PCNT MOUSE PERICENTRIN [M.musculus], RIKEN cDNA 4932408L24 gene, myosin heavy chain, cardiac muscle, adult, myosin heavy chain-like, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, beta

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0		GenBank Acc.	1 1 1 1 1 1	S. W. T.	Attv. Ref. 44921-5090-01-WO/2105485
اً ع	GLGC DIND.	D No.		Model Code Human Ho nologous Known Gene Name	Human Homologus Sentrative Chiefer THIS
					ESI, Highly similar to MYH/_RAI Myosin heavy chain, cardiac muscle beta isotorm (MyHC-beta) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs. Weakly similar to
				myosin heavy chain, cardiac muscle, adult, myosin,	MYHB_MOUSE MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) [M.musculus], ESTs, Weakly similar to PCNT MOUSE PERICENTRIN [M.musculus], RIKEN CONA 4032A081 24 2020.
1979	i i	20484 NM_017240	Ф	heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1), myosin, heavy polypeptide 7, cardiac muscle, beta	muscle, adult, myosin, heavy chain-like, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy
					EST, Weakly similar to MYH6_RAT Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY
	,			myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 6, cardiac muscle, alnha	CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA
1978	1497	1497 NM_017239	g	(cardiomyopathy, hypertrophic 1), myosin, heavy polypeptide 7, cardiac muscle, beta	adult, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy
					EST, Highly similar to MY1A_RAT Myosin IA (Myosin I alpha) (MMI-alpha) (MMIa) (Myosin heavy chain myr 1) [R.norvegicus], EST, Weakly similar to MYOSIN I
2463	17653	17653 NM_053986	cc, dd	myosin IB	Part in partitional wide musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010010B23:myosin, heavy polypeptide-like (110kD), full insert semience, myosin IB.
					Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730519L10:myristoylated alanine rich motein kingso Contactor 4.11:
470	24329	24329 AA899253	aa, bb		Sequence, myristoylated alanine rich protein kinase C substrate, myristoylated alanine rich protein kinase C substrate, myristoylated
2041	20938	20938 NM_019223	듔	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase), NADH dehydrogenase Fe-S protein 6	ESTs, Highly similar to NUMM MOUSE NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT [M.musculus], NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-menyme O requirese)
2282	18389	18389 NM_031545	a, d, y, ee, fff	natriuretic peptide	EST, Moderately similar to ANFB MOUSE BRAIN NATRIURETIC PEPTIDE PRECURSOR [M.musculus], natriuretic peptide precursor B, natriuretic peptide
					אכסמוסטו ואום ה

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<u></u>	GLGC ID No.	No.	. •	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1762		638 NM_012613	aa, bb	E3 PF natriuretic peptide receptor 1, natriuretic peptide receptor na A/guanylate cyclase A (atrionatriuretic peptide receptor A)(A)	STs, Weakly similar to ATRIAL NATRIURETIC PEF RECURSOR [M.musculus], Mus musculus, Similar clone IMAGE:5052434, mRNA, partial cds, natriur triuretic peptide receptor Aguanylate cyclase A (a
1761		1298 NM_012610	<del>.</del>	nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16)	Mus musculus, clone IMAGE:5097359, mRNA, partial cds, nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16), p75-like apoptosis-inducing death domain profein PI AIDD
1761		1; 99 NM_012610	cc, dd	nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16)	Mus musculus, clone IMAGE:5097359, mRNA, partial cds, nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16), p75-like
1945		NM_017130	u, v	alidase)	neuraminidase 2 sialidase 2 (cytosolic sialidase)
2441	1780	1780 NM_053846	۵, ر	neurexin 2, neurexin II	ESTs, Highly similar to C40228 neurexin II-alpha precursor - rat [R.norvegicus], ESTs, Moderately similar to NX1A_MOUSE_2 [Segment 2 of 2] Neurexin 1-alpha (Neurexin 1-alpha) (Fragments) [M.musculus], ESTs, Weakly similar to NX1A_MOUSE_1 [Segment 1 of 2] Neurexin 1-alpha (Neurexin 1-alpha) (Fragments) [M.musculus], RIKEN cDNA 4933401A11 gene, chondroitin sulfate
2298	197.22	NM_031609	j, kk	ession of tumorigenicity 1	dante, neuroblastoma suppression of timoricanicity 4
2098	20450	NM_022239	l, m, u, v		neuromedin, neuromedin U
2047	24849	24849 NM_019248	aa, bb	osine kinase, receptor, type 3	RIKEN cDNA 0710005A05 gene, neuropeptide Y neurotrophic tyrosine kinase recentor tyne 3
2629	1715	U72660	a, jj, kk		ninjurin 1, ninjurin 2
1649	20127/	20127 AJ011116	j, k, n, o	Initric oxide synthase 3 (endothelial cell), nitric oxide fit synthase 3, endothelial cell synthase 3, endothelial cell s	ESTs, Moderately similar to A Chain A, Human Endothelial Nitric Oxide Synthase With Arginine Substrate (SUB 66-492 [H.sapiens], Homo sapiens cDNA FLJ14885 fis, clone PLACE1003711, nitric oxide synthase 3 (endothelial cell), nitric oxide synthase 3, endothelial cell
1840	7641	764 NM_012988	ee, ff	nuclear factor I/A	nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)
743	17963	17963 AB012231	ji, kk	nuclear factor I/B - 7	Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)
1331	24763 A	247 63 AI176488	jj, kk	nuclear factor I/B	Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)

TABLE 3	,			は 一日 一日 一日 日本 D LAND LAND LAND LAND LAND LAND	
SEO	١.	GenBank Acc.			
಼	GUGC DINS	N.	Model Code	Model Code Human Ho notogous Known Gene Name	Human Homologous Sequence Cluster Title
				nuclear far for of kappa light chain gene enhancer in B-	
2870		25/00/1/52504	2	cells inhibitor, alpha, nuclear factor of kappa light	
200	- 1	A03034	y .	polypeptide gene ennancer in B-cells inhibitor, alpha	
8C07		24674 NM_019328	,, K	nuclear receptor subfamily 4, group A, member 2	nuclear receptor subfamily 4, group A, member 2
2303		567 NM_031628	p, q	nuclear receptor subfamily 4, group A, member 3	
				nuclear RNA export factor 1, nuclear RNA export factor 1	
755	18731	18731 AF093139	d	homolog (S. cerevisiae)	
				nuclear transcription factor Y, gamma, nuclear	
238 238	4339,	4339 AA875121	jj, Kk	transcription factor-Y gamma	
				nuclear transcription factor Y, gamma, nuclear	
1870	4338	4338 NM_012866	u, v	transcription factor-Y gamma	
				nucleophosmin (nucleolar phosphoprotein B23,	
1841	17394	17394 NM_012992	hh, kk	numatrin), nucleophosmin 1	ESTs. Highly similar to A32915 nucleophosmin IH saniens1 nucleophosmin 1
					ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] IR norvegicus]
					ESTs, Highly similar to SET HUMAN SET PROTEIN IH. sapiens1. SET
					translocation, SET translocation (myeloid leukemia-associated), nucleosome
152	16006/	16006 AF062594	<u>66</u>	nucleosome assembly protein 1-like 1	assembly protein 1-like 1
		_			ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus],
					ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], SET
Í					translocation, SET translocation (myeloid leukemia-associated), nucleosome
72,	16007/	16007 AF062594	£	nucleosome assembly protein 1-like 1	assembly protein 1-like 1
					ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus],
					ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], SET
-					translocation, SET translocation (myeloid leukemia-associated), nucleosome
976	/665/	7665/AI030668	а	nucleosome assembly protein 1-like 1	assembly protein 1-like 1
				omithine carbamoyltransferase, ornithine	
1862	13283	13283 NM_013078	p	transcarbamylase	ornithine carbamoyltransferase, ornithine transcarbamylase
					ESTs, Weakly similar to ODCI_MOUSE Omithine decarboxylase antizyme inhibitor
2141	Z1062N	Z106Z NM_0Z2585	99	ornithine decarboxylase antizyme inhibitor	[M.musculus], ornithine decarboxylase antizyme inhibitor
77.77	2000				ESTs, Weakly similar to ODCL_MOUSE Ornithine decarboxylase antizyme inhibitor
1417	V 2017		Ζ,	omithine decarboxylase antizyme inhibitor	[M.musculus], ornithine decarboxylase antizyme inhibitor
2333	15840 N	15840 NM 031817	h, i	osteomodulin	osteoglycin, osteomodulin

TABLE 3		*** *** * * * * * * * * * * * * * * *	4 6 13 4 2mg.		
SEQ		GenBank Acc.			Atty. Ref. 44921-5090-01-WO/2105485
ف	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					ESTs, Weakly similar to JE0111 lectin-like oxidized LDL receptor - mouse [M.musculus], Mus musculus NKRP1F mRNA, complete cds, killer cell lectin-like receptor subfamily B member 1A, killer cell lectin-like receptor subfamily B member
2515		4318 NM_133306	b,q	oxidised low density lipoprotein (lectin-like) receptor 1, oxidized low density lipoprotein (lectin-like) receptor 1	18, killer cell lectin-like receptor subfamily B member 1C, killer cell lectin-like receptor subfamily B member 1D, oxidised low density lipoprotein (lectin-like) receptor 1, oxidized low density linguation flectin like)
1690	7	20549 K01701	Q	oxytocin, oxytocin, prepro- (neurophysin !)	ESTs, Moderately similar to NEU1 MOUSE OXYTOCIN-NEUROPHYSIN 1
2289	- 1	1918 NM 031576	gg	P450 (cytochrome) oxidoreductase	i reconder [w.iiiusculus], oxytodin, oxytodin, prepro- (neurophysin I)
2289		16:20 NM_031576		P450 (cytochrome) oxidoreductase	
2289		NM_031576	j, k, s, t	P450 (cytochrome) oxidoreductase	
1843	.	24563 NM_012999		paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6	EST, Highly similar to 153282 gene PACE4 protein - rat [R.norvegicus], RIKEN cDNA A930029K19 gene, paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin tyne 6
1843	24:-64	24:64 NM_012999	9.0	paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6	EST, Highly similar to 153282 gene PACE4 protein - rat [R.norvegicus], RIKEN cDNA A930029K19 gene, paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6
2046	13.8		; = 	virod like homes.	ESTs, Weakly similar to PIX3_RAT Pituitary homeobox 3 (Homeobox protein PTX3) [R.norvegicus], RIKEN cDNA 1600026O01 gene, diencephalon/mesencephalon-expressed brain homeobox 1, newborn ovary homeobox gene, paired-like
2066	18819N			paireu-like itorrieoudinain transcription factor 3 palmitovl-profein thioesterase 2	homeodomain transcription factor 3
2066	18620N			palmitoyl-protein thioesterase 2	parmitoyi-protein thioesterase 2 palmitoyi-protein thioesterase 2
					EST, Moderately similar to CL36_HUMAN LIM DOMAIN PROTEIN CLP-36 [H.sapiens], ESTs, Weakly similar to PDL1_RAT PDZ and LIM domain protein 1 (LIM domain protein CLP-36) (C-terminal LIM domain protein 1) (Elfin) [R.norveoicus]. Mus musculus, clone McC-37634 (MACE-3000000)
2014	1581 N	1581 NM_017365	l, p, q, s, t Pl	PDZ and LIM domain 1 (elfin)	complete cds, PDZ and LIM domain 1 (effin), PDZ and LIM domain 3, Rattus norvegicus LIM-domain protein LMP-1 mRNA, complete cds, actinin alpha 2 associated LIM protein
1974	18148NI	18148 NM_017226 r	n, o	peptidyl arginine deiminase, type II	ESTs, Highly similar to PROTEIN-ARGININE DEIMINASE [M.musculus], peptidyr arginine deiminase, type II

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				は、100mmの対象をは、100mmのが、100mmの対象をは、100mmの対象をは、100mmの対象をは、100mmの対象をは、100mmの対象をは、100mmのが、100mmののが、100mmののが、100mmののが、100mmののが、100mmののが、100mmののののののののののののの	
3		GenBank Acc.	3.7.	ŀ	Atty. Ker. 44921-5090-01-WO/2105485
≘	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Clister Title
1974		15108 NM 017226	A II	الاستامات المتاسات مواماتها والمالية	ESTs, Highly similar to PROTEIN-ARGININE DEIMINASE [M.musculus], peptidyl
		011250	2,0	peping) alginine deiminase, type ii	arginine deiminase, type II, ribosomal protein S18
					EST, Moderately similar to A Chain A, Cyclophilin A [H.saplens], ESTS, Highly similar to CYPH MOUSE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A
					[M.musculus], ESTs, Moderately similar to A Chain A, Human Cyclophilin A
					Complexed With 2-Thr Cyclosporin [H.sapiens], ESTs, Weakly similar to A Chain A.
					Cyclophilin A [H.sapiens], ESTs, Weakly similar to A Chain A, Human Cyclophilin A
					Complexed With 2-Thr Cyclosporin [H.sapiens], ESTs, Weakly similar to
					CYPH_RAT Peptidyl-prolyl cis-trans isomerase A (PPlase) (Rotamase) (Cyclophilin
					A) (Cyclosporin A-binding protein) (P31) [R.norvegicus], RIKEN cDNA 2510026K04
1939	43911	4391 NM 017101	+	Pepudyipi uyi isolilerase A, pepudyiprolyi isomerase A	gene, expressed sequence Al256741, expressed sequence AW457192,
	3	10110	16	(cyclopniiin A)	peptidylprolyl isomerase A
					EST, Weakly similar to period homolog 2 (Drosophila) [Rattus norvegicus]
					[R.norvegicus], ESTs, Highly similar to period homolog 2 (Drosophila) [Raffus
2310	15041 N	15041 NM 031678	 ₹	period homolog 2 (Droscophila)	norvegicus] [R.norvegicus], period homolog 1 (Drosophila), period homolog 2
				Period in the protein 22 period in the protein	(Drosophila)
1917	4500N	4500 NM 017037	_:=	Porpreta inyenin protein 22, peripriera myenn protein, 22. kDa	
745	225G7 A	22567 ABN17544			peripheral myelin protein 22, peripheral myelin protein, 22 kDa
2	7 10077	##C/100	aa	peroxisomal biogenesis factor 14	peroxisomal biogenesis factor 14
1848	20178N	20178 NM 013014	×	al dereathin	EST, Weakly similar to persephin [Rattus norvegicus] [R.norvegicus], artemin,
		T			persephin
					ESTS, Weakly SIMILIAT TO PIEN MOUSE PROTEIN-TYROSINE PHOSPHATASE
			_	<u> </u>	FIEN [M.musculus], Mus musculus mRNA for tyrosine phosphatase (Tpte gene),
					isotorm A, splice variant A, phosphatase and tensin homolog, phosphatase and
2297	11296IN	11296 NM 031606	<u> </u>	priospirates and tensin nomolog, phosphatase and	tensin homolog (mutated in multiple advanced cancers 1), phosphatase and tensin
				Chair notifying (mutated in mulliple advanced cancers 1) In	construction of the trade of the trade of the concers of the conce
					Homo sapiens, clone MGC:22776 IMAGE:4700840, mRNA, complete cds, RIKEN
1977	15598 NI	15598 NM 017236	<u></u>	nanolamine binding protein, prostatic	cDNA 1700023A18 gene, RIKEN cDNA 1700081D17 gene,
		200	2	d  unang bing in	phosphatidylethanolamine binding protein, prostatic binding protein

2% 2%	GLGC ID No.	F		· · · · · · · · · · · · · · · · · · ·	Auy, Ker. 44921-5090-01-WO/2105485
GLG 63 75 24	O O				
75			Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Tifle
	24598 NM_017231	231 hh		phosphatidylinositol transfer protein, phosphotidylinositol transfer protein	IDYLINOSITOL TRANFER PROTEIN ALPH Sitol transfer protein,
	945 NM_138882		, k, s, t	phosphatidy/serine-specific phospholipase A1, phosphatidy/serine-specific phospholipase A1aloha	ESTs, Weakly similar to A34671 triacylglycerol lipase [M.musculus], ESTs, Weakly similar to S15893 triacylglycerol lipase [M.musculus], Homo sapiens membranebound phosphatidic acid-selective phospholipase A1 mRNA, complete cds, expressed sequence AA986889, lipase, endothelial, pancreatic lipase-related profesion?
	14250 AA799729	9 .; k		phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase 4B, cAMP-specific
1916 14;	14247 NM_017031	31 h,		phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase 4B, cAMP-specific
2320 13	1340 NM_031715	75 jij. 茶		phosphofructokinase, muscle	ESTs, Highly similar to phosphofructokinase, muscle; phosphofructokinase-1 A isozyme [Mus musculus] [M.musculus], expressed sequence Al131669, phosphofructokinase, muscle
1021	12058 12058				ESTs, Highly similar to K6PP_MOUSE 6-PHOSPHOFRUCTOKINASE, TYPE C (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO- 1-KINASE ISOZYME C) (PFK-C) [M.musculus], ESTs, Moderately similar to A53047 6-phosphofructokinase [R.norvegicus], ESTs, Weakly similar to JC2055 6- phosphofructokinase [H.sapiens], ESTs, Weakly similar to K6PL MOUSE 6- PHOSPHOFRUCTOKINASE, LIVER TYPE [M.musculus], phosphofructokinase,
	25377 L25387	두		prosproringse, platelet phosphofructokinase, platelet	platelet
2365 13	1311 NM_053291	<u>ө</u>	<u>a</u>		ESTs, Highly similar to A33792 phosphoglycerate kinase (EC 2.7.2.3) - rat [R.norvegicus], phosphoglycerate kinase 2
2003 245	24533 NM_017328	9 п, о		phosphoglycerate mutase 2, phosphoglycerate mutase 2 r (muscle)	EST, Weakly similar to PMGM MOUSE PHOSPHOGLYCERATE MUTASE, MUSCLE FORM [M.musculus], EST, Weakly similar to PMHUYM phosphoglycerate mutase [H.sapiens], phosphoglycerate mutase 2, phosphoglycerate mutase 2 (muscle)

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بار		GenBank Acc			Attv. Ref. 44921:5090_01.WOP2105485
آء	GLGC ID No.	No.		Model Code Human Hr mologous Known Gene Name	Human Homologous Saguence Chreter Title
2446		11.05 NM_053866		phospholit ase A2, activating protein, phospholipase A2-activating protein	phospholipase A2, activating protein, phospholipase A2-activating protein
					FSTs Highly similar to EGDA LI MAAN DI TATILITY OF CO.
		,			NUCLEOTIDE EXCHANGE FACTOR (H.sapiens), ESTS, Weakly similar to B39898
					phospholipase A2 [M.musculus], ESTs, Weakly similar to FGD1 MOUSE PUTATIVE
					Weakly similar to FGD1. HUMAN PUTATIVE RHO/RAC GLIANINE NI ICI ECTINE
					EXCHANGE FACTOR [H.sapiens], FGD1 family, member 3, Homo sapiens cDNA
					FLJ32732 fis, clone TESTI2001141, highly similar to Rattus norvegicus actin-
					filament binding protein Frabin mRNA, Mus musculus actin-binding protein frabin-
					alpha mRNA, complete cds, RIKEN cDNA 2310026J01 gene, RIKEN cDNA
			a, j, k, y, z,	phospholipase A2, group IVA (cytosolic, calcium-	2610311B01 gene, RIKEN cDNA 5830461L01 gene, faciogenital dysplasia
2528	244		, kk		Calcium-denendent) absorbalisase A2 group IVA (cytosolic,
1362	9378	9378 NM_017174	jj, kk	phospholipase A2, group V	phospholinase A2 grain V
2106					Homo sapiens mRNA: cDNA DKFZn434F235 (from clone DKFZn434E225)
2017	100007	20303 MINI 024333	- 'u	phospholipase C, beta 4	phospholipase C, beta 1
				3	ESTs, Moderately similar to KPBG_HUMAN PHOSPHORYLASE B KINASE
					GAMMA CATALYTIC CHAIN, SKELETAL MUSCLE ISOFORM [H.sapiens],
2288	546 N	546 NM_031573	h, ii	pirospirorytase kinase garima, prosphorytase kinase, le gamma 1 (muscle)	endoplasmic reticulum (ER) to nucleus signalling 2, phosphorylase kinase gamma,
			2		priospriolyrase kinase, gamma 1 (muscle)
35	4832 A	4832 AA800190	a, e, ii, kk	phosphorylase, glycogen; brain	ilver grycogeri priosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen; brain
2595	4834N	4834 NM 153821		ili	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase,
		Τ			glycogen; brain
2423	13369 N	13369 NM_053742	п, о		ESTs, Highly similar to PPI2_HUMAN PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM IH sanians1 phospholidulinosital transfer activity
				pha, platelet-derived	platelet derived growth factor, alpha, platelet-derived g
2/0	1332 A	1332 AI013222 B			polypeptide
	2	T	cc, dd	ig.	
1995	82 Ni	82 NM_017297  ii			
					potassium inwardly-rectifying channel, subfamily J, member 5

TABLE 3	23			77	
S		GenBank Acc			Atty. Ref. 44921-5090-01-WO/2105485
۵	GLGC ID No.	No.		Model Gode Human Homologous Known Gene Name	ter Tifle
1938	- 1	15517 NM_017099	ပ	potassium inwardly-rectifying channel, subfamily J, member 8	1 7
1997		1028 NM_017304	:=	potassium voltage-gated channel, shaker-related subfamily, beta member 2	potaceium voltace anted channel, subiatrilly J, member 8
1091		13267 A1101847	<u>f</u>	potassium voltage-gated channel, shaker-related subfamily, member 5	Potassium voltage-gated Grammer, Shaker-related Subtamily, beta member 2
1940		15776 NM_017108	ה' א	potassium voltage-gated channel, subfamily H (eag- related), member 3	RIKEN cDNA C030044P22 gene, expressed sequence AU019351, potassium
1982	$\sqcup 1$	16601 NM_017252		POU domain, class 3, transcription factor 4	Vollage-gated channel, subramily H (eag-related), member 3
2524		NM_133528	s, t		neimplantation profess 3, utalison page 4
2361	238951	23895 NM_033485	aa	PRKC, apoptosis, WT1, regulator	ESTs, Weakly similar to Ser/Arg-related nuclear matrix protein; plenty-of-prolines-101; serine/arginine repetitive matrix protein 1 [Mus musculus] [M.musculus], Mus musculus, Similar to hypothetical protein MGC13125, clone MGC:38070 IMAGE:5252666, mRNA, complete cds, PRKC, apoptosis, WT1, regulator, expressed sequence Al480556, glucocorticoid-induced gene 1, serine/arginine repetitive matrix 1
2043	15503 N	15503 NM_019237	o 'e	procollagen C-endopeptidase enhancer, procollagen C-proteinase enhancer protein	EST, Weakly similar to PCO1_HUMAN PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PCO1_RAT Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal proteinase enhancer) (Type 1 procollagen C-proteinase enhancer protein) [R.norvegicus], expressed sequence A1043106, membrane frizzled-related protein, procollagen C-endopeptidase enhancer, procollagen C-endopeptidase enhance
1842	19393 N	19393 NM_012998		procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55), prolyl 4-hydroxylase, beta polypeptide	de de la company
8	V 96707	ZUZ38 NM_0193/4	E,	prodynorphin	
2088	17936NI	17936 NM_021766		progesterone receptor membrane component 1	Homo sapiens, clone MGC:32124 IMAGE:4877960, mRNA, complete cds, RIKEN cDNA 4631434019 gene, progesterone receptor membrane component 1
2107	11454NI	11454 NM_022381	o, I, m, n, o, s, t	proliferating cell nuclear antigen	Droliferating cell nuclear antinen
					and a support of the

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SEC.	·   ·   ·   ·   ·   ·   ·   ·   ·   ·	SEC   GenBank Acc.	•		**************************************
Q	G.G	D GLGC ID No.		Model Code Human Hi mologous Known Gene Name	Himan Homologogic Commence Office of the Commence Office of the Commence Office of the Commenc
23.0	11/35   11/35   13/30	5 NM 022381	S	proliferating cell nuclear antigen	Inditional residence of the contract of the co
4077				prosaposin, prosaposin (variant Gaucher disease and	Promoteury cen nuclear anagen
1847	1	Z3545 NM 013013	m,	variant metachromatic leukodystrophy)	
9//1		501 NM_012704	:=:	prostaglandin E receptor 3 (subtyne FP3)	
1776		NM_012704	o ʻu	prostaglandin E receptor 3 (subtype EP3)	
					RIKEN cDNA 4833439O17 gene, immunoglobulin superfamily, member 2,
2045		21108 NM_019243	<b>9</b>	prostaglandin F2 receptor negative regulator	Innuhoglobulin superfamily, member 3, immunoglobulin superfamily, member 8, prostaglandin F2 recentor negative requirements.
					EST, Highly similar to PTGL_RAT Prostacyclin synthase (Prostaclandin 12 synthase)
2285		692 NM_031557	s, t,	prostaglandin I2 (prostacyclin) synthase	[R.norvegicus], cytochrome P450, subfamily VIIIB (sterol 12-alpha-hydroxylase),
				prostaglandin-endoperoxide synthase 2 prostaglandin-	polypepiloe 1, prostagiandin 12 (prostacyclin) synthase
1976	20193	20193 NM_017232	b,q	endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	prostaglandin-endoperoxide synthase 2, prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclopymense)
				Droteasome (prosome macronain) enhinet alaboration	מיים ביים לו וויות מיים מיים לו היססיל לפוומאבל
1991	15:42	15:42 NM_017278	l, m	proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type, 1 (macropain) subunit, alpha type, 1	proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type, 1 (macropain) subunit, alpha type, 1 (macropain) subunit, alpha type, 1
					meachaint abhla type, I
					EST, Weakly similar to SNHUC8 multicatalytic endopeptidase complex [H.sapiens], ESTs, Highly similar to PRC8 MOLISE PROTER COMPONIENT OF
				omeonic of the second control of the second	[M.musculus], ESTs, Weakly similar to PRC8 MOUSE PROTEASOME
99	18673	18673 AA849028		proteasonie (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha ture, 3	proteasonie (prosome, macropain) subunit, alpha type 3, COMPONENT C8 [M.musculus], proteasome (prosome, macropain) subunit, alpha proteasome (prosome, macropain) subunit, alpha
_				de la	Solution apria type, 3 lype 3, Proteasome (prosome, macropain) subunit, alpha type, 3
			•		ESTs, Weakly similar to JX0230 multicatalytic endopentidase complex (FC
1992	15538N	15538 NM_017283		proteasome (prosome, macropain) subunit, alpha type 6, [3.4.99.46) iota chain in proteasome (prosome macropain) arkiniti alpha type 6,	proteasome (prosome, macropain) subunit, alpha type 6, (3.4.99.46) iota chain - rat [R.norvegicus], proteasome (prosome, macropain)
				recommend (proporties, macropaint) subutilit, alpha type, 6 1:	Subtinit alpha type &

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ָ ט פ	:	- Genbank Acc.			Auy, Rel. 44921-5090-01-WO/2105485
	GLGC ID No.	ONo.	Model Co	Model Code Human Homologous Known Gene Name	Human Homologous. Sequence: Cluster. Title
					EST, Highly similar to PSAZ_HUMAN PROTEASOME SUBUNIT ALPHA TYPE 7
					(crocleasonine subdivit Rcb-1) (PROTEASOME SUBUNIT XAPC7) [H.sapiens] [EST. Highly similar to S60038 multicatalyric and open fidelity similar to S60038 multica
					alpha chain RC6-1 - rat R.norvenicus I Homo sanions, similar to Destandance
					Subunit alpha type 7 (Proteasome subunit RCG-1) clone MCC-36605
		<del></del>			IMAGE:4829939, mRNA, complete cds, RIKEN cDNA 2410072D24 gene.
1662		9029 D30804	<u>£</u>	proteasome (prosome, macropain) subunit, alpha type 7, professome (prosome macropain) subunit alpha type 7,	
				professome (prosome, macropain) sublinit heta type, o	madropain) subunit, alpha type, 7
1777	40 )3	40 )3 NM 012708	a	macropain) subunit, beta type 9 (large multifunctional	
		23.7	,	חוטובמסב ל)	multifunctional protease 2)
2346	176,01	176.31 NM_031976	a, <u>;;</u> ₹	protein kinase, AMP-activated, beta 1 non-catalytic suburit	expressed sequence AW049591, protein kinase, AMP-activated, beta 1 non-
1839	21237	212/37 NM_013065	E,	protein phosphatase 1. catalytic subunit heta isoform	vacajuro suburiii
					Process prospirates 1, catalytic subunit, beta isotorm RIKEN CENA 2040/407/40 CCC BUYEN CONTRACTOR
					phosphatase 1 regulation (in bilities) and 4933415F23 gene, protein
					Principlinates 1, regulatory (infiliplicity) Subunit 14A, protein phosphatase 1, regulatory
2503	96.33	9633 NM_130403	<u>≔</u> ≵	protein phosphatase 1 regulatory (inhihipr) subunit 444	(Inhibitor) subunit 14B, protein phosphatase 1, regulatory (inhibitor) subunit 14C,
_				ליייווחנות (יייווחנות) ליייווחנות ליייווחנות אלייייות אלייייים אליייים אליייים אליייים אליייים אליייים אליייים אליייים אליייים אליייים אלייים אליייים אליים אליים אליים אליים אלייים אליי	protein phosphatase 1, regulatory (inhibitor) subunit 14c
_					EST, Weakly Similar to IPP1_HUMAN PROTEIN PHOSPHATASE INHIBITOR 1
					H. Sapiens], ESTs, Moderately similar to PROTEIN PHOSPHATASE INHIBITOR 1
					R.norvegicus], Mus musculus, clone MGC:18770 IMAGE:4164563, mRNA,
2148	24564	24564 NM 022676	••-	profein phosphafase 1 regulatory (inhihities)	complete cds, RIKEN cDNA 4930565W23 gene, protein phosphatase 1 regulatory
_				atase 2 (formerly 2A), catalytic submit	subunit 1A, protein phosphatase 1, regulatory (inhibitor) subunit 1A
				protein phosphatase 2a, catalytic subunit	Protein phosphatase 2 (formaria 24)
1918	3203	3203 NM_017039	ပ		phosphatase 2a. catalytic subunit alpha isoform
			•		Mus musculus adult female placenta cDNA, RIKEN full-length enriched library.
					clone:1600017J22:protein phosphatase 2a, catalytic subunit, beta isoform, full insert
1919	24597 N	24597 NM_017040	b, l, m, u, v	b, I, m, u, v   beta isoform	sequence, protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform,
					protein prospitatase Za, catalytic subunit, beta isoform

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SEQ C	Gen	GenBank Acc.			Afty, Ref. 44921-5090-01-WO/2105485
2	GLGC IE	INO.	Model Code	Model Code Human Homologous Known Gene Name	Human Hômologous Sequence Gluster Title
2292		24219 NM_031579	d, p, q, y, z, Kk	d, p. q, y, z, protein tyrosine phosphatase 4a1, protein tyrosine kk	protein tyrosine phosphatase 4a1, protein tyrosine phosphatase 4a3, protein tyrosine phosphatase type IVA, member 1, protein tyrosine phosphatase type IVA,
					EST, Moderately similar to A34845 protein-tyrosine-phosphafase (FC 3.1.3.48)
1767		1841 NM 012637	<u>ئ</u> =: ح	nrofoin travaira - Learning	nonreceptor type 1B - rat [R.norvegicus], ESTs, Moderately similar to PTN1_HUMAN PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1
			W iff to	process tyrosine prosphatase, non-receptor type 1	[H.sapiens], protein tyrosine phosphatase, non-receptor type 1
					nonreceptor type 18 - rat [R.norvegicus]. ESTs. Moderately similar to
1767		1844 NM_012637	p, q, y, z	protein tyrosine phosphatase, non-receptor tyne 1	PTN1_HUMAN PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1
					ESTS, Weakly similar to 2103274A recentor type northern Tvr phosphatase
2021	14973	14973 NM_019140	ឧធ	protein tyrosine phosphatase, recentor tyne. D	[M.musculus], RIKEN cDNA 1600019004 gene, expressed sequence AU040377,
					Forein Viosine priospratase, receptor type, S FSTs. Highly similar to TUVA. LITHAM PROST IN A SOCIAL ASSESSMENT OF TUVA.
2085	22916	22916 NM 021740		prothymosin alpha, prothymosin, alpha (gene sequence	RIKEN cDNA 2610009E16 gene, prothymosin alpha, prothymosin, alpha (gene
				Dirinerdic recentor DOX lingual actual ica channel 4	sequence 28)
1510	4716/	4716 AI232313		purincials receptor 1 2.7, ligaringated for channel 4, purinergic receptor P2X, ligand-gated ion channel, 4	purinergic receptor P2X, ligand-gated ion channel 4, purinergic receptor P2X, ligand- pated ion channel 4
2499	363	363 NM 080780	d, e, p, q,	Plittingeric recorder DOV licend	מינים נסו מומונים ל
				purinergic receptor P.Z.A, ilgand-gated ion channel, 5	purinergic receptor P2X, ligand-gated ion channel, 5
					G protein-coupled receptor 31, G protein-coupled receptor 35, Mus musculus, clone
1983	1496N	1496 NM 017255		coupled 2, purinergic	ivico. 28142 liviade: 3982042, mRNA, complete cds, RIKEN cDNA 2610302102 gene, RIKEN cDNA 5830408N17 gene, expressed sequence AI662791, purineraic
		Т		eceptor PZT, G-protein coupled, 2	receptor P2Y, G-protein coupled 2, purinergic receptor P2Y, G-protein coupled, 2
					Mus musculus, similar to pyruvate dehydrogenase kinase, isoenzyme 1, clone MGC:28719 IMAGE:4458562, mRNA, complete cds. Mus musculus, similar to
				DVRUVafe dehydronenase C esenenorhydde dehydronenase	pyruvate dehydrogenase kinase, isoenzyme 3, clone MGC:6383 IMAGE:3500763,
2208	1928N	1928 NM_030872 s	s, t		MKNA, complete cds, pyruvafe dehydrogenase 2, pyruvafe dehydrogenase kinase,   isoenzvme 2

SEQ   GLGC   19   2208   19   2012   204	GLGC ID No.		Model Code Human Homologous Known Gene Name	Atty: Ref. 44921:5090-01-WO/2105485
2 8 CEC	ID No.		e Human Homologous Known Gene Name	5100110
~				Human Homologous Sequence Cluster Title
	1929 NM_030872	표	pyruvate dehydrogenase 2, pyruvate dehydrogenase kinase, isoenzyme 2	Mus musculus, Similar to pyruvate dehydrogenase kinase, isoenzyme 1, clone MGC:28719 IMAGE:4458562, mRNA, complete cds, Mus musculus, Similar to pyruvate dehydrogenase kinase, isoenzyme 3, clone MGC:6383 IMAGE:3500763, mRNA, complete cds, pyruvate dehydrogenase 2, pyruvate dehydrogenase kinase, isoenzyme 2
	20417 NM_017359	h, l, hh	RAB10, member RAS oncogene family	ESTS, Weakly similar to RAB8_HUMAN RAS-RELATED PROTEIN RAB-8 [H.sapiens], RAB10, member RAS oncogene family, RAB12, member RAS oncogene family, RAB38, member RAS oncogene family, expressed sequence AM107754
	20229 NM_013018		RAB3A, member RAS oncogene family	ESTs, Weakly similar to C34323 GTP-binding protein Rab3A [H.sapiens], RAB3A, member RAS oncogene family
2231 1830	18308 NM_031091	w, x W, X	RAB3B, member RAS oncogene family RAB3B, member RAS oncogene family	RAB3B, member RAS oncogene family
١	6577 NM_022532	>	raf-related oncogene, v-raf murine sarcoma 3611 viral oncogene homolog 1	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200013E08:raf-related oncogene, full insert sequence, expressed sequence AW495444, raf-related oncogene, v-raf murine sarcoma 3611 viral oncogene
2351 2180 1661 2527	21809 NM_032067 25278 D30734	66	Ral-interacting protein 1, ralA binding protein 1 Ral-interacting protein 1, ralA binding protein 1 RAS p21 protein activator 2	Ral-interacting protein 1, ralA binding protein 1 Ral-interacting protein 1, ralA binding protein 1
1547 22165	22152 AI234822	,;; K	RAS, dexamethasone-induced 1	Mus musculus small GTP-binding tumor suppressor 1 (Gbts1) mRNA, complete cds, Mus musculus, Similar to RAP1A, member of RAS oncogene family, clone MGC:18653 IMAGE:3600519, mRNA, complete cds, RAP2B, member of RAS oncogene family, RAS, dexamethasone-induced 1, RIKEN cDNA 1110065D03 gene, RIKEN cDNA 2010200P20 gene, RIKEN cDNA 5830461H18 gene, rap2A-like
1898 23362	23362 NM_013216	ф. Э.	RAS-homolog enriched in brain, Ras homolog enriched in brain 2	RAS-homolog enriched in brain, Ras homolog enriched in [M.musculus], RAS-homolog enriched in brain, RIKEN cDNA 1810036J22 gene, brain 2  Ras homolog enriched in brain 2, ras-like protein VTS58635
2373 1609	1609 NM_053338	j, p, q, y, z R	Ras-related associated with diabetes	ESTs, Weakly similar to Ras-related associated with diabetes [Rattus norvegicus] [R.norvegicus], GTP binding protein (gene overexpressed in skeletal muscle), GTP binding protein overexpressed in skeletal muscle, Ras-related associated with diabetes, rad and gem related GTP binding protein

TABIFIS	• 1				
W.	· ;ar	GenBank Acc			Atty. Refr 44924-5090-01-WO/2105485
7	GLGC ID No.	No.		Model Code Human Hr mologous Known Gene Name	Human Homolonous Societores Office Fells
ر ا	16(62	16' 62 NM 031646	n, o	ein 2	or (column) and the column
2062		2(:88 NM_019341	aa, bb	-protein	receptor (variounit) activity modifying protein 2
1947	20916	20916 NM_017132	ס	n 2, reticulocalbin 2, EF-hand calcium binding	ESTs, Weakly similar to 156519 taipoxin-associated calcium binding protein-49  2, reticulocalbin 2, EF-hand calcium binding precursor - rat [R.norvegicus], calumenin, reticulocalbin, reticulocalbin 2, reticulocalbin 2 EF-hand calcium binding domains.
1658	17264	17264 D25233	٥	EST, M [M.mus [M.mus obtained] (including ASSOC osteosarcoma)	EST, Moderately similar to RETINOBLASTOMA-ASSOCIATED PROTEIN [M.musculus], ESTs, Highly similar to RB MOUSE RETINOBLASTOMA- ASSOCIATED PROTEIN [M.musculus], retinoblastoma 1, retinoblastoma 1
1419	1377/	1377 AI227715	a, ee, ff	Mus mu library, cretinoblastoma-like 2 (p130)	Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700054A06:retinoblastoma-like 1 (p107), full insert sequence, retinoblastoma-like 1 (p107), full insert sequence,
2233	1376 N	1376 NM_031094	:=		Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700054A06:retinoblastoma-like 1 (p107), full insert sequence, retinoblastoma-like 1 (p107), full insert sequence,
1782	23806 N	23606 NM_012733			ESTs, Weakly similar to RET1_RAT Retinol-binding protein I, cellular (Cellular retinol-binding protein) (CRBP) [R.norvegicus], retinoid binding protein 7, retinoid binding protein 1, cellular, retinoid binding protein 5, cellular, retinoid binding protein 7, cellular, retinoid protein 7, cel
1850	1338 N	1338 NM_013022	<u>.</u>	Rho-associated coiled-coil forming kinase 2, Rho-Rho-associated, coiled-coil containing protein kinase 2 protein ki	Rho-associated coiled-coil forming kinase 2, Rho-associated, coiled-coil containing protein kinase 2, expressed semience Al In44030
					EST, Moderately similar to RIB2_HUMAN DOLICHYL- DIPHOSPHOOLIGOSACCHARIDEPROTEIN GLYCOSYLTRANSFERASE 63 KDA SUBUNIT PRECURSOR [H.sapiens], ESTs. Moderately similar to
2314	21575NI	21575 NM_031698	w, x	RIB2_HU   GLYCOS   GLYCOS   Il   Il   Il   Il   Il   Il   Il   I	RIB2_HUMAN DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE—PROTEIN GLYCOSYLTRANSFERASE 63 KDA SUBUNIT PRECURSOR [H.sapiens], ribophorin 2. related seminance 1. ribophorin 1.
2227	11849 NA	11849 NM_031065	h, l, n, o rit	ribosomal protein L10A, ribosomal protein L10a [M.muscu	EST, Moderately similar to R10A MOUSE 60S RIBOSOMAL PROTEIN L10A [M.musculus], ribosomal protein L10A, ribosomal protein L10a

	05485	. d	c 60S	<u>-</u>	<u></u>	mal	EIN L19	[5] [5]	is is
	Atty. Ref. 44921:5090-01-WO/2105485	Human Homologous Sequence Cluster Trile	EST, Moderately similar to JC2368 ribosomal protein L13, cytosolic [validated] - rat [R.norvegicus], EST, Weakly similar to JC2368 ribosomal protein L13, cytosolic [validated] - rat [R.norvegicus], ESTs, Highly similar to ribosomal protein L13.	Indosomal protein L13; breast basic conserved protein 1 [Homo sapiens] [H.sapiens], ESTs, Moderately similar to RL13 MOUSE 60S RIBOSOMAL	FEBRA2007458, Human RPL13-2 pseudogene mRNA, complete cds, ribosomal	ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L18 [M.musculus], ribosomal	EST, Weakly similar to RL19 MOUSE 60S RIBOSOMAL PROTEIN L19 [M.musculus], ESTs, Weakly similar to RL19_HUMAN 60S RIBOSOMAL PROTEIN L1 [M.musculus], ESTs, Weakly similar to RL19_HUMAN 60S ribosomal protein L19] R provenius	EST, Moderately similar to 2113200B nbosomal protein L21 [H.sapiens], EST, Moderately similar to 2113200B nbosomal protein L21 [H.sapiens], EST, Moderately similar to 2113200B nbosomal protein L21 [H.sapiens], EST, Weakly similar to 2113200B nbosomal protein L21 [H.sapiens], EST, Similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weakly similar to RL21_HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ESTs, Highly similar to 2113200B nbosomal protein L21 [H.sapiens], ESTs, Highly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], ESTs, Moderately similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus].	EST, Moderately similar to 2113200B ribosomal protein L21 [H.sapiens], EST, Moderately similar to 2113200B ribosomal protein L21 [H.sapiens], EST, Moderately similar to RL21_RAT 60S RIBOSOMAL PROTEIN L21 [R.norvegicus], EST, Weakly similar to 2113200B ribosomal protein L21 [H.sapiens], EST, Similar to RL21_HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], EST, Weakly similar to RL21_HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], EST, Highly similar to 2113200B ribosomal protein L21 [H.sapiens], ESTs, Highly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], ESTs, hibosomal protein L21 [M.musculus],
		Hur	ESI (R.n (vali	H.S.	FEB 4	EST	EST, [M.m. L1 [N	EST, Mode EST, Mode EST, Simila Simila Weak ESTs, Simila Moder	EST, Modern Modern EST, V Similar Weakly ESTS, I Similar Modera ribosom
		ene Name							
	H 1	omológous Known Gene Name			ribosomal protein L13	ribosomal protein L18	rrotein L19	otein 1.21	
		Wodel Code Human Homol			ribosomal	ribosomal	ribosomal protein L19	ribosomal protein	ribosomal protein i
:. :.		Iwodel Cod			f, w, x,	h, l	D		, w, x
	GenBank Acc.	į.			23854 NM_031101	20#62 NM_031102		053330 e	
	ي ز				23854 NN	20462 NN	16w38 NM_031103	14927 NM_053330	14929 NM_053330 5667 X58200
ABL	SEO ID				2237	2238	2239	2371	2371

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		GenBank Acc.		(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	- Atty: Ref. 44921-5090-01-14-01-
٥	GLGC ID No.	No.		Model Code Human Hemologous Known Gene Name	=
2125		2696 NM_022515	cc, dd	ribosomal protein L24	Homo sapiens, clone MGC:27044 IMAGE:4793412, mRNA, complete cds, Mus musculus, Similar to 60S ribosomal protein L30 isolog, clone MGC:6735 IMAGE:3590401, mRNA, complete cds, ribosomal protein 104
2125		NM_022515	f, g, gg	ribosomal protein 1 24	Homo sapiens, clone MGC:27044 IMAGE:4793412, mRNA, complete cds, Mus musculus, Similar to 60S ribosomal protein L30 isolog, clone MGC:6735
2124		3027 NM_022514	W, X	ribosomal protein L27	IMAGE:3590401, mRNA, complete cds, ribosomal protein L24
2152		17729 NM_022697	f, g, w, x, cc, dd		ribosomal profein I 28
2658		18611 X58200			EST, Moderately similar to RL29_HUMAN 60S RIBOSOMAL PROTEIN L29 [H.sapiens], EST, Moderately similar to RL29_RAT 60S RIBOSOMAL PROTEIN L29 (P23) [R.norvegicus], ESTs, Highly similar to S65784 ribosomal protein 1.20
2078		15335 NM_021264	o ≥	ribosomal protein (35a	cytosolic [H.sapiens], ribosomal protein L29
2120	4259 N	4259 NM_022504	f, g	ribosomal protein L36	EST, Moderately similar to ribosomal protein L36 [Rattus norvegicus]
2564	15380 N	15380 NM_139083	u, v, cc, dd	ribosomal protein L41	ESTS, Highly similar to YZA1_HUMAN HYPOTHETICAL PROTEIN [H.sapiens], ribosomal protein L36
					EST, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus], EST, Weakly similar to JN0923 ribosomal protein L8, cytosolic IH.saniens1 FSTs, Highly
					similar to R5RTL8 ribosomal protein L8, cytosolic [validated] - rat [R.norvegicus], ESTs, Highly similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L IM musculus]
2666	15875 X62145	62145	ı, r	ribosomal protein L8	ESTs, Moderately similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], expressed sequence AI 024098, ribosomal protein to
<del></del> -					EST, Moderately similar to S65792 ribosomal protein L9, cytosolic [H.sapiens], EST, Weakly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 IR nonvenious ESTs
2650	18250 X51706		w, ×	ribosomal protein L9	Weakly similar to 60S RIBOSOMAL PROTEIN L9 [M.musculus], RIKEN cDNA 4930401B11 gene, ribosomal profein I a
2653	20427 X53378		ų ų	ribosomal protein S13	ESTs, Moderately similar to RS13_HUMAN 40S RIBOSOMAL PROTEIN S13
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SEO		GenBank Acc.		The state of the s	Atty-Ref. 44921-5090-01-00-01-01-01-01-01-01-01-01-01-01-01
므	GLGC ID No.	No.	Model Code	Human Homologoûs Known Gene Name	Human Homologuis Carmano Olindo Trus
1955		16953 NM_017151	Б	ribosomal protein S15	EST, Moderately similar to R3HU15 ribosomal protein S15, cytosolic [H.sapiens], ESTs, Highly similar to RS15_HUMAN 40S RIBOSOMAL PROTEIN S15
1955		16954 NM_017151	66	ribosomal protein S15	EST, Moderately similar to R3HU15 ribosomal protein S15, cytosolic [H.sapiens], ESTs, Highly similar to RS15_HUMAN 40S RIBOSOMAL PROTEIN S15_IMMuscullus  ribosomal protein S15
1955		16955 NM_017151	l, m, s, t	ribosomal protein S15	EST, Moderately similar to R3HU15 ribosomal protein S15, cytosolic [H.sapiens], ESTs, Highly similar to RS15_HUMAN 40S RIBOSOMAL PROTEIN S15
2648		15£ 26 X17665	W, X	ribosomal protein S16	EST Al317031, EST, Weakly similar to R3HU16 ribosomal protein S16, cytosolic
2651	20€ 72	208 72 X51707	l, w, x	ribosomal protein S19	EST, Moderately similar to R3RT19 ribosomal protein S16 [R.norvegicus], EST, Weakly similar to RS19_HUMAN 40S RIBOSOMAL PROTEIN S19 [H.sapiens]
2492	104981	10498 NM_078617	c, g, w, x	ribosomal protein S23	ESTs, Highly similar to 40S RIBOSOMAL PROTEIN S23 [H.sapiens], ESTs, Weakly similar to ribosomal protein S23 [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to mitochondrial ribosomal protein S12, clone MGC:13892 IMAGE:4209358, mRNA, complete cds. mitochondrial ribosomal protein S12, ribosomal
					ESTs, Highly similar to ribosomal protein SZ7a [Mus musculus] [M.musculus], ESTs, Highly similar to ubiquitin / ribosomal protein SZ7a [Mus musculus], similar to ribosomal protein SZ7a [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to ubiquitin-like 4, clone MCC14422 (MACE144150)
2246	20839 N	20839 NM_031113	w, x	ribosomal protein S27a	complete cds, neural precursor cell expressed, developmentally down-regulated 8, ribosomal protein \$27a
1813	17305N	17305 NM_012876	g, hh	ribosomal protein S29	EST, Moderately similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 [M.musculus], ESTs, Weakly similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 IH.sapiens], ribosomal protein S29
1813	17306 <sub>N</sub>	17306 NM_012876   f	程	ribosomal protein S29	EST, Moderately similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 [M.musculus], ESTs, Weakly similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 IH.sapiens], ribosomal protein S29
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SEO		GenBank Acc			Atty. Ref. 44921;5090;01:WO/2105485
⊖	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologue Source Clineter Tata
					EST, Moderately similar to RS3 MOLISE this characteristics
					EST, Weakly similar to RS3 MOLISE 408 ribosomal protein S2 for notices.
	-				ESTs, Highly similar to RS3 MOUSE 40S ribosomal protein S3 Included to RS3 MOUSE 40S ribosomal protein S3 IR nonzeniens
					ESTs, Moderately similar to RS3 HUMAN 408 RIBOSOMAI DEOTEIN C
					[H.sapiens], ESTs, Weakly similar to RS3 MOLISE 40S RIBOSOMAL DEDUTEIN 52
2640		754500			[M.musculus], hypothetical protein FLJ11252, hypothetical protein FI 123059 miss
2070	- 1	10019/201330	99	ribosomal protein S3	inositol 1-phosphate synthase A1, ribosomal protein S3
7043		X51536	w, x, hh	ribosomal protein S3	On Higher Principles 1
0					EST. Moderately similar to 2113200F ribosomal protein SETU conional EST
8007	- [	25/02 X58465	g, w, x	ribosomal protein S5	Weakly similar to 2113200E ribosomal profein SS I'll sanians Tribosomal archain SE
					Command the control of the control o
0					EST. Moderately similar to 2113200E rithosomal protein SE ID comissor.
607	- 1	10109 X58465	g, w, x	ribosomal protein S5	Weakly similar to 2113200E ribosomal protein SE III conjunt
					EST, Moderately similar to R3HU6 ribosomal protein SS, cybrolic III sanions   EST
					Moderately similar to RS6 HI MAM And Displacement of Street,
					FOT Models designed to the control of the control o
					E31, Weakly Similar to K3HU6 ribosomal protein S6, cytosolic [H.sapiens], ESTs,
					Highly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ESTs.
1957	17104	17104 NIM 017160		7	Weakly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 IH, sapiens]
	5	T		noosomal protein So	ribosomal protein S6
					EST, Moderately similar to R3HU6 ribosomal protein S6, cytosolic IH, sapiens]. EST
					Moderately similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 IH.sapiens1
	<del></del>				EST, Weakly similar to R3HU6 ribosomal protein S6, cytosolic IH saniens. ESTs
					Highly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 IH saniens I FSTs
1057	47405				Weakly similar to RS6_HUMAN 40S RIBOSOMAL PROTFIN S6 IN saniens1
25	2017	OQL/IO WAIGOI/I	ם, ה	ribosomal protein S6	ribosomal protein S6
			_		EST, Moderately similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens]. EST.
		70			Moderately similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 IH.sapiens]
					EST, Weakly similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], ESTs.
	• • • • •				Highly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ESTs.
1957	17106N	17106 NM 017160	- 'E	thosomol profoir Oc	Weakly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens],
		1		nosonilal protein So	ribosomal protein S6

TABLE 3	3		À		
OH.	· •	GenBank Acc.	ŀ	· · · · · · · · · · · · · · · · · · ·	Attv. Ref. 44921-5090-01-1WO/210519E
۵	GLGC ID No.	O No.		Model Code Human Homologous Known Gene Name	DOCUMENT THE PROPERTY OF THE P
				EST, Moderately similar to CST, Weakly similar to RST (M.musculus), EST, Weakly	EST, Moderately similar to JC4388 ribosomal protein S7, cytosolic [H.sapiens], EST, Weakly similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [M.musculus], EST, Weakly similar to RS7_HI MANI 40s. shooting
2287		9620 NM 031570		[R.norvegicus], ESTs, Highly [H.sapiens], ESTs, Highly si [H.sapiens], ESTs, Highly si [H.sapiens], ESTs, Moderate	[R.norvegicus], ESTs, Highly similar to JC4388 ribosomal protein S7, cytosolic [H.sapiens], ESTs, Highly similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [H.sapiens], ESTs, Moderately similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7
2315	16204	16204 NM_031706		ribosomal protein S8	S7 [H.sapiens], ribosomal protein S7 [EST, Weakly similar to 40S RIBOSOMAL PROTEIN S8 [M.musculus], ESTs, Highly similar to S25022 ribosomal protein S8, cytosolic [H.sapiens], ESTs, Moderately similar to RS8_HUMAN 40S RIBOSOMAL PROTEIN S [H.sapiens], RIKEN cDNA 110008P08 gene ribosomal protein S9
2315	16205	16205 NM 031706	jj. KK	EST, Weakly similar to 40S similar to 40S ribosomal protein S8	EST, Weakly similar to 40S RIBOSOMAL PROTEIN S8 [M.musculus], ESTs, Highly similar to \$25022 ribosomal protein \$8, cytosolic [H.sapiens], ESTs, Moderately similar to RS8_HUMAN 40S RIBOSOMAL PROTEIN S [H.sapiens], RIKEN cDNA
28	18061	18061 AA799735		RuvB-like protein 1	Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene, 1
2316	18054	18054 NM_031707	f, g, n, o	RuvB-like 1 (E. coli), RuvB-like protein 1	Homer, neuronal immediate early gene, 18, homer, neuronal immediate early gene,
2316	18057	18057 NM_031707		RuvB-like 1 (E. coli), RuvB-like protein 1	Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene,
2316	18059 N	18059 NM_031707	p, q, ee, ff	RuvB-like 1 (E. coli), RuvB-like protein 1	Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene,
2247	19040 N	19040 NM_031114	a, c, h, l, y, ee, ff	0	EST, Moderately similar to S110_RAT Calpactin I light chain (P10 protein) (P11) (Cellular ligand of annexin II) (Nerve growth factor induced protein 42C) [R.norvegicus], S100 calcium binding protein A10 (annexin II ligand, calpactin I, light
1764	20589 NI 16394 NI	20589 NM_012618 16394 NM_053485	h, l, n, o, w, x h, l, w, x	h, I, n, x S100 calcium binding protein A4, S100 calcium binding protein A (calcium protein, calvasculin, metastasin, murine placental homolog)  S100 calcium binding protein A4, S100 calcium binding protein A6, A6, A6, A6, A6, A6, A6, A6, A6, A6,	Protypepude (p.11), S100 calcium binding protein A10 (calpactin) S100 calcium binding protein A2, S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
			]		

TABI F. 2		**************************************	A Comment of the Comm	The state of the s	
ŭ		GenBank Acc.			Atty, Ref. 44921-5090-01-WO/2105485
۽ ا	GLGC ID No.	ONo.		Model Code Human Hr mologous Known Gene Name	Human Homologous Sequence Cluster Title
	, ר <b>י</b>				rolase-like 1, clone MGC:18748
1967		20779 NM 017201	E. J.	Sadenosylhomonysteine bydologo	adenosylhomocysteine hydrolase, related sequence 3, expressed sequence
2214		15682 NM 031011	n. 0	S-adenosylmethionine decathoxyloco 4	AL024110
2214		15683 NM_031011	cc, dd, gg	S-adenosylmethionine decarboxylase 1	S-adenosylmethionine decarboxylase 1, S-adenosylmethionine decarboxylase 2
1770		NIM OTOCCO		secreted acidic cysteine rich glycoprotein, secreted	Secreted acidic cysteine rich alvooprotein, secreted protein acidic cysteine rich
		1021/ INM_012656	c, aa, bb	protein, acidic, cysteine-rich (osteonectin)	(osteonectin)
1770		16218 NM_012656	0,0	, secreted	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich
1770		16219 NM 012656		, secreted	(osteonectin) secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich
		00710	66 1		(osteonectin)
1770		16220 NM_012656	h, I, aa, bb		secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)
1770		16221 NM_012656	9	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich
				sphoprotein 1, secreted phosphoprotein 1	
1814		23651 NM_012881	h, I, n, o, w, (osteopontin, x	(osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	
1851	17894	17894 NM_013027	s 56	selenoprotein W, 1, selenoprotein W, muscle 1 s	ESTs, Weakly similar to SELW MOUSE SELENOPROTEIN W [M.musculus], selenoprotein W, 1, selenoprotein W, muscle 1
1718	21400	21400 M36410	s ee, ff, gg d	Sepiapterin reductase, sepiapterin reductase (7,8-	ESTs, Highly similar to A36024 sepiapterin reductase (EC 1.1.1.153) - rat [R.norvegicus], sepiapterin reductase, sepiapterin reductase (7,8-dihydrohionterin NADE+ exidence.
1765	15540 1	15540 NM_012620	s a, kk p	e e	יין אינטייניין אינטיין
			<b>ω</b> 7	heat	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1,
1961	17301N	17301 NM_017173	c, f, g, j, k, pu v, z	proceduce protein 47), mentiber 1, serine (or cysteine) ser proteinase inhibitor, clade H (heat shock protein 47), (commember 1, collanen hinding protein 4)	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1), serine (or cysteine) proteinase inhibitor, clade H (heat
		1		iagen binding protein 1)	shock protein 47), member 2

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<u>S</u> . 0	GI GC ID No	GenBank Acc.	Model Code		Atty: Ref. 44921-5099-01-WO/2105485
			anonai cone	model Code Indinan Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2322		15507 NM_031735	3	serine/threonine kinase 3 (STE20 homolog, yeast), serine/threonine kinase 3 (Ste20, yeast homolog)	serine/threonine kinase 24 (STE20 homolog, yeast), serine/threonine kinase 25 (STE20 homolog, yeast), serine/threonine kinase 25 (yeast), serine/threonine kinase 3 (STE20 homolog, yeast), serine/threonine kinase 3 (Ste20, yeast homolog), serine/threonine kinase 4
2042		20 33 NM_019232	ر بې پې	serum/glucocorticoid regulated kinase	EST, Weakly similar to SGK_RAT Serine/threonine-protein kinase Sgk (Serum/glucocorticoid-regulated kinase) [R.norvegicus], Mus musculus, hypothetical protein MGC11287 similar to ribosomal protein S6 kinase ., clone MGC:38756 (IMAGE:5358742, mRNA, complete cds, RIKEN cDNA 1190006F07 gene, serine/threonine protein kinase CISK, serum/glucocorticoid regulated kinase, serum/hlucocorticoid regulated kinase,
					ESTS, Highly similar to SNK_RAT Serine/threonine-protein kinase-like inducible kinase) [R. Norvegicus], ESTS, Weakly similar to SNK (Serum inducible kinase) [R. norvegicus], ESTS, Weakly similar to SNK MOUSE SERINE/THREONINE-PROTEIN KINASE SNK [M. musculus], ESTS, Weakly similar to SNK_RAT Serine/threonine-protein kinase SNK (Serum inducible kinase)
2334	2955 N	2655 NM_031821	Q	[i   Serum-inducible kinase	[R.norvegicus], Homo sapiens cDNA FLJ30246 fis, clone BRACE2002202, weakly similar to SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1), NIMA (never in mitosis gene a)-related expressed kinase 1, NIMA (never in mitosis gene a)-related kinase 4, serum-inducible kinase
				H	EST, Moderately similar to SSRD_RAT TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR (TRAP-DELTA) (SIGNAL SEQUENCE RECEPTOR DELTA SUBUNIT) (SSR-DELTA) [R.norvegicus], EST, Weakly similar as SED III MAN TRANSLOCOM
1966	9124 N	9124 NM_017199  F	si h, i, hh	P signal sequence receptor, delta, signal sequence α receptor, delta (translocon-associated protein delta) as	PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:4038523, mRNA, partial cds, signal sequence receptor, delta, signal sequence receptor, delta, signal sequence receptor, delta.

ABL	:		.:	The second secon	
850		GenBank Arc.			Atty, Ref. 44921-5090-01-WO/2105485
<u>ء</u>	31.GC DIN	N.		Model Gode Human Ho nologous Known Gene Name	Human Homologous Sequence Cluster Title
					EST, Highly Similar to 142626 secreted religine-rich repeat-containing protein SCLTZ
					MGC7599; clone MGC:7599 [Mus musculus] [M.m.sculus]. ESTs. Weakly similar to
			<del></del>		integral membrane glycoprotein [Mus musculus] [M.musculus], ESTs, Weakly similar to ALS MOUSE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN
					COMPLEX ACID LABILE CHAIN PRECURSOR [M.musculus], ESTs, Weakly
					similar to J60193 G protein-coupled receptor FEX - mouse [M.musculus], ESTs,
					Weakly similar to Slit-1 protein [H.sapiens], Mus musculus, Similar to leucine-rich
	-				repeat-containing 3, clone MGC:30505 IMAGE:4481142, mRNA, complete cds,
2167	15727	15727 NM_022953	n' n	slit homolog 1 (Drosophila)	RIKEN GUNA 95300/4E10 gene, slit homolog 1 (Drosophila), slit homolog 2 (Drosophila) elit homolog 2
					EST, Weakly similar to S07723 immediate-early serum-responsive protein. IF
			2 d 7 pp	emal individual outobing A control of individual leads	precursor - rat [R.norvegicus], expressed sequence Al323594, small inducible
2277	20448	20448 NM_031530	ff, jj, kk	(monocyte chemotactic protein 1)	cytokine A2, small inducible cytokine A24, small inducible cytokine subfamily A (Cys-
					EST Wooth civilar to 207773 in the state of
					Decursor - rat R.norvegicus] expressed sequence 4/3/3/504 email inclusive
1400	- 07700	000000	a, z, ee, ff,	I inducible cytokine A2	Cytokine A2, small inducible cytokine A24, small inducible cytokine subfamily A / Cyc.
1177	204469	ZU449 NM 031530	X.		Cys), member 24
		_		small inducible cytokine subfamily D (Cys-X3-Cys),	
2545	19077	19077 NM 134455	44	neurotactin), small inducible	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine,
			aa, uu	Cytoknire subrarnily L., 1	neurotactin), small inducible cytokine subfamily D, 1
1801	202461	20246 NM_012807	l, m, s	smoothened homolog (Drosophila)	ES1, Moderately similar to SMO_HUMAN SMOOTHENED HOMOLOG PRECURSOR IH saniens! smoothened homolog (Drecorbing)
					Mus musculus brain and heart sodium channel beta 3 subunit mRNA, complete cris
1993	20579 N	20579 NIM 047288	44		sodium channel beta 3 subunit, sodium channel, voltage-gated, type 1, beta
200	2001	1		sogium channel, voltage-gated, type I, beta polypeptide	polypeptide

TABLE 3	3			のでは、	The state of the s
SEO		GenBank Acc.			Atty, Ker. 44921-5090-01-WO/2105485
₽	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					ESTs, Weakly similar to EAA3_RAT Excitatory amino acid transporter 3 (Sodium-dependent glutamate/aspartate transporter 3) (Excitatory amino-acid carrier 1)
					[R.norvegicus], Mus musculus adult male testis cDNA, RIKEN full-length enriched
			-		library, clone:4931413K05:solute carrier family 1, member 1, full insert sequence,
					Rattus norvegicus mRNA for sodium-dependent neutral amino acid transporter,
				solute carrier family 1 (neuronal/epithelial high affinity	ASCT2, solute carrier family 1 (neuronal/epithelial high affinity glutamate
1664		21147 D63772	ر بر ا	glutamate transporter, system Xag), member 1, solute	transporter, system Xag), member 1, solute carrier family 1, member 1, solute
				solute carrier family 11 (proton-complet divalent metal icon	Califer Lathiny 1, Member /
2279		1005 NM_031537	l, m		
					Mus musculus strain ILS K-Cl cotransporter (SIc12a5) mRNA complete cds cation-
			-:-		chloride cotransporter 6. cation-chloride cotransporter 9. cation-chloride
				family 12 (sodium/potassium/chloride	cotransporter-interacting protein 1, solute carrier family 12
				member 2, solute carrier family 12,	(sodium/potassium/chloride transporters), member 2, solute carrier family 12
2331	2114	2114 NM_031798	aa, bb		member 2
1770		VIII 040740		amily 16 (monocarboxylic acid	RIKEN cDNA 1110004H10 gene, RIKEN cDNA 1200003C15 gene, solute carrier
2		2000 NWI 012/10	e '5'	member 1	family 16 (monocarboxylic acid transporters), member 1
4770	00000	0707070		family 16 (monocarboxylic acid	RIKEN cDNA 1110004H10 gene, RIKEN cDNA 1200003C15 gene, solute carrier
2	18007 70007	ZU009 INM 012/16	e, aa, bb	transporters), member 1	family 16 (monocarboxylic acid transporters), member 1
					solute carrier family 19 (folate transporter), member 1, solute carrier family 19
					(sodium/hydrogen exchanger), member 1, solute carrier family 19
				family 19 (folate transporter), member 1,	(sodium/hydrogen exchanger), member 3, solute carrier family 19 (thiamine
4006	30000	0000170		rier family 19 (sodium/hydrogen exchanger),	transporter), member 2, solute carrier family 19 (thiamine transproter), member 2,
022	73073	667/10 MINI C7967	cc, ad		solute carrier family 19, member 3
2554	10707	700007 711		пег family 2 (facilitated glucose transporter),	Mus musculus, clone MGC:8298 IMAGE:3593581, mRNA, complete cds, solute
7007	104701	10240 NW 13882/	y, z		carrier family 2 (facilitated glucose transporter), member 1
0554	2000	100007		rier family 2 (facilitated glucose transporter),	Mus musculus, clone MGC:8298 IMAGE:3593581, mRNA, complete cds, solute
7331	1074311	10249 MM 13882/	I, K	member 1	carrier family 2 (facilitated glucose transporter), member 1

GELGC ID No. Model Code Human Homologous Krown Gene Name  1510 NM_017224 II member 6  18018 D12771 f, g mucleotide translocator), member 5  20735 NM_013030 cc, dd solute carrier family 3 (activators of dibasic and neutral solute carrier family 34 (anion exchanger), member 1  20735 NM_013030 cc, dd solute carrier family 34 (sodium phosphale), member 1  18355 A1045744 b, u, v group)  24859 NM_017048 u, v, ii solute carrier family 4 (anion exchanger), member 2  24859 NM_01706	TABLE	TABLE 3 Comments	رُزِيْنَ مُنْ مِنْ الشَّمْعِيقَ ا		The state of the s	CONTRACTOR CONTRACTOR
Solute carrier family 22 (organic anion transporter), member 6   Solute carrier family 22 (organic anion transporter), member 6   Solute carrier family 23 (mitochondrial carrier; adenine of nucleotide translocator), member 5   Solute carrier family 28 (mitochondrial carrier; adenine of nucleotide translocator), member 5   Solute carrier family 3 (activators of dibasic and neutral solute carrier family 3 (activators of dibasic and neutral solute carrier family 3 (activators of dibasic and neutral solute carrier family 4 (anion exchanger, member 1   Solute carrier family 4 (anion exchanger, member 1   Solute carrier family 4 (anion exchanger, member 1   Solute carrier family 4 (anion exchanger, member 2   Solute carrier family 4 (anion exchanger, member 2   Solute carrier family 4 (anion exchanger, member 2   Solute carrier family 4 (anion exchanger, member 2   Solute carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter, second carrier family 6 (neurotransmitter transporter) (second carrier family 6 (neurotransmitter) (second carrier family 6 (neurotransmitter) (second carrier family 6 (neurotransmitter) (second carrier family 6 (neurotransmitter) (second carrier) (second carrier family 6 (neurotransmitter) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (second carrier) (se	SEO		GenBank Acc.			AUY: Kei, 448ZI-508U-U-WU/ZIU5485
solute carrier family 22 (organic anion transporter), member 6 18018 D12771	으	GLGC ID	No.	Moděl-Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5  20743 NM_031684  a, x, z, kk member 1  20734 NM_019283  kk mino acid transport), member 2  i, k, t, y, z, solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2  i, k, t, y, z, solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2  i, k, t, y, z, solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2  i, k, t, y, z, solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 1  solute carrier family 4 (anion exchanger), member 1  solute carrier family 4, anion exchanger, member 2  solute carrier family 4 (anion exchanger), member 2  solute carrier family 4, anion exchanger, member 2  solute carrier family 4, anion exchanger, member 2  solute carrier family 6 (neurotransmitter transporter, solute carrier family 6 (neurotransmitter transporter, solute carrier), member 6  in v, ii (arvine), member 6  solute carrier family 6 (neurotransmitter transporter, solute carrier)  solute carrier family 6 (neurotransmitter transporter, solute carrier), member 6	1973		NM 017224	-		Homo sapiens, Similar to ust3, clone MGC:23972 IMAGE:4714598, mRNA, complete cds, Mus musculus, Similar to solute carrier family 22 (organic anion transporter), member 7, clone MGC:18877 IMAGE:4236556, mRNA, complete cds, Rattus norvegicus mRNA for organic anion transporter 5, complete cds, expressed sequence Al648912, putative integral membrane transport UST1r, solute carrier family 22 (organic anion transporter), member 6, solute carrier family 22 (organic
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5  20743 NM_031684 a, x, z, kk member 1  20734 NM_019283 kk member 1  j, k, t, u, v, jj, solute carrier family 3 (activators of dibasic and neutral mino acid transport), member 2  j, k, t, y, z, solute carrier family 3 (activators of dibasic and neutral mino acid transport), member 2  j, k, t, y, z, solute carrier family 3 (activators of dibasic and neutral mino acid transport), member 2  solute carrier family 4 (anion exchanger), member 1  (erythrocyte membrane protein band 3, Diego blood group)  solute carrier family 4 (anion exchanger), member 2  solute carrier family 4 (anion exchanger), member 2  solute carrier family 4, anion exchanger, member 2  solute carrier family 4, anion exchanger, member 2  solute carrier family 4, anion exchanger, member 2  solute carrier family 6 (neurotransmitter transporter, solute carrier family 6, neurotransmitter transporter, solute carrier family 6 (neurotransmitter transporter, solute carrier family 6)						Cauor varisporter Fixe 2, usts EST, Moderately similar to S03894 ADP,ATP carrier protein T3 [H.sapiens], EST, Weakly similar to A29132 ADP,ATP carrier protein T2 [H.sapiens], Homo sapiens, clone IMAGE:5215220, mRNA, Mus musculus, Similar to CG4995 gene product, clone MGC:7958 IMAGE:3584570, mRNA, complete cds, RIKEN cDNA
solute carrier family 29 (nucleoside transporters),  20734 NM_019283 Kk amino acid transport), member 2  20735 NM_019283 kk amino acid transport), member 2  i, k, t, y, z, solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2  i, k, t, y, z, solute carrier family 34 (sodium phosphate), member 1  solute carrier family 4 (anion exchanger), member 1  (erythrocyte membrane protein band 3, Diego blood (erythrocyte membrane) (erythrocyte me	1655		D12771	f, g	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	carrier, adenine nucleotide translocator), member 5, solute carrier family 25 (mitochondrial (mitochondrial carrier; adenine nucleotide translocator), member 5, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
1, K, t, u, v, ij, solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2  20735 NM_019283 kk amino acid transport), member 2  18076 NM_013030 cc, dd solute carrier family 34 (sodium phosphate), member 1  solute carrier family 4, anion exchanger, member 1, solute carrier family 4, anion exchanger, member 1  (erythrocyte membrane protein band 3, Diego blood group)  solute carrier family 4 (anion exchanger), member 2, solute carrier family 4, anion exchanger, member 2, solute carrier family 4, anion exchanger, member 2, solute carrier family 4, anion exchanger, member 2, solute carrier family 6 (neurotransmitter transporter, taurine), member 6	2311	20743	NM_031684	a, x, z, kk	solute carrier family 29 (nucleoside transporters), member 1	ESTs, Weakly similar to solute carrier family 29 (nucleoside transporters), member 1 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 4933435C21 gene, solute carrier family 29 (nucleoside transporters), member 1
18076 NM_019283 kk amino acid transport), member 2  18076 NM_013030 cc, dd solute carrier family 34 (sodium phosphate), member 1, solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)  24697 NM_017048 u, v, ii (erythrocyte membrane protein band 3-like 1)  24859 NM_017206 h, i taurine), member 6	2052	20734	NM_019283	j, k, t, u, v, jj, kk	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
18076 NM_013030 cc, dd solute carrier family 34 (sodium phosphate), member 1, solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group) solute carrier family 4 (anion exchanger), member 2, solute carrier family 4, anion exchanger, member 2, solute carrier family 4, anion exchanger, member 2, solute carrier family 6 (neurotransmitter transporter, taurine), member 6	2052	20735	NM_019283	, t, y, z,	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
16335 Al045744 b, u, v group) 24697 NM_017206 lu, v, ii (erythrocyte membrane protein band 3-like 1) solute carrier family 4 (anion exchanger), member 1 (erythrocyte membrane protein band 3, Diego blood group) 24859 NM_017206 lu, v, ii (erythrocyte membrane protein band 3-like 1) solute carrier family 6 (neurotransmitter transporter, taurine), member 6	1852	180761	NM_013030		solute carrier family 34 (sodium phosphate), member 1	Rattus norvegicus mRNA for Na+/Pi-cotransporter type IIc, complete cds, Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, expressed sequence Al649385, solute carrier family 34 (sodium phosphate), member 1
24697 NM_017048 u, v, ii (erythrocyte membrane protein band 3-like 1) solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1) solute carrier family 6 (neurotransmitter transporter, taurine), member 6	985	16335	A1045744		solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	ESTs, Moderately similar to B3AT MOUSE BAND 3 ANION EXCHANGE PROTEIN [M.musculus], expressed sequence Al503023, solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3. Dieno blond grann)
24859 NM_017206 (h, l taurine), member 6	1920	24697	VM_017048		solute carrier family 4 (anion exchanger), member 2, solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	solute carrier family 4 (anion exchanger), member 2, solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein hand 3-like 1)
	1969	24859 N			solute carrier family 6 (neurotransmitter transporter, taurine), member 6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6

<b>TABLE 3</b>	3			· 一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个	- CALLED CO. CO. CO. CALL D. C. TAR.
SEO		GenBank Acc.			AUV., TREI: 448 Z 1-50 UP-U1-WO/Z105485
	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1923	ł	1876 NM_017052	w, x	sorbitol dehydrogenase, sorbitol dehydrogenase 1	ESTs, Highly similar to A54674 L-iditol 2-dehydrogenase [H.sapiens], sorbitol dehydrogenase, sorbitol dehydrogenase 1
					ESTs, Weakly similar to SFRS MOUSE SPLICING FACTOR, ARGININE/SERINE-RICH 5 [M.musculus], Mus musculus, clone MGC:36924 IMAGE:4945988, mRNA,
					complete cds, RIKEN cDNA 1210001E11 gene, RIKEN cDNA 6330415C05 gene,
				splicing factor, arginine/serine-rich 5, splicing factor,	sprous racios, arginine/serine-rich 1 (spriong ractor 2, attemate spriong ractor), splicing factor, arginine/serine-rich 4, splicing factor, arginine-rich 5, splicing
2049	-	23419 NM 019257		arginine/serine-rich 5 (SRp40, HRS)	factor, arginine/serine-rich 5 (SRp40, HRS)
240		16681 NM_01/136		squalene epoxidase	Homo sapiens cDNA FLJ30795 fis, clone FEBRA2001124, squalene epoxidase
2294		14542 NM_031596	_	squamous cell carcinoma antigen recognised by T cells, squamous cell carcinoma antigen recognized by T-cells 1	
2294		14543 NM_031596	, u, d	squamous cell carcinoma antigen recognised by T cells, squamous cell carcinoma antinen recognized by T-rells 1	
865		20924 AI012832	<u></u>	stannin	RIKEN cDNA 2810407J07 gene. stannin
2491	15707	15707 NM_058208	ō	STAT induced STAT inhibitor-2, cytokine inducible SH2- containing protein 2	ESTs, Weakly similar to cytokine inducible SH2-containing protein CiS4 [Mus musculus] [M.musculus], JAK binding protein, RIKEN cDNA 5830401B18 gene, STAT induced STAT inhibitor-4, Socs-5, cytokine inducible SH2-containing protein 2
					ESTs, Highly similar to 137186 arylsulfatase D [H.sapiens], ESTs, Weakly similar to STS MOUSE STERYL-SULFATASE PRECURSOR [M.musculus], ESTs, Weakly
					similar to STS_RAT STERYL-SULFATASE PRECURSOR (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYI SIJI FATASE C) (ASC)
1771	21087	21087 NM_012661	s pp 'so	steroid sulfatase, steroid sulfatase (microsomal), arylsulfatase C, isozyme S	[R.norvegicus], arylsulfatase E (chondrodysplasia punctata 1), arylsulfatase F, steroid sulfatase. C isozume S
1236	15393/	15393 AI170663	cc, dd	sterol regulatory element binding transcription factor 2	sterol regulatory element binding factor 1, sterol regulatory element binding factor 2, sterol regulatory element binding transcription factor 2
1694	17508 L08814	.08814	<i>.</i>	structure specific recognition protein 1	ESTs, Weakly similar to S35637 high mobility group 1 protein homolog - rat (fragment) [R.norvegicus], Mus musculus, clone IMAGE:4948318, mRNA, partial cds, Mus musculus, clone IMAGE:5355658, mRNA, structure specific recognition protein 1

23.36 4748 NM_031834 to 1922 20875 NM_017050 re 1922 20875 NM_017050 re 2130 4601 NM_022524 re 1930 4601 NM_022524 re 1930 4601 NM_022524 re 1930 4601 NM_022524 re 1930 4601 NM_022524 re 1930 NM_022524 re 1930 4601 NM_022524 re 1930 4601 NM_022524 re 1930 NM_022524 re 1930 4601 NM_022524 re 1930 NM_	ank Acc. Model 53752 aa, bb 1834 s, t, aa, 1834 s, aa, 1834 s, t, aa, 1834 s, t, aa, 1834 s, t, aa, 1834 s, t, aa, 1834 s, aa, 1834 s, t, aa, 1834 s, aa, 18	Code		Alty: Ref. 44921-5090-01-WG/2105485
24 GLGC D No. 24 187 75 NM 053 2336 4748 NM 0318 2336 4749 NM 0318 1922 20875 NM 0170 2164 18738 NM 0229 2130 4601 NM 0225	33752 aa, 1834 s, t,	Code	Human Ho nologous Known Gene Name	distribution of the second of
24 % 18175 NM_053 2336 4748 NM_0318 2336 4749 NM_0318 1922 20875 NM_0170 2164 18038 NM_0229 2130 4601 NM_0225;	33752 aa, 1834 s, t,			Human Homologoris Segmence, Chreter Tilla
22 22 31			succinate-oo ligase, GDP-forming, alpha subunit	
2 2		s, t, aa, bb	sulfotransferase family 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	sulfotransferase family 1A, phenol-preferring, member 1, 1110030E23 gene, sulfotransferase family 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1, sulfotransferase
	1834 t, bb		sulfotransferase family 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	Aryl sulfotransferase cytosolic, 1A, phenol-preferring, member 3, RIKEN cDNA 1110030E23 gene, sulfotransferase family 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2
	7050 hh	- 5, 4-	superoxide dismutase 1, soluble, superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	EST, Weakly similar to SODC MOUSE SUPEROXIDE DISMUTASE [M.musculus], superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
	7050 r	o ←	superoxide dismutase 1, soluble, superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)	EST, Weakly similar to SODC MOUSE SUPEROXIDE DISMUTASE [M.musculus], superoxide dismutase 1, soluble (amyotrophic lateral solocosis 1 fodulus)
	2947	s a	JC	(duli)
				ESTs, Weakly similar to down-regulated by v-src gene [Rattus norvegicus] [R.norvegicus], Homo sapiens mRNA; cDNA DKFZp586N2022 (from clone DKFZp586N2022), RIKEN cDNA 1110039C07 gene. RIKEN cDNA 2610001517
	524 l, m	<u>∞</u> 5.	sushi-repeat-containing protein, sushi-repeat-containing grotein, X chromosome	gene, sushi-repeat protein, sushi-repeat-containing protein, sushi-repeat-containing protein, X chromosome
833 15917 AI011498	<u>م</u>	လ ရူ	SWI/SNF related, matrix associated, actin dependent segulator of chromatin, subfamily d, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2, SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
2027 20440 NM_019166	166 b, I, m		Synaptogyrin 1	ESTs, Moderately similar to SNG1_RAT SYNAPTOGYRIN 1 (P29) [R.norvegicus], synaptogyrin 1, synaptogyrin 3, synaptogyrin 4

TABIE2	~ -	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	. 4 4 7		
		4		Control of the second of the s	Ah Ref Algor snon na monantage
<u>0</u>	GLGC ID No.	Senbank Acc.		Model Code Human Homologous Known Gene Name	Himan Homologous Seguence Cluster Title
					H.V. Micely, ameles & Journal
		_			EST, Weally Stiffliar to JWU to Synaptojanin 2 alpha protein - mouse [M.musculus],
					ESTS, Moderately similar to PW0049 synaptojanin 2 zeta protein - mouse
					(fragment) [M.musculus], ESTs, Weakly similar to JW0105 synaptojanin 2 alpha
				-	protein - mouse [M.musculus], ESTs. Weakly similar to T42384 innefine 4.4.5.
					Hisphoenhate S-nhoenbataco (M. misoscilla Llomo, contra to the contrata to the
			_		unspring Spring Spring Pringspring as Eliv. Husculus, nomo sapiens CDNA: PLJ23105 fls,
					cone LNGU/6/7, inositol polyphosphate 5-phosphatase, oculocerebrorenal
					syndrome of Lowe, phosphatidylinositol (4,5) bisphosphate 5-phosphatase
0300		1	,		homolog; phosphatidylinositol polyphosphate 5-phosphatase type IV
7007	-	11-11 NM 0320/1	y, z	synaptojanin 2	phosphatidylinositol (4.5) hisphosphate 5-phosphatase A synaptician o
2015	- 1	205 36 NM 019122	b, l, m, u, v	synaptotagmin 3, synaptotagmin III	(1-7) - chirachina a hisabilatasa, A, synapinjaliii z
1769		94 23 NM_012649	j, k, y, z	syndecan 4, syndecan 4 (amphiglycan, ryudocan)	Synderan A synderan A (amphichaea anderen)
2250		NM_031124	n' v	1 55	Symbolic Description 2 American 2
				Americal of the second of the	Sympaxin 3, Sympaxin 3A
000		207070		synuciein, aipna, synuciein, aipha (non A4 component of	
0707		74"30 INM_019169	n, o	amyloid precursor)	synuclein, alpha, synuclein, alpha (non A4 component of amyloid precursor)
					ESTs, Weakly similar to S58222 PQ-rich protein [H.sapiens]. T-cell death
					associated gene, pleckstrin homology-like domain, family A member 1 pleckstrin
7				T-cell death associated gene, pleckstrin homology-like	homology-like domain, family A. member 3. tumor suppressing subtransferable
3 5	3815	190 1/180 U1/180	6	domain, family A, member 1	candidate 3, tumor-suppressing subchromosomal francerable francer 3
7797	200/3	UZ6310	66	tensin	O HIGH BOTT DESCRIPTION OF THE PROPERTY OF THE
					RIKEN cDNA 4833428C18 gene. RIKEN cDNA 4930584N22 gene hynothetical
-	!				profein BC007901, testis specific profein kinase 1, testis specific broties
2291	21715	21715 NIM_031578		testis specific protein kinase 1, testis-specific kinase 1	Specific kinase 2
2299	24234	24234 NM_031614	r, y, z, jj, kk	thioredoxin reductase 1	thioredoxin reductase 1 thioredoxin reductase 2
2299	24235	24235 NM_031614	y, z, kk	thioredoxin reductase 1	thioredoxin reductace 1 thioredoxin reductace 2
2140	21076	21076 NM_022584			thioradoxin radiofase 2
450	12031/	12031 AA893860		g	through to the control of the contro
					uneonly-triva synthetase
1815	16871	16871 NM 042887			ES IS, Highly similar to THPA_HUMAN THYMOPOIETIN ALPHA [H.sapiens],
2000	3	WIN 012007	=		RIKEN cDNA 5630400D24 gene, thymopoietin
//07	101802	208 10 NIM 021261	- 1		
7.07			ď, Ľ	thyrotropin releasing hormone, thyrotropin-releasing	
CC01	등  -  -	11113 NM_013046	v, gg		thyrotropin releasing hormone, thyrotropin-releasing hormone
0.00			K, n, o, y, z, 1	n releasing hormone, thyrotropin-releasing	
1822	11114 N	11114 NM_013046	芝		thyrotropin releasing hormone, thyrotropin-releasing hormone

TABI E 3				この 一	
SEO	ŀ·	GenBank Acc.		The second secon	(Atty. Ref. 44921-5090-01-WO)2105485
₽	GLGC DN).	N.	Model Code	Model Code Human Ho nologous Known Gene Name	Human Homologous Sequence Chister Tille
2092		243 NM_021989	h, l, n, o, ll	tissue inhibitor of metalloproteinase 2	7 (from clone D
				tissue inhibitor of metalloproteinase 3, tissue inhibitor of	decide minister of metallobiotellase z
229		17236 AA858903	s, t, gg	metanoproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundis dystronby peandoinflammetany)
				tissue inhibitor of metalloproteinase 3, tissue inhibitor of	Cores Transaction, pseudoninaminatory
,			:	metalloproteinase 3 (Sorsby fundus dystrophy,	tissue inhibitor of metalloproteinase 3. fissue inhibitor of metalloproteinase 3.
21.0		17231 AA924107	=	pseudoinflammatory)	(Sorsby fundus dystrophy, pseudoinflammatory)
				tissue inhibitor of metalloproteinase 3, tissue inhibitor of	
000			:	metalloproteinase 3 (Sorsby fundus dystrophy,	lissue inhibitor of metalloproteinase 3 fissue inhibitor of metalloproteinase 3
/Ro		17232 AA965161	=	pseudoinflammatory)	(Sorsby fundus dystrophy, pseudoinflammatory)
				formicomogna (PNIA) II -1-1- 1	ESTs, Moderately similar to A40493 DNA topoisomerase [H.sapiens], ESTs, Weakly
476	- 1	23778 AA899854	C	apple (170kD)	similar to topoisomerase (DNA) II alpha [Rattus norvegicus] [R.norvegicus], topoisomerase (DNA) II alpha tonoisomerase (DNA) II alph
					ESTs, Moderately similar to A40493 DNA topoisomerase IH.sapiens1, ESTs. Weakly
2094	23780	23780 NM_022183	: <u>:</u>	(DNA) II apha, topoisomerase (DNA) II apha, topoisomerase (DNA) II	similar to topoisomerase (DNA) II alpha [Rattus norvegicus] [R.norvegicus],
	<del>  -</del> -			(aug. 1) aud.	topoisomerase (DNA) II apha, topoisomerase (DNA) II beta
2378	6221	622 NM_053369	a, j, k	transcription factor 4	ES1, rignly similar to TRANSCRIPTION FACTOR 4 [M.musculus], transcription factor 4
2378	623	623 NM_053369	r, hh	transcription factor 4	EST, Highly similar to TRANSCRIPTION FACTOR 4 [M.musculus], transcription
				transforming growth factor, beta 1, transforming growth	ממנטן א
2079	18729	18729 NM_021578		factor, beta 1 (Camurati-Engelmann disease)	
1723	457 N	457 M60666	aa	topomyosin 1 (albha). tropomyosin 1 -alpha	Homo sapiens cDNA FLJ30635 fis, clone CTONG2002520, expressed sequence
					Homo sanions CNNA El 130635 fis along CTON CROSSON
2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	455N	455 NM_019131	b, u, v	tropomyosin 1 (alpha), tropomyosin 1, alpha	A834628, expressed sequence C76867, tropomyosin 4, hiffelin 1
2018	461	461 NM 019131	m E	frontomore ( sinhs) transmissin 4 sinhs	Homo sapiens cDNA FLJ30635 fis, clone CTONG2002520, expressed sequence
					Alababased sequence C76867, tropomyosin 4, tuftelin 1
1773	24854 N	24854 NM_012676	aa, bb t	troponin T2, cardiac	EST, Weakly similar to TRT2 MOUSE TROPONIN T, CARDIAC MUSCLE ISOFORMS IM musculus], hypothetical protein EL 110408
					יייייייייייייייייייייייייייייייייייייי

TABLE 3	٠ د			(新年は、こう) - 一方が、 - 一が、 - 一	The state of the s
SEO		GenBank Acc.			Atty. Ref. 44921-5090-01-WO/2105485
۵	GLGC ID No.	No.		Model Code Human Hornglogous Known Gene Name	Human Homologous Sequence Cluster Title
	-				tumor necrosis factor receptor superfamily, member 11a, tumor necrosis factor receptor superfamily, member 11a, activator of NFKB, tumor necrosis factor
1811		24617 NM_012870	:=	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	superfamily, member 21, tumor necrosis factor receptor superfamily, member 5,
1935		23665 NM_017092	n, v	rosine kinase, TYRO3 protein tyrosine	AXL receptor tyrosine kinase, TYRO3 protein tyrosine kinase, TYRO3 protein tyrosine kinase 3
2295		192 11 NM_031603	<u>–</u>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	ESTs, Highly similar to 138947 14-3-3 protein epsilon isoform [H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
554		3£ 17 AA926328	p, q	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX activation protein, zeta polypeptide protein, zeta polypeptide protein, zeta polypeptide
1846	252 79	252 79 NM_013011	ъ <u>.</u>	fyrosine 3-monooxygenase/tryptophan 5-monooxygenase [activation protein, zeta polypeptide	ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX activation protein, zeta polypeptide protein, zeta po
1846	34.04	3434 NM_013011	p,q	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase [activation protein, zeta polypeptide	ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX activation protein, zeta polypeptide protein, zeta polypeptide protein, zeta polypeptide
1712	15049	15049 M24542	aa, bb	Rieske iron-sulfur	EST, Weakly similar to UCRI_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], ESTs, Moderately similar to UCRI_HUMAN UBIQUINOL- CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], RIKEN cDNA 4430402G14 gene, ubiquinol-cytochrome c reductase. Rieske iron-sulfur nolynewide 1
2477	151251	15125 NM_057105	jj, kk, ll	UDP glycosyltransferase 1 family, polypeptide A6	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A8
133	23828 /	23828 AA817823	 :=	ransferase,	Mus musculus, Similar to xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I), clone MGC:28643 IMAGE:4224150, mRNA, complete cds, UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1, UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2, UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase
2426	7927 N	7927 NM_053765	9	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	UDP-N-acety/glucosamine-2-epimerase/N-acety/mannosamine kinase

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SEO		ConBony Ago		が開発している。 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	A COMPANY OF A C
2	GLGC ID No.	Oelibalik AG D No.		Model Code Human Homologous Known Gene Name	Auy. Ker. 44921-5090-01-W6)2105485
2023		278 NM_019150	aa, bb	urocortin	ruman Homologous Sequence Cluster Title
2688		19279 Y00350	a, aa, bb, jj, kk		Urocortin
1215		6888 A1169615	s, t	VAMP (vesicle-associated membrane protein)-associated protein A (33kD), vesicle-associated membrane protein, associated protein A (33 kDa)	
1439		16203 AI229196	w, x, cc, dd	vesicle-associated membrane protein 1, vesicle-associated membrane protein 1 (synaptobrevin 1), vesicle-associated membrane protein 2, vesicle-associated membrane protein 2 (synaptobrevin 2)	vesicle-associated membrane protein 1, vesicle-associated membrane protein 2,
1772		16197 NM_012663	j, k	vesicle-associated membrane protein 2, vesicle-associated membrane protein 2 (synaptobrevin 2)	volución de la filiplante protein 4
2472		23250 NM_057097	f, g	vesicle-associated membrane protein 3, vesicle-associated membrane protein 3 (cellubrevin)	ESTs, Weakly similar to vesicle-associated membrane protein 3 [Rattus norvegicus] [R.norvegicus], vesicle-associated membrane protein 3, vesicle-associated membrane protein 3 (cellubrevin), vesicle-associated membrane protein
2026	24362	24362 NM_019156		vitronectin, vitronectin (serum spreading factor, somatomedin B, complement S-protein)	
1956	21975	21975 NM_017154	d, e, j, k, n, o, y, z, kk	xanthene dehydrogenase, xanthine dehydrogenase	
1960	209191	20919 NM_017172	a 2	zinc finger protein 36, C3H type-like 1	ESTs, Weakly similar to S10471 cMG1 protein - rat [R.norvegicus], zinc finger protein 36 C3H tune.like 1 zinc finger sectors
2511	25730	25730 NM_133290	, k, p, q h	ain 36, C3H type,	zinc finger protein 36 zinc finger protein 36, C3H type-like 2
2541	8692 N	8692 NM_134387	ł.		2,4-dienoyl CoA reductase 1, mitochondrial, 2,4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, RIKEN cDNA
	19451	19451 AA819788	O		28kD interferon responsive protein, RIKEN cDNA 5830458K16 nene
1646	23219 A.	23219 A.1000347		The state of the s	3(2), 5-bisphosphate nucleotidase 1, ESTs, Moderately similar to INPP MOUSE INOSITOL POLYPHOSPHATE 1-PHOSPHATASE [M.musculus], bisphosphate 3'-nucleotidase 1, hypothetical protein FLJ20421, inositol polymbosphate 1.
			0 (=)	1	phosphatase

TABLE 3	: 3 :		意味を	The same design and a service of the
SEQ	ļ	GenBank Acc.		
₽	GLGC ID No.	No.	Model Code Human Hom	tuman Homologous Known, Gene Name Human Homologous Sequence Cluster Title-
1715		15580 M33648	y, z	nase 2, 3-hydroxy-3-methyle
				3-hydroxybutyrate dehydrogenase (heart, mitochondrial), ESTs, Weakly similar to
		<u>.                                      </u>		BDH_RAT D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor (BDH)
				(3-rl)droxybutyrate denydrogenase) [R.norvegicus], RIKEN cDNA 0610039E24
2465		17739 NM_053995	9	gene, rancin cuna zatuuazazu gene, retinol dehydrogenase 7, retinol dehydrogenase 7, retinol
				3-hydroxyisobutyrate dehydrogenase, ESTs, Highly similar to D3HI HUMAN 3-
888	_	21950 AI013861	, t,	HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
				6-phosphofructo-2-kinase/fructose-2.6-biphosphatase 1. 6-phosphofructo-2-kinase/fructose-2.6-biphosphatase 1.
2060		1238 NM 019333	5	kinase/fructose-2,6-biphosphatase 4, ESTs, Moderately similar to F26L MOUSE
		0000 I 0 10000	66	6PF-2-K/FRU-2,6-P2ASE LIVER ISOZYME IM.musculus
2076		13486 NM 020306	4	a disintegrin and metalloproteinase domain 17, a disintegrin and metalloproteinase
	1	00000	da, Do	domain 17 (tumor necrosis factor, alpha, converting enzyme)
2323		20724 NM_031753	<u>ت</u>	activated leucocyte cell adhesion molecule, activated leukocyte cell adhesion
2198	938	938 NM 024486	u, v	almaiour A riviero
				activity A receptor, type 1, activin A receptor, type 1
2083	19661	19661 NM_021686		acuvin receptor interacting protein 1, connector enhancer of KSR2, expressed
472	4636 ₽	4636 AA899491	Ð	adaphraplated motion complex 4 miles in the protein PIP3-E
2522	4074	4074 MIN 400500	a, ee, ff, jj,	adaptor-related protein complex 3, mu 1 subunit, adaptor-related protein complex
2347	2408414	24084 NIM 034709	¥,	AP-3, mu 1 subunit
1	13047	00 1 LO	D 6	adhesion regulating molecule 1
1445	15212A	15212 AI229753	p, q, t, y, z, ee, ff	ADB-riboevlation factor 4 ADB showdestee feet and and a second at the se
2178	1742N	1742 NM_024150	p, q, y, ee, ff	A DD-ribonylation factor 1 ADD -it- 1100sylation 1 ADD
2127	4145 <sub>N</sub>	4145 NM 022518	ii. Kk	ADP-ribosylation factor 1, ADP-ribosylation-like 6, ESTs, Weakly similar to ADP-
2127	4151N	ļ	b. f. m	ADP-ribosylation factor 1, ADP-ribosylation-like 6, ESTs, Weakly similar to ADP-
2179	17517NI	17517 NM 024151		KIBUSYLATION FACTOR 1 [M.musculus], expressed sequence T25534
	<del> </del>			AUP-nbosylation factor 4

TAB	C T			1970	
9	6	GenBank Acc.		Atty: Ref: 44921-5090-01-WO/2105486	2105485
	GEOCUNY	CN	Model Code	Model Code Human Ho nologous Known Gene Name Human Homologous Sequence Cluster Title	· · · · · · · · · · · · · · · · · · ·
				ADP-ribosylation factor 6, ESTs, Weakly similar to ARF6_HUMAN ADP-	
				ADP-ribosylation factor 6 [R.norvegicus]. RIKEN cDNA 1110033P22 nene. RIKEN	HUMAN-
2180		21696 NM 024152	Σ'λ	cDNA 2310075M17 gene, RIKEN cDNA 9130014L17 gene, SAR1 protein, SAR1a	AR1a
	1		211	gene homolog (S. cerevisiae), hypothetical protein FLJ22595   ADP-rihosvlation factor-like 5, ADP-rihosvlation like 6, commonded	
225		20327 AA926265	cc, dd	T25534, hypothetical protein DKF24341 1123 similar to mouse Aris	
				AFG3 ATPase family gene 3-like 1 (yeast), BCS1-like (yeast), EST, Weakly similar	similar
				to PRS4_HUMAN 26S protease regulatory subunit 4 (P26S4) [M.musculus], ESTs,	ESTs,
				Highly similar to PRS4_HUMAN 26S protease regulatory subunit 4 (P26S4)	•
				[H.Sapiens], Homo sapiens cDNA FLJ31926 fis, clone NT2RP7005502, moderately	erately
				similar to Homo sapiens mRNA for paraplegin-like protein, protease (prosome,	ď
2480		727 NM 057123	vi	macropain) 26S subunit, ATPase 1, proteasome (prosome, macropain) 26S	
				Subunit, A.I.Pase, 1	
				Ar 53 A I Pase family gene 3-like 2 (yeast), AFG3(ATPase family gene 3)-like 1	_
				(yeast), Mus musculus, clone IMAGE:5040761, mRNA, partial cds, YME1-like 1 (S.	31 (S.
2418		2063 NM 053682	_ <b>a</b>	Oefevisiae), spastic paraplegia 7, paraplegin (pure and complicated autosomal	<del>-</del>
				(PCESSIVE)	
				Agrin, ES1s, Weakiy similar to A38096 perlecan precursor [H.sapiens], ES1s,	
				PROTEORY VOAN CORE DECTINED IN THE PROPERTY OF THE PROPERTY OF THE PARAM SOLFALE	
				Similar to PGBM_HUMAN BASEMENT MEMBRANE-SPECIFIC HEPARAN	
				SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR IH.sapiens), Mus	- sn
				musculus, clone IMAGE:3494258, mRNA, partial cds, heparan sulfate proteoglycan	lycan
		•		2 (pertecan), pertecan (heparan sulfate proteoglycan 2), serine protease inhibitor.	for.
1403		01170700	£	Kazal type, 5, sialoadhesin, transmembrane protein with EGF-like and two follistatin-	istatin-
280		16074 AA874874	D, 1, 111	like domains 1	
3		40140	p, q	alcohol dehydrogenase 5, alcohol dehydrogenase 5 (class III), chi polypentide	
				aldehyde dehydrogenase 3 family, member B1, aldehyde dehydrogenase 3 family,	mily,
2343	24644 N	24644 NM 031972	5	member B2, aldehyde dehydrogenase 3 family, memberA1, aldehyde	
			25 (25	dehydrogenase family 3, subfamily A1	

I ADLE 3	2				
S T T	•	GenBank Acc.			Atty-Ref. 44921-5090-01-WO/2105485
Ω	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Himan Homologous Common Clouds Him
					de l'alla l'originations ocquerice ciuster. I me
					Alpna-z-macroglobulin, CCR4 carbon catabolite repression 4-like (S. cerevisiae),
					ESIS, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN
					PRECURSOR [M.musculus], Homo sapiens, clone MGC:1119 IMAGE:2959975.
				<u>je</u>	mRNA, complete cds, Mus musculus, clone MGC:29037 IMAGE:3598248, mRNA.
				18	complete cds, Mus musculus, clone MGC:29167 IMAGE:5052974, mRNA, complete
485		4725 AA900290	4	<del>8</del>	cds, alpha-2-macroglobulin, carbon catabolite repression 4 homolog (S. cerevisiae)
		000000	ار، ۴، 2, 55, 11	pre	pregnancy-zone protein
2171		8269 NM 023103	£	die .	alpha-2-macroglobulin, murinoglobulin 1, murinoglobulin 2, murinoglobulin
1076	1	07070	1, 1,	DSE	pseudogene 1
0/0	ı	10049 NIM 013132	c, gg		annexin A5
				AP	APC11 anaphase promoting complex subunit 11 homolog (yeast) ESTs. Highly
222		15%60 0088848	,	sim	similar to T51146 ring-box protein 1 [H.sapiens], ESTS. Weakly similar to T51146
1		0100000	6'1	ring	g-box protein 1 IH.sapiens), ring finger protein 7, ring how 1
				AR	ARPZ actin-related protein Z homolog (yeast), ARP3 actin-related protein 3 homolog
				(yex	(yeast), EST, Weakly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin)
				<u> </u>	Rnorvegicus], ESTs, Highly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1
				[M.r	M.musculus], ESTs, Weakly similar to A29861 actin gamma [H.sapiens], ESTs.
			-	Wee	Weakly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1 IM.musculus]. Homo
				ides	sapiens cDNA FLJ31247 fis, clone KIDNE2005296, weakly similar to ACTIN.
				L\o	CYTOPLASMIC 1, Homo sapiens cDNA FLJ32120 fis, clone PEBLM1000068.
-				high	highly similar to ACTIN, CYTOPLASMIC TYPE 5, Homo sapiens mRNA; cDNA
				DYK	DKFZp434B2115 (from done DKFZp434B2115), RIKEN cDNA 1700052K15 gene.
687	18830	18830 AA964496	7	actir	actin, beta, actin, beta, cytoplasmic, calcitonin gene-related peptide-receptor
	1000		4, 4	(COM	component protein, expressed sequence AV259599

TABLE				- 一一一一一一一一一一一一一一一一一一一一一一一一一一一一一一一一一一一一	3	
SEO		GenBank Acc		"Water considered to the second secon	The State of the S	Transport 1-5090-01-WO/2105485
₽	50	No.	Model Code	Model Code Human Honologous Known Gene Name	ame.	Human Homologous Sequence Cluster Title
						AKYZ acun-related protein 2 nomolog (yeast). AKP3 acti
						(yeast), EST, Weakly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin)
						[R.norvegicus], ESTs, Highly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1
						[M.musculus], ESTs, Weakly similar to A29861 actin gamma [H.sapiens], ESTs,
						Weakly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1 [M.musculus], Homo
						sapiens cDNA FLJ31247 fis, clone KIDNE2005296, weakly similar to ACTIN,
						CYTOPLASMIC 1, Homo sapiens cDNA FLJ32120 fis, clone PEBLM1000068,
			1			highly similar to ACTIN, CYTOPLASMIC TYPE 5, Homo sapiens mRNA; cDNA
						DKFZp434B2115 (from clone DKFZp434B2115), RIKEN cDNA 1700052K15 gene,
1127	`	100004	1		•	actin, beta, actin, beta, cytoplasmic, calcitonin gene-related peptide-receptor
2 6		A1104337	00 :			component protein, expressed sequence AV259599
730		5867 AA858953	茶			asparaginyl-tRNA synthetase, hypothetical protein FLJ23441
						AT2 receptor-interacting protein 1, Homo sapiens cDNA FLJ32157 fis, clone
1202		07.505.51				PLACE6000205, moderately similar to TRANSCRIPTIONAL REPRESSOR
200		13031 A11/6/40	CC, GG			PROTEIN YY1, YY1 transcription factor
					,	ATP synthase, H+ transporting, mitochondnal F1 complex, O subunit, ATP
						synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin
						sensitivity conferring protein), EST, Weakly similar to ATPO_HUMAN ATP
						SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR,
						MITOCHONDRIAL [H.sapiens], ESTs, Highly similar to ATPO_HUMAN ATP
						SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR,
						MITOCHONDRIAL [H.sapiens], ESTs, Moderately similar to ATPO_HUMAN ATP
0000	1001	000007			,	SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR,
RCC7	CRS/	/ 385 MN 138883	_			MITOCHONDRIAL [H.sapiens]
						ATPase, Ca++ transporting, type 2C, member 1, ATPase, Ca++ transporting,
					<del></del>	ubiquitous, Homo sapiens cDNA: FLJ21771 fis, clone COLF7779, Homo sapiens
2509						mRNA; cDNA DKFZp434L231 (from clone DKFZp434L231), KIAA0703 gene
2440	- 1	200 30 NIM 151307	اد			product, putative secretory pathway Ca-ATPase SPCA2
0447	- [		99		7	ATPase, H+ transporting, lysosomal 14kD, V1 subunit F

	TABLE 3	က		,	1	
Human Homologous Knjown Gene Name   Human Homologous Sequence Cluster T     ATPase, Hit Traisporting, 1950somal international files     Vacadar ATP Synthase subunit St presulations   Participated ATP Synthase subunit St presulations     Vacadar ATP Synthase subunit St presulations   Vacadar ATP Synthase subunit St presulations     Vacadar ATP Synthase subunit St presulations   Vacadar ATP Synthase subunit St presulations     Vacadar ATP Synthase subunit s soform     Vacadar ATP Synthase subunit St presulations     Vacadar ATP Synthase subunit St presulations     Vacadar ATP Synthase subunit St presulations     Vacadar ATP Synthase subunit St presulations     Vacadar ATP Synthase subunit St presulations     Vacadar ATP Synthase subunit St presults     Vacadar ATP Synthase subunit St presults     Vacadar ATP Synthase subunit St presults     Vacadar ATP Synthase subunit St presults     Vacadar ATP Synthase subunit St presults     Vacadar ATP Synthase subu	SEO		GenBank Acc.			14921-5090-01-WO/2105485
22710 INM_013178		GLĠC ID	No.	Model Code	ológous Known Gene Name Human-Homologous Seguence Cluster T	
22661 A1169265 9g   1   1   1   1   1   1   1   1   1					ATPase, H+ transporting, lysosomal interacting prote 154197 hypothetical protein [H.sapiens], ESTs, Weakl	1, EST, Weakly similar to similar to VAS1_RAT
22661 A169265 gg ff ff					Vacuolar ATP synthase subunit S1 precursor (V-ATP   Vacuolar ATP   V-A	e S1 subunit) (V-ATPase S1
22661 A169265 99  7 16: 78 INM_031785 f 23709 INM_013113 hh 2350 A1235738 r 24146 A169668 ii hA					Sapiens cDNA FLJ12563 fis, clone NT2RM4000820, the Sapiens CDNA FLJ12563 fis, clone NT2RM4000820, the Sapiens CDNA FLJ12563 fis, clone NT2RM4000820, the Sapiens Sapiens Sapiens CDNA FLJ12563 fis, clone NT2RM4000820, the Sapiens Sa	akly similar to VACUOLAR
7 16: 78 NM_031785 f 20640 NM_031604 cc, dd 23709 NM_013113 hh 23710 NM_013113 hh 3650 AI235738 r 60 cl	1209	22661	AI169265	99	sequence AW108110	6.1.34), expressed
20540 NM_031785 f 20540 NM_031604 cc, dd 23709 NM_013113 f,g 23710 NM_013113 hh 23710 NM_01313 f,g R A 3650 A1235738 r In M M M M M M M M M M M M M M M M M M M					ATPase, H+ transporting, lysosomal interacting protein	, EST, Weakly similar to
7 16: 78 NM_031785 f  20640 NM_031604 cc, dd  23709 NM_013113 f, g  23710 NM_013113 hh  3650 Al235738 r  6 cl  6 cl  6 cl  6 cl  7 16: 78 NM_031785 f  8 cl  8 cl  9 cl  9 cl  10 cl  24146 Al169668 ii					Vacuolar ATP synthase subunit S1 precursor (V-ATPs	imilar to VAS1_RAT
7 16; 78 NM_031785 f 20540 NM_031604 cc, dd 23700 NM_013113 f, g 23710 NM_013113 hh 23710 NM_01313 hh 3650 Al235738 r 24146 Al169668 ii					accessory protein) (V-ATPase Ac45 subunit) (C7-1 pr	in) [R.norvegicus]. Homo
7 16: 78 NIM_031785 f 20640 NIM_031604 cc, dd 23709 NIM_013113 hh 23710 NIM_013113 hh 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8					sapiens cDNA FLJ12563 fis, clone NT2RM4000820, w	akly similar to VACUOLAR
2370 NM_031604 cc, dd 2370 NM_013113 f, g 23710 NM_013113 hh 2370 NM_01313 hh 3650 A1235738 r 24146 A1169668 ii	2327	16: 78	NM_031785	<b>-</b>	ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC.	3.1.34), expressed
23710 NM_031604 cc, dd 23710 NM_013113 hh 23710 NM_013113 hh 3650 A1235738 r					ATPase. H+ transnorting lysosomal V/A cultumit A incet	
23709 NM_031604 cc, dd 23709 NM_013113 f, g 23710 NM_013113 hh 3650 AI235738 r 24146 A1169668 ii					transporting, lysosomal V0 subunit a isoform 1. ATPas	H+ transporting typesomal
23710 NM_031604 cc, dd 23710 NM_013113 hh 23710 NM_013113 hh 3650 Al235738 r 24146 Al169668 ii					V0 subunit a isoform 2, ATPase, H+ transporting, lysos	nal V0 subunit a isoform 4.
3650 AI235738 r 24146 A1169668 ii					EST, Weakly similar to B38656 vacuolar proton pump	6K chain - rat
23710 NM_013113		20640 N		- <del>-</del> -	[R.norvegicus], ESTs, Moderately similar to B38656 va	olar proton pump 116K
23710 NM_013113 hh 3650 Al235738 r 24146 Al169668 ii	1	23709IN		f o	chain - rat [R.norvegicus]	
3650 AI235738 r 24146 A1169668 ii		23710N	Τ-	1, 0 1, 0	ATPase, Na+/K+ transporting, beta 1 polypeptide	
3650 A1235738 r 24146 A1169668 ii			Т		ATPase, Na+/K+ transporting, beta 1 polypeptide	
3650 A1235738 r 24146 A1169668 ii					ATP-binding cassette, sub-family C (CFTR/MRP), men	er 4, ATP-binding cassette,
3650 A1235738 r 24146 A1169668 ii					sub-ramily C (CF I K/MRP), member 9, ESTs, Weakly s	llar to ATP-binding
3650 A1235738 r 24146 A1169668 ii					cassette, sub-family C, member 9, isoform c; sulfonylur	-binding protein 2;
3650 A1235738 r 24146 A1169668 ii					sulfonylurea receptor 2 [Mus musculus] [M.musculus], I	mo sapiens cDNA
3650 AI235738 r 24146 AI169668 ii					FLJ31957 fis, clone NT2RP7007381, highly similar to S	onylurea receptor 2A,
3650 A1235738 r 24146 A1169668 ii					Mus musculus adult male pituitary gland cDNA, RIKEN	I-fength enriched library,
24146 A1169668   ji	1560	3650 AI	1235738 r		clone:5330439B14:ATP-binding cassette, sub-family C	FTR/MRP), member 9, full
	1217	24146 AI	1169668		Insert sequence	
					ATP-binding cassette, sub-family F (GCN20), member 2	

TABLE 3	ш 3				
SEO		GenBank Acc		Affect Adol-snon of Amountaine	74 MO1940E40E
<u>.</u> ⊡	GLGC ID No.	ID No.		Model Code Human Homologous Known Gene Name	395C017/0AA-10
				Introfein/encyl Construct A Exercise For the Anydratase, AU RNA binding	ling
				Produite Indianal Produit Prod	5 AU-specific
				ruvr-binding protein / enoyl-CoA hydratase homolog [H.sapiens], Mus musculus,	is musculus,
				Similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase, clone MGC:31364	364
248		20582 AA859688	w, hh	IIMAGE: 4238681, mRNA, complete cds, RIKEN cDNA 1300017C12 gene,	lene,
				uncharacterized hypothalamus protein HCDASE	
				B-cell translocation gene 1, anti-proliferative, ESTs, Highly similar to TOB1 HUMAN	TOB1 HUMAN
798		22545 AI009747	- CO	TOB1 PROTEIN [H.sapiens], transducer of ERBB2, 1, transducer of ERBB2, 2	RBB2 2
2055		23679 NM 019290	0.0	transducer of ErbB-2.1	
				B-cell translocation gene 3, BTG family, memher 3	
2500		23033 NM 080888		BCL2/adenovirus E1B 19 kDa-interacting protein 3-like, BCL2/adenovirus E1R 19kD	inis F1R 10kh
2153		17757 NM 022698	- Job 30	interacting protein 3-like	OWO 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
				BCL2-antagonist of cell death. Bcl-associated death promoter	
781		21632 AI009167	a, v, z, ee, ff	BINING TO THE PROPERTY OF THE	
				BCL2-associated athanogene 2	
1493		15171 AI231792	ee, ff	BCL2-associated athanogene 3, BCL2-associated athanogene 5, Bcl2-associated	-associated
558	22677		S. t. kk	athanogene 3, RIKEN cDNA 1700081D05 gene	
999	23957			BCL2-related ovarian killer, Bcl2-like	
1466	22387	22387/A/230753	0	brain expressed, X-linked 1, hypothetical protein FLJ10097	
			0	brain protein 13	
412	11997	11997 AA892828	-	branched chain ketoacid dehydrogenase E1, beta polypeptide, pyruvate	93
				dehydrogenase (lipoamide) beta	
1313	5876	5876 AI176117	- -	branched chain ketoacid dehydrogenase E1, beta polypeptide, pyruvate	9
				dehydrogenase (lipoamide) beta	
				bubb budding uninhibited by benzimidazoles 3 homolog (yeast), ESTs, Weakly	Weakly
				Similar to guanine nucleotide-binding protein, beta-1# subunit [Rattus norvegious]	lorvegicus
				[K.norvegicus], Mus musculus, clone MGC:7934 IMAGE:3583848, mRNA, complete	VA. complete
			_	cds, budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae), quanine	auanine
2209	21801	21801 NM_030987	cc. dd. ji	nucleotide binding protein, beta 1, neural precursor cell expressed, developmentally	elopmentally
				down-regulated gene 1	

Atty. Ref. 44921-5090-01-WO/2105485	Model Code Human Homologous Known Gene Name  BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast), ESTs, Weakly similar to guanine nucleotide-binding protein, beta-1# subunit [Rattus norvegicus] [R.norvegicus], Mus musculus, clone MGC:7934 IMAGE:3583848, mRNA, complete cds, budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae), guanine nucleotide binding protein, beta 1, neural precursor cell expressed devicement.	down-regulated gene 1	calcium binding protein, 140 kDa, heat shock 70 kDa protein 4, heat shock 70kD protein 4, heat shock 70kD protein 4, heat shock protein (hsp110 family), osmotic stress protein 94 kDa, oxygen requilated protein (160, 20).	(130KD) (calmedin, calmexin	Carboxypeptidase E, ESTs, Weakly similar to carboxypeptidase E [Raftus norvegicus] [R.norvegicus], carboxypeptidase E, carboxypeptidase X 1 (M14 family), expressed sequence AAE00220	CARD only protein, ESTs, Moderately similar to A57511 interleukin-1 beta converting enzyme [H.sapiens], ESTs, Weakly similar to A56084 interleukin-1 beta converting enzyme [H.sapiens], Homo sapiens mRNA; cDNA DKFZp586A181 (from clone DKFZp586A181); partial cds, ICEBERG caspase-1 inhibitor, caspase 1, apoptosis-related cysteine protease (interleukin 1.	CARD only protein, ESTs, Moderately similar to A57511 interleukin-1 beta converting enzyme [H.sapiens], ESTs, Weakly similar to A56084 interleukin-1 beta converting enzyme beta isozyme [H.sapiens], Homo sapiens mRNA; cDNA DKFZp586A181 (from clone DKFZp586A181); partial cds, ICEBERG caspase-1 inhibitor, caspase 1, caspase 1, apoptosis-related cysteine protease (interleukin 1	Deta, convertase)  cargo selection protein (mannose 6 phosphate receptor binding protein)	Cathepsin S Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2,
_	Model 6	99	a	66	cc, dd	aa, bb	Φ	n, o b, I, m, kk	p, q, r, bb, ee, ff, jj, kk
GenBank Acc.	21805 NM 030987	2582 AA965164	157 11 NM_153629	11333/44033328	17875 AA799755	18066 NM_012762		24270 AI230758 1894 NM_017320	
SEQ In		869	2594		67	1791		1467 24 2002 1	1343 161

TABI F.3	6.		ない意動い		
Ш —	   	CenBank Acc			Atty. Ref. 44921-5090-01-WO/2105485
2	GLGC ID No.	No.		Model Code Human H mologous Known Gene Name	
					oxy-terminal domain 1,
2419		16122 NIM 052508	¥ 6	Cop/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	oxy-terminal domain, 1, oxy-terminal domain, 2
		000000	p, q, ee, II	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain	oxy-terminal domain 4
				Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain 1,	oxy-terminal domain 1,
2419		16123 NM_053698	d, p, q, jj, kk	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2,	oxy-ferminal domain, 2,
707		4700 A A O O O R E	3 3	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	oxy-terminal domain, 4
		Cionery	= '22	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-ferminal domain. A	xy terminal domain 4
		_		CD 81 antigen, CD81 antigen (target of antiproliferative antibody 1), ESTs, Weakly similar to CD81 ANTIGEN [M.musculus]. ESTs. Weakly ENAT CD81	ibody 1), ESTs, Weakly
1867		8899 NM 013087	d f	antigen (26 kDa cell surface protein TAPA-1) (Target of the antiproliferative	antiproliferative
			a, j, k, q, hh,	antibody 1) [R.norvegicus]	
2086		19710 NM_021744	文	CD14 antioen	
				CD151 antigen, EST AI426782, ESTs, Moderately similar to C151 MOUSE PLATELET-ENDOTHELIA! TETRASPAN ANTIGEN 3 IM SUIGEN DIFFERENTE PLATE OF THE PROPERTY OF THE	C151 MOUSE
2129	4412IN	4412 NM_022523	m'j	1110014F12 gene, RIKEN cDNA 2210021G21 gene, RIKEN cDNA 2610042G18	usculusj, Kinely CDNA I CDNA 2610042G18
1932	1523 N	1523 NM_017079	h, l, n, o, w, x	CD1B antigen, b polypeptide, CD1D antigen, d polypeptide, CD1E antigen, e	uperfamily member 6 CD1E antigen, e
				polypeptide, CD1d1 antigen, CD1d2 antigen, expressed sequence Al747460   CD2 antigen family. member 10. CD48 antigen. CD48 antigen. (P. 2011)	uence Al747460
				protein), CD84 antigen, ESTs, Weakly similar to CD48_RAT MRC OX-45 surface	MRC OX-45 surface
2567	17854 N	17854 NM_139103		antigen precursor (BCM1 surface antigen) (BLAST-1) (CD48) [R.norvegicus].	(R.norvegicus),
				CD3 antigen, zeta polypeptide. CD3Z antigen, zeta polypeptide.	1234 de /TiT3 comploy Es
				fragment of IgE, high affinity I, receptor for, gamma polypeptide, Fc receptor. IgE.	de, Foreceptor, IqE.
			_	high affinity I, gamma polypeptide, Homo sapiens, Similar to Fc fragment of IgE,	Fc fragment of IgE,
999	24040 A	24040 AA957422	n, o, w, x	high affinity I, receptor for; gamma polypeptide, clone MGC:22620 IMAGE:4704425,	2620 IMAGE:4704425,
				illikivik, complete cas, 1-cell receptor CD3, subunit zeta	

TABLE	: ::	in the second second		Version and a second	
SEO		GenBank Acc.	-	AND THE STATE OF	5/185
<u>ء</u>	GLGC ID No.	No.	Model Code Human Hom	Ologous Known Gene Name	3
393	_	24873 <u>44892</u> 408	- <u>-</u>		) gg '
		064700000	II, NA	transmembrane 4 superfamily member 8	<u>.</u>
			a, p, q, cc, dd, ee, ff ii	CD72 antigen, Mus musculus strain BALB/c dectin-2 gamma isoform mRNA.	7
2111		22499 NM 022393	天 ( )	complete cds, alternatively spliced, NK receptor Ly 49Q, asialoglycoprotein receptor	ptot
				CD9 antinen CD9 an	
				CDS amgent, CDS amgent, CDS amgent, CDS inginity similar to 2103288A CD9 protein  [Rattus norvegicus] [R.norvegicus]. Mus muscrifus Clone MCC-38363	
2523		20990 NM 133526		IMAGE:5344986, mRNA, complete cds, RIKEN cDNA 6330415F13 gene.	
				transmembrane 4 superfamily member 3, uroplakin 1A	_
88		15: 72 AA875205	y, z	CDA02 protein, ESTs, Weakly similar to IF39_HUMAN EUKARYOTIC	Τ
1				IransLATION INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]	
28 28		15/74 H34186		TRANSLATION INITIATION 5 SUBJINIT OF 129—HUMAN EUKARYOTIC	
		_		Suaides ui a livogoo o coloco	Т
				CDw92 antigen, ESTs, Weakly similar to CTL2 gene fHomo sapiens] fH saniens	
				ESTs, Weakly similar to transporter-like protein [Rattus norvedicus] IR norvedicus	- 7
				Homo sapiens, clone MGC:34032 IMAGE:4828797, mRNA, complete cds. Mus	
	<u>.</u>			musculus, Similar to transporter-like protein, clone MGC:7894 IMAGE:3582543	_
2387	14904 N	14904 NM_053492	s, t	mRNA, complete cds, RIKEN cDNA 1110028E10 gene, RIKEN cDNA 2210409B01	
	 			gene, chromosome 6 open reading frame 29, expressed sequence AW547365	
2530	1627 N	1827 NM_133572	r, u, v	cell division cycle 25 homolog B (S. cerevisiae), cell division cycle 25 homolog C (S.	(s)
0530	1600			Cell division cycle 25 cell division cycle 25 cell division cycle 25 cell division cycle 25 cell division cycle 25 homolog R/S cerevision cycle 25 cell division cycle 25 homolog R/S cerevision cycle 25 homolog R/S cerevision cycle 25 cell division cycle 25 homolog R/S cerevision cycle 25 cell division cycle 25 homolog R/S cerevision cycle 25 cell division cycle 25 cell division cycle 25 cell division cycle 25 homolog R/S cerevision cycle 25 cell division	1
7000	N N N	1930 NM 1335/2	>	cerevisiae), cell division cycle 25B, cell division cycle 25C.	· i
2530	1831 N	1831 NM 133572		cell division cycle 25 homolog B (S. cerevisiae), cell division cycle 25 homolog C (S.	lu
416	22871 A	.[		Gerevisiae), cell division cycle 25B, cell division cycle 25C	
33	23294 A	23294 AA799472	88.4	cerebral cell adhesion molecule	<del>_</del>
		T		CGI-116 protein	7
443	19505 AA893634			CGI-120 protein, COPZ2 for nonclathrin coat protein zeta-COP, coatomer protein	_
1588	3368 AI237331			complex, subunit zeta 1	-
1029	18 A		X W	CGI-143 protein	Т
			, , , , , , , , , , , , , , , , , , ,	CGI-20 protein	_
					_

S S S	]:	GenBank Acc.		Atty. Ker. 44921-5090-01-WO/2105485
2	GLGC ID No.	No.		Model Code Human Hr mologous Known Gene Name Human Homologous Sequence Cluster Title
1520		3*00 AI232741	hh	CGI-51 protein, EST, Weakly similar to CG51_HUMAN PROTEIN CGI-51
647		14327 AA956111	h, í	CGI-69 protein, EST, Moderately similar to 743493 hypothetical protein
				CGI-74-like SR-rich, DNA segment, Chr 17, human D6545, EST, Weakly similar to
				SRA4_HUMAN CTD-BINDING SR-LIKE PROTEIN RA4 [H.sapiens], ESTs, Highly
				Similar to T31420 C-terminal domain-binding protein rA8 - rat [R.norvegicus], ESTs,
				PROTEIN IM musculus]. ESTs. Weakly similar to Tataon C-terminal domain
				binding protein rA8 - rat [R.norvegicus], KIAA1116 protein. expressed sequence
2565		734 MM 120004		Al447644, expressed sequence Al448652, hypothetical protein FLJ10290, pre-
2007		INIVI_IOSOS4	66	mRNA splicing SR protein rA4
	-		-	CGI-86 protein, DKFZP566O084 protein, ESTs, Weakly similar to T17307
1629		17215 AIR39268	5 5 1 1 1 1 1 1 1	hypothetical protein DKFZp5660084.1 [H.sapiens], hypothetical protein MGC4172,
292		16319 AAR75047	¥ 0	retinal short chain dehydrogenase reductase
607	22615	22615 A A O A S G 42	D 3	Chaperonin containing TCP1, subunit 6A (zeta 1), chaperonin subunit 6a (zeta)
2246	4004	4004 MM 004045	KK :	chitinase 3-like 1, chitinase 3-like 1 (cartilage glycoprotein-39)
2246	1024	14IM 031016	S, U, V	cholinergic receptor, muscarinic 2
27	10201	010150_WW_C2010	۸٬۰	cholinergic receptor, muscarinic 2
84	18881	18881 44799992	c, h, l, n, o,	
ā	18882	18882 A 700000	۷ ' <u>۱</u>	Chromosome 11 open reading frame 17, predicted gene ICRFP703B1614Q5,6
5 02	100001	10003 447 99992	C, n, o, KK	chromosome 11 open reading frame 17, predicted gene ICRFP703B1614O5 6
0/0	107	1013448	D	chromosome 20 open reading frame 30
1861	17181N	17181 NM 013073	2	chromosome 20 open reading frame 36, protein-L-isoaspartate (D-aspartate) O-
			200	methyltransferase, protein-L-isoaspartate (D-aspartate) O-methyltransferase 1
1861	21830N	21830 NM 013073	, p	chromosome 20 open reading frame 36, protein-L-isoaspartate (D-aspartate) O-
77	21000A	21000 AA799816	h I	methyltransferase, protein-L-isoaspartate (D-aspartate) O-methyltransferase 1
2602	9518	951 S69206		chromosome / open reading frame 2, lipocalin-interacting membrane receptor
				Chymase 1, mast cell, mast cell protease 1
2438	17154 N	17154 NM_053835	b, gg	Cathrin, light polypeptide (Lca), clathrin, light polypeptide (Lcb), expressed sequence AV026556
2438	17155N	17155 NM 053835		clathrin, light polypeptide (Lca), clathrin, light polypeptide (Lcb), expressed
3	1	000000	6	sequence AV026556

I ABLE 3	3		N. A. S. S. S. S. S. S. S. S. S. S. S. S. S.	١
		GenBank Acc.		
₽	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name
2438		18065 NM 053835	0	clathrin, light polypeptide (Lca), clathrin, light polypeptide (Lcb), expressed
				Sequence AV026556
				Occess protein, Ed.1, rugniy similar to 330363 G9a protein [H.sapiens], ESTs, Weakly similar to 117453 ERG-associated protein FSFT - mones IM misconing
1604	1710R	17108 41630017	=	SET domain, bifurcated 1, euchromatic histone methyltransferase 1, suppressor of
		I DOODIN	=	variegation 3-9 (Drosophila) homolog 2; hypothetical protein FLJ23414
				CLST 11240 protein, DKFZP564K247 protein, ESTs, Highly similar to T14766
				hypothetical protein DKFZp564K247.1 [H.sapiens], ESTs, Weakly similar to
				hypoxia induced gene 1 [Rattus norvegicus] [R.norvegicus], Homo sapiens mRNA:
				cDNA DKFZp434A1627 (from clone DKFZp434A1627), RIKEN cDNA 2010110M21
2501	96,52	NM DROGO	- <del>-</del>	gene, RIKEN cDNA 2310056K19 gene, hypothetical protein MGC2198, hypoxia
1856	2 2 2	246 74 NIM 0490ET	77	induced gene 1
3	±	/COC10_WIN		Coagulation factor III, coagulation factor III (thromboniastin fissus factor)
				Cocoacrisp, EST, Highly similar to epididymal glycoprotein [Rattus norvegicus]
2546	10501	1050A NIA 120510	=	[R.norvegicus], acidic epididymal glycoprotein 1, acidic epididymal glycoprotein 2
	5	120210	=	epididymal glycoprotein, glioma pathogenesis-related profein
				Complement component 4 binding protein, alpha, Mus musculus decay accelerating
				factor glycosylphoshatidylinositol-anchored form (DAF) mRNA, partial cds,
				complement component 4 binding protein, complement component 4 binding
994	80H2/	8042 A1058330	11 # 00	protein, alpha, decay accelerating factor 1, expressed sequence Al195242,
36	24178/		55, 11, AA	expressed sequence Al323748, zona pellucida 3 receptor
1358	24120	24129 A1177590	2 4	component of oligomeric golgi complex 4
2404	GEREIN	1.	13	component of oligomeric golgi complex 4
4730	2000		d, rk	connective tissue growth factor
0741	101677		8	craniofacial development protein 1
				Creatine transporter [human, brainstem/spinal cord, mRNA, 2283 nt], ESTS, Highly
-				similar to G02277 creatine transporter [H.sapiens], Mus musculus, Similar to solute
				carrier family 6 (neurotransmitter transporter, GABA), member 13, clone
				MGC:28956 IMAGE:4240641, mRNA, complete cds, X transporter protein 3,
5000	468 N	468 NM 017348		expressed sequence AA589632, solute carrier family 6 (neurotransmitter
	1	7	, v	transporter, creatine), member 8

TABLE 3	m			The state of the s	
SEO		GenBank Acc.	-	The second secon	Atty. Ref. 44921-5090-01-WO/2105485
٥	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Hömölösous Senuence Cluster Title
					CTAGE-1 protein, ESTs, Moderately similar to MEA6_HUMAN MENINGIOMA- EXPRESSED ANTIGEN 6/11 (MEA6) (MEA11) IH sapiens1 ESTs, Maakh, similar to
				MEAG_HUMAN MI	MEA6_HUMAN MENINGIOMA-EXPRESSED ANTIGEN 6/11 (MEA6) (MEA11)
1254		22958 AI171374	p, q, t	[H.sapiens], KIAA0	<ul><li>[H.sapiens], KIAA0268 protein, meningioma expressed antigen 6 (coiled-coil proline- rich)</li></ul>
				C-type (calcium de	C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily
1451	7650	7650 AI230142	W, X	member 13, ESTs,	member 13, ESTs, Weakly similar to KUCR_RAT Kupffer cell receptor
			e, aa, bb,	It violagions), vii	i vitor vegicus), Aupilei celi receptor, Langemans celi specific c-type lectin
1792	- [	17257 NM_012766	ee, ff	cvalin D3	
1/92	17261	17261 NM_012766	n, m	cyclin D3	
736	2782	2782 AA998565	c, I, m	cyclin-dependent ki	cyclin-dependent kinase inhibitor 1C (P57), cyclin-dependent kinase inhibitor 1C
0			y, z, ee, ff,	(Adv. , 104)	
8977	11258	11258 NM_031327	66	cysteine rich proteil	Cysteine rich protein 61. cysteine-rich angiogenic inducer 64
3	70//07	2017UNM 024160	0, n	cytochrome b-245, alpha polypeptide	alpha polypeptide
1795	449	449 NM_012786	hh	cytochrome c oxida	Cytochrome c oxidase, subunit VIIIh, heme-remulated initiation foots 2 class 1
1705	4037	000070 711			est coording them est egulated illinguon lactor z-alpha Kinase
25 75	1004	5227 AA925924	i, nh	cytochrome c oxida:	cytochrome c oxidase, subunit VIIIb, heme-regulated initiation factor 2-alpha kinase
1528	5228	5228 A1932344	1, U, NR	cytokine receptor-like factor 1	ke factor 1
272	7777	11000711	0,11,11	Cytokine receptor-like factor 1	(e factor 1
				DEADIH (Asp-Glu-A	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 20, DEAD/H (Asp-Glu-Ala-Asp/His)
	_			box polypeptide 20,	box polypeptide 20, 103kD, DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 39,
				DEAD/H (Asp-Glu-A	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD), DEAD/H
		_		(Asp-Glu-Ala-Asp/Hi	(Asp-Glu-Ala-Asp/His) box polypeptide 7 (RNA helicase, 52kD), EST, Moderately
			2 2	similar to HLA-B-as	similar to HLA-B-associated transcript 1A; DNA segment, Chr 17, human D6S81E
2395	4327 N	4327 NM 053563	1, 1, 0, 7, 4, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	1; nuclear RNA helic	1; nuclear RNA helicase Bat1 [Mus musculus] [M.musculus], HLA-B-associated
		1	YM off	transcript 1A	
				death-associated kin	death-associated kinase 3, death-associated protein kinase 1, death-associated
2139	12422N	12422 NM 022546	0	protein Kinase 3, exp	protein Kinase 3, expressed sequence Al120141, serine/threonine kinase 17a
1		1	- -	(apoptosis-inducing)	(apoptosis-inducing), serine/threonine kinase 17b (apoptosis-inducing)
				•	

TABLE 3	E3			
S S		GenBank Acc.		
ੂ	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name Human Homologous Seguence Chister Title
233		16155 NM 031810	12	
2132		NM 022531	0	defensin beta 1, defensin beta 2, defensin, beta 1, expressed sequence AW260221
250%	ı	4739 NM 130400	44.00	desmin
		001001	da, DD	dihydrofolate reductase
2182		4504 NM 024159		disabled homolog 1 (Drosophila), disabled homolog 2 (Drosophila), disabled
939		7880 AI043714	· :=	homolog 2, mitogen-responsive phosphoprotein (Drosophila)
				UNTZP434BU335 protein
				DKFZP4341216 protein, ESTs. Highly similar to DBS MOLISE GLIANINE
				NUCLEOTIDE EXCHANGE FACTOR DBS IM. musculus I FSTs Weakly similar to
				DBS MOUSE GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS IM miscrifies
				ESTs, Weakly similar to TIAM MOUSE T-LYMPHOMA INVASION AND
				METASTASIS INDUCING PROTEIN 1 [M.musculus]. Homo saniens CONA
				FLJ21933 fis, clone HEP04337, KIAA0861 protein, KIAA1209 protein, MCF 2 cell
				line derived transforming sequence, MCF.2 cell line derived transforming sequence-
				like, RIKEN cDNA 2410008H17 gene, T-cell lymphoma invasion and metastasis 2
2453		531 NM 053951		expressed sequence AA408740, hypothetical protein MGC2780, likely ortholog of
			000	mouse common-site lymphoma/leukemia GEF, mcf.2 transforming segmence
				DKFZP564D0764 protein, ESTs, Weakly similar to zinc finger protein 319 IMus
				musculus] [M.musculus], KIAA1805 protein, Mus musculus, clone MGC:29358
2401	24875 N	24875 NM_053583  ii	—— ≅: :=:	IIMAGE:5038671, mRNA, complete cds, OLF-1/EBF associated zinc finger gene,
				NIKEN CUNA 4931408L03 gene, early B-cell factor associated zinc finger protein
				Chain produced by Meakly Similar to S59856 collagen alpha 1(III)
			-	Contain prevail soil - Informace [in. musculus], hypothetical protein DKFZp547D065,
1166	10780 A	10780 AI136555 c	_	inypoineucal protein FLJ13725, mucin and cadherin-like, splicing factor 3a, subunit
482	11268A	11268 AA899969	E	Z, bokU
			-	DKFZP566C0424 protein
				DKFZP566D213 protein, EST, Moderately similar to EPIDERMAL GROWTH
			_	FACTOR PRECURSOR [M.musculus], Homo sapiens mRNA; cDNA
1015	8347 A	8347 A1059519	0.0	DKFZp434O0213 (from clone DKFZp434O0213); partial cds, hypothetical protein
	<del> </del> 			MGC11256, nidogen 2

TAB	TABLE			The state of the s	
ŭ,	!!	GenBank Acc.	_		VO/2105485
أ	GEGC ID No.	Ŋo.	Model Code	Model Code, Human Hr mologous Known Gene Name	
			. ,	DKFZP586G011 protein, ESTs, Weakly similar to T08767 probable lamina- associated protein DKFZp586G011.1 IH saniens Mus museulus olong MCC 2557	1a- MCC:6267
70007		1948 NM 145092	D, I, m	IMAGE:3493883, mRNA, complete cds	1000.00M
			-	DNA (cytosine-5-)-methyltransferase 1, DNA methyltransferase (cytosine-5) 1, EST,	-5) 1, EST,
				Weakly similar to JE0378 DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - rat	.37) - rat
				In the vegicus, r-box and leucine-rich repeat protein 11, Mus musculus DNA control repeat protein 11, Mus musculus DNA control repeats methyl 20 hinding domein	NA
742		21666 AB012214	o'u	containing CXXC domain 2	, protein
				DNA polymerase epsilon, subunit 3, ESTs, Moderately similar to CCAAT-BINDING	BINDING
				I RANSCRIP I ION FACTOR SUBUNIT A [M.musculus], ESTs, Weakly similar to	milar to
				AZ3692 transcription factor, CCAAT-binding, chain A1 - rat [R.norvegicus], RIKEN	J, RIKEN
				CDINA 1610U34K18 gene, down-regulator of transcription 1, down-regulator of	or of
				uanscription 1, 1 BP-binding (negative cotactor 2), nuclear transcription factor Y,	ctor Y,
2283		1822 NM 031553		beta, nuclear transcription factor-Y beta, polymerase (DNA directed), epsilon 3 (p17	ion 3 (p17
1650		2401 AJ011607	3	Subunit)	
				Drive printase, poo suburin, printase, polypeptide 2A (58KD)	
				DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed, EST, Weakly	r, Weakly
				Similar to Suppression or tumorigenicity 13 (colon carcinoma) Hsp70-interacting	acting
<b></b>				fundrinenicity 13 (Anlan Carrings) Heazo information and information matter to suppression of	ession of
				Raines norvegicus    Research	regicus]
2248	23568 N	23568 NM 031122		expressed sequence AW538196, sperm associated antigen 1, suppression of	o gene, n of
0177	70007	$\top$	D I	tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	
				DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed, EST, Weakly	Weakly
			-	similar to suppression of tumorigenicity 13 (colon carcinoma) Hsp70-interacting	acting
				protein [Kattus norvegicus] [R.norvegicus], ESTs, Weakly similar to suppression of	ession of
				Immorigenicity 13 (colon carcinoma) Hsp70-interacting protein [Rattus norvegicus]	egicus]
-				Investigate   Investigate	3 gene,
2248	23569N	23569 NM_031122  r		tumoridenicity 13 (colon carcinoma) (Henzo intermiting anatoin)	
				(mind gainer) (color calculotte) (15p/o litteraculig protein)	

TABLE 3	33		44.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
SEQ		GenBank Acc.		number of the state of the stat	Atty. Ref. 44921:5090-01-WO/2105485
Ω	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					DNA segment, Chr 10, ERATO Doi 398, expressed, EST, Weakly similar to 2102279A protein Tyr phosphatase [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to 41 MOUSE PROTEIN 4.1 M muscrifus] protein process
2526		1824 NM_133545	j, k, r		phosphatase, non-receptor type 14, protein tyrosine phosphatase, non-receptor type 21
2255		13358 NM_031135	ס		DNA segment, Chr 12, ERATO Doi 427, expressed, RIKEN cDNA 7420700M05 gene, TGFB inducible early growth response, TGFB inducible early growth response 2
2255		13; 59 NM_031135	s, t		DNA segment, Chr 12, ERATO Doi 427, expressed, RIKEN cDNA 7420700M05 gene, TGFB inducible early growth response, TGFB inducible early growth response 2
					DNA segment, Chr 17, ERATO Doi 479, expressed, EGF-like module containing, mucin-like, hormone receptor-like sequence 1, EST, Highly similar to T08685
					MOUSE CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR [M.musculus], ESTs, Weakly similar to EMR1 ESTs, Weakly similar to EMR1 MOUSE CELL SURFACE GLYCOPROTEIN EMR1
2570	146631	14663 NM_139110	<u> </u>		PRECURSOR [M.musculus], KIAA0758 protein, cadherin EGF LAG seven-pas G-type receptor 2, hynothetical profesion 11,12584, latrachilin
					DNA segment, Chr 17, ERATO Doi 479, expressed, EGF-like module containing, mucin-like, hormone receptor-like sequence 1, EST, Weakly similar to EMR1 MOUSE CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR IM musculus)
2103	23511 N	23511 NM_022294	0,0		ESTs, Weakly similar to EMR1 MOUSE CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR [M.musculus], egf-like module containing, mucin-like, hormone
					DNA segment, Chr 3, University of California at Los Angeles 2, EST, Weakly similar to RL10 MOUSE 60S RIBOSOMAL PROTEIN L10 [M.musculus], EST, Weakly similar to RI 10 MOUSE 60S ribosomal profein 140 / OM profein Landing
2236	20812 N	20812 NM_031100	g, h, I		[R.norvegicus], ribosomal protein 10, ribosomal protein L10, ribosomal protein L10-like
2625	1283 061729		cc, dd, ll		DNA segment, Chr 4, Brigham & Women's Genetics 0593 expressed, ESTs, Moderately similar to JC4899 proline rich protein - rat [R.norvegicus], RIKEN cDNA 0610011F17 nene hynothetical protein El 190312
					וסווסו וביי אפיפ, וואסטופטסו אוטופווו רבאבטאנל, אנאוחה חכח 2

ا ا ا	G G G	GenBank Acc.		<del>(</del>	. Ref. 44921-5090-01-WO
		The state of the s	Iwinger Code	Model Code Human Honologous Known Gene Name	Human Homologous Sequence Cluster Title
				DNA se	DNA segment, Chr 4, ERATO Doi 429, expressed, EST, Weakly similar to
				2113200	2113200G nbosomal protein S10 [H.sapiens], EST, Weakly similar to ribosomal
				protein	protein S10 [H.sapiens], ESTs, Highly similar to 2113200G ribosomal protein S10
				(H.sapie	H. Sapiens], ESTs, Highly similar to RS10 RAT 40S RIBOSOMAL PROTEIN S10
2242		16847 NM 031109	<u>&gt;</u>	Rnorve	R.norvegicus], ESTs, Moderately similar to RIKEN cDNA 2210402A09 [Mus
	1		V (1 1)	ninosnui	musculus] [M.musculus], RIKEN cDNA 2210402A09 gene, ribosomal protein S10
				DNA seg	DNA segment, Chr 9, ERATO Doi 394, expressed, Mus musculus, Similar to
				electron-	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II), clone
461		16434 AA894174	_	MGC:646	MGC:6481 IMAGE:2646522, mRNA, complete cds, electron-transfer-flavoprotein.
				alpha po	alpha polypeptide (glutaric aciduria II)
				DNA seg	DNA segment, Chr X, Celltech Chiroscience 3, Mus musculus, serine threonine
2145		21115 NM 022602	د.	kinase pi	kinase pim3, clone MGC:27707 IMAGE:4924687, mRNA, complete cds, pim-1
			u .	negano	e, pim-2 oncogene, proviral integration site 1
				DNA seg	DNA segment, EST 1068184, ESTS, Highly similar to S68418 protein phosphatase
				1M chain	IM chain M110 isoform - rat [R.norvegicus], ESTs, Weakly similar to S68418
				protein pl	protein phosphatase 1M chain M110 isoform - rat (fragment) [R.norvegicus], ESTs.
				Weakly si	Weakly similar to T42713 ankyrin 3, splice form 1 - mouse [M.musculus], RIKEN
				CDNA 18	cDNA 1810037003 gene, ankyrin repeat and SOCS box-containing 1, ankyrin
				repeat an	repeat and SOCS box-containing 2, ankyrin repeat and SOCS box-containing 3,
2	_	17137 44799438	33 :: #	leukocyte	eukocyte receptor cluster (LRC) member 3, protein phosphatase 1, regulatory
		00400	CC, 11, JJ, KK	(inhibitor)	(inhibitor) subunit 12A
				DNA segr	DNA segment, KIST 6, ESTs, Moderately similar to 147177 hypothetical protein
			_	DKFZp76	DKFZp762H157.1 [H.sapiens], ESTs, Weakly similar to MOES MOUSE MOESIN
2207		1048 NM 030863		[M.muscu	[M.musculus], RIKEN cDNA 4933415103 gene, expressed sequence AA408511.
107	1	1	S, t, mn	moesin, ra	moesin, radixin, villin 2 (ezrin)

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SEQ		GenBank Acc.			2105485
≘	GLGC ID No.	No.	Model Code	Inefer Ti	
2262		23097 NM_031145	n, o, cc, dd	3, ESI ib [H.s ing protein) (( tein) (( ated, o mRNA	ens], n lytic nmplete
246	163 I8 A	163 18 AA859648	b á	DnaJ (Hsp40) homolog, subfamily A, member 1, DnaJ (Hsp40) homolog, subfamily A, member 4, DnaJ (Hsp40) homolog, subfamily B, member 1, DnaJ (Hsp40) homolog, subfamily B, member 12, ESTs, Weakly similar to DJA1_MOUSE DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) [R.norvegicus], ESTs, Weakly similar to HSJ2_HUMAN DNAJ PROTEIN HOMOLOG 2 [H.sapiens], Homo sapiens cDNA FLJ13992 fis, clone Y79AA1002139, weakly similar to DNAJ PROTEIN HOMOLOG 1, RIKEN cDNA 1700014P03 gene, RIKEN cDNA 2010306G19 gene, RIKEN cDNA 5730551F12	ofamily naJ
103	6892/A	6892 AA800551 e	e, ee, ff, ii	UnaJ (HSp4u) homolog, subtamily A, member 1, DnaJ (HSp4u) homolog, subtamily A, member 1, DnaJ (HSp4u) homolog, subtamily A, member 1, DnaJ (HSp4u) homolog, subtamily A, member 1, DnaJ (HSp4u) homolog, subtamily A member 1, DnaJ (HSP4u) homolog, subtamily A member 1, DnaJ (HSP4u) homolog subfamily A member 1 (Heat shock 40 kDa protein homolog 2) (HSJ-2) [R.norvegicus], ESTs, Weakly similar to DnaJ-like protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to HS44 MOUSE HEAT SHOCK 40 KDA PROTEIN 4 [M.musculus], Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 730912, Mus musculus SEC63 (Sec63) mRNA, complete cds, similar to DNAJ	amily amily :AT sert nplete

11 6891 NIM_022834 ee, ff 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	TABLE 3 SEQ ID G	E.3 GLGC ID No.	GenBank Acc.		Model Code Human Homologous Known Gene Name	Jous Known G	ene Name		**************************************
18047 A1171359 bb	2161		NW 02034	#					Promiser Portugues Sequence Cluster Little  [DnaJ (Hsp40) homolog, subramily A, member 1, DnaJ (Hsp40) homolog, subramily  A, member 4, ESTs, Highly similar to HS44 MOUSE HEAT SHOCK 40 KDA  PROTEIN 4 [M.musculus], ESTs, Moderately similar to DJA1_MOUSE DnaJ  homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein  homolog 2) (HSJ-2) [R.norvegicus], ESTs, Weakly similar to DnaJ-like protein  homolog 2) (ASJ-2) [R.norvegicus], ESTs, Weakly similar to HS44 MOUSE HEAT  SHOCK 40 KDA PROTEIN 4 [M.musculus], Homo sapiens mRNA full length insert  cDNA clone EUROIMAGE 730912, Mus musculus SEC63 (Sec63) mRNA.
390 AA956907 u, v 18946 NM_021584 s, t 399 U31668 p, q 17586 NIM_022694 w, x	1252	=======================================	A1171359	e qq					ods, similar to DNAJ  DnaJ (Hsp40) homolog, subfamily A, member 1, DnaJ (Hsp40) homolog, subfamily  Rember 6, DnaJ-like protein, ESTs, Highly similar to HS44 MOUSE HEAT  HOCK 40 KDA PROTEIN 4 [M.musculus], Homo sapiens mRNA full length insert
7 5990 AA956907 u, v 18946 NM_021584 s, t 399 U31668 p, q	692	3808;	A1008643	p, q, ee, ff				<u> </u>	Durk Gone EURUIMAGE 730912, RIKEN cDNA 4930483N21 gene DnaJ (Hsp40) homolog, subfamily B, member 1, DnaJ (Hsp40) homolog, subfamily B, member 5, Homo sapiens cDNA FLJ25366 fis, clone TST01784, RIKEN cDNA 700014P03 gene, RIKEN cDNA 2010306G19 gene, RIKEN cDNA 5730551F12
399 U31668 p, q  24375 A1104979 j, k  17586 NIM_022694 w, x	657	5990	AA956907	n, v				<u> </u>	ene, hyponieucal protein FLJ14281 had (Hsp40) homolog, subfamily C, member 8, Homo sapiens cDNA FLJ13613 fis one PLACE1010856, Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone KFZp434C2016). hypothetical protein DKFZp434R222
399 U31668 p, q 24375 A1104979 j, k 17586 NIM_022694 w, x	7007	10346	NM_021584	ڻ' <del>د</del>				<u>ещ ў ; ў</u>	oublecortex; lissencephaly, X-finked (doublecortin), doublecortin  ZF transcription factor 4, p107/p130-binding, E2F transcription factor 5, E2F  anscription factor 5, p130-binding, ESTs, Moderately similar to E2F5 MOUSE  RANSCRIPTION FACTOR E2F5 [M.musculus], ESTs, Moderately similar to  1.F5, RAT TRANSCRIPTION FACTOR F2F5 (F2F, N.D. paracely similar to
24375 Al104979 j, k 17586 NM_022694 w, x	2621	399	J31668	b d				ΞΞ	usculus, Similar to E2F transcription factor 4, p107/p130-binding, clone GC:37558 IMAGE:4987691, mRNA, complete cds
17586 NM_022694   w, x	1146	24375 A	V104979	j, k				<u>。</u> 四	3NA1 binding protein 2, ESTs, Moderately similar to EBNA1 binding protein 2; icleolar protein p40; homolog of yeast EBNA1-binding protein; nuclear FGF3 iding protein; EBNA1-binding protein; 2 (Homo graping) in a contein;
	2151	17586N		W, X				<b>出 8</b>	3NA-2 co-activator (100kD), ESTs, Moderately similar to 138968 100 kDa activator (H.sapiens).

TABLE 3	E3	14 To 17 To 18	", 190g)	. Are
SEO		GenBank Acc		Alty-Ref. 44974-5090-01-WOID40K49E
₽	GLGC ID No.	No.		Homologous Segments Chiefor
1667		22762 D89730	qq	
2568		17868 NM_139104	7, S, t	EGF-like-domain, multiple 6, ESTs, Moderately similar to T17324 hypothetical protein DKFZp564P2063.1 [H.sapiens], ESTs, Weakly similar to MEGF6 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to fibulin 5 [Mus musculus] [M.musculus], ESTs, Weakly similar to T03065 hypothetical protein - mouse [M.musculus], ESTs, Weakly similar to T17324 hypothetical protein DKFZp564P2063.1 [H.sapiens], ESTs, Weakly similar to TIE1 MOUSE TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR [M.musculus], MEGF6, NEU1 protein, RIKEN cDNA 6130401L20 gene, expressed sequence AW047140
1550	13293 A 17358 A	13293 AI235032 17358 AI179147	h h	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B), ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D), ESTs, Highly similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus], ESTs, Moderately similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus], ESTs, Weakly similar to HUD_HUMAN PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD [H.sapiens]
1328	17920 A	17920 AI176422	==	electron-transferring daynosptide
943	7913AI	7913 AI043849	<b>₩</b>	ELL-related RNA polymerase II, elongation factor, ESTs, Weakly similar to ELL MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL [M.musculus], Musmusculus, clone IMAGE:3583970, mRNA, partial cds, RIKEN cDNA 9430098F02
699	23732 A		# # # # # # # # # # # # # # # # # # #	gene, eleven-nineteen lysine-rich leukemia gene, hypothetical protein FLJ22637 Ena-vasodilator stimulated phosphoprotein, RNB6, enabled homolog (Drosophila), expressed sequence Al528774, likely ortholog of mouse NPC derived proline rich
352	6635A	6535 AA891746	l, m	protein 1, vasodilator-stimulated phosphoprotein endothelial differentiation-related factor 1
				1 CAPURATION IN CAPULATION IN

TABLES					
ŭ	  -	GenBank Acc.		Control of the contro	Atty. Ref. 44921-5090-01-WO/2105485
اء	GLGC ID No.	Ŋo.	Model Code	Model Code Human Hr mologous Knovin Gene Name Human Homologous Sequence Clister Title	
					ated substrate related).
				expressed sequence Al385681, neural precursor cell expressed, developmentally	ressed, developmentally
1828		18694 NM_012931	j, k, gg	امown-regulated gene 9, signal transduction protein (SH3 containing), v-crk- Jassociated hyrocing Lings ويتأمين	containing), v-crk-
				pubancer of filamentation 4 (Act ill. 4 - 1).	
				Paringued in maniferration of the property of the property of the paring	ated substrate related),
				Capacasaca sequence Ansocioo I, lieural precursor cell expressed, developmentally	ressed, developmentally
1828		18695 NM 012931	ikva	down-regulated gene 9, signal transduction protein (SH3 containing), א-כילי	containing), v-crk-
386		23194 AA892417	71, 71, 71	associated tyrosine kinase substrate	
2005		21500 NIM 020047	66	ephrin A1, ephrin-A1	
247	7	14INI_030047	n, ı, n, o	epithelial membrane protein 3	
				ER to nucleus signalling 1, ESTs, Weakly similar to A34366 Ca2+tralmodulin-	36 Ca2+/calmodulin-
				dependent protein kinase (EC 2.7.1.123) II delta chain - rat IR novecious I Mus	at IR.norvegicus Mus
				musculus, clone MGC:18731 IMAGE:3980838, mRNA, complete cds	molete cds
				calcium/calmodulin-dependent protein kinase (CaM kinase) !! alnha	a) II alnha
1	1			Caldium/calmodulin-dependent profein kinase (CaM kinase) II delta	) II delta
15	100002	25355 MN 012519	u, v, "	Calcium/calmodulin-dependent protein kinasa II dalta	ין זו טפונס,
			-	ER to nucleus signalling 1 FSTs prosent in Journal 1 FSTs prosent in Section 1 FSTs prosent in S	
				dependent protein kinase (FC 2 7 1 123)   John and India about a rot ID managing   Managing	o caz+/calinodulin-
				Imusculius clone MGC:48741 IMAGE:3080838	r inclini vegicusį, ivius
				Configuration (Color)	ripiere cas,
				calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha,	) II alpha,
1737	2735 N	2735 NM 012519		calcium/calmodulin-dependent protein kinase (CaM kinase) II detta,	i) II delta,
				Calcium/calmodulin-dependent protein kinase II, delta	
	-			EK to nucleus signalling 1, ESTs, Weakly similar to A34366 Ca2+7calmodulin-	6 Ca2+/calmodulin-
				dependent protein kinase (EC 2.7.1.123) II delta chain - rat [R.norvegicus], Mus	R.norvegicus), Mus
				musculus, clone MGC:18731 IMAGE:3980838, mRNA, complete cds.	nplete cds,
				calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	i alpha.
1737	9736 NI	2736 NW 043540		calcium/calmodulin-dependent protein kinase (CaM kinase) II delta.	) Il delta.
	3		۱ ا	calcium/calmodulin-dependent protein kinase II, delta	
				ER transmembrane protein Dri 42, RIKEN cDNA 1810019D05 gene, phosphatidic	005 gene, phosphatidic
	<u> </u>			acid phosphatase 2a, phosphatidic acid phosphatase type 2A, phosphatidic acid	2A, phosphatidic acid
2136	8596 NA	8596 NM 022538		phosphatase type 2B, phosphatidic acid phosphatase type 2C, phosphatidic acid	2C, phosphatidic acid
		200		phosphatase type 2c	

TABLI	С		これのないないます リーン	control
SEO		GenBank Acc	$\vdash$	2000-01-WO/2105485
Ω	GLGC ID No.	No.		į
2136		8597 NM_022538	aa, bb, kk, Il	ER transmembrane protein Dri 42, RIKEN cDNA 181 acid phosphatase 2a, phosphatidic acid phosphatase phosphatase type 2B, phosphatidic acid phosphatase
2071		16 NM_019386	cc, dd, kk	erythrocyte membrane protein band 4.2, transglutaminase 2 (C polypeptide, protein- glutamine-gamma-glutamytransferase), transglutaminase 2, C polypeptide, transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamytransferase),
2230		4684 NM_031083	b, l, m	EST AA437822, Homo sapiens, Carisyludarinidase 3, transgludarinidase 2, an an aguidamnase 2.  EST AA437822, Homo sapiens, Similar to phosphatidylinositol 4-kinase, catalytic, alpha polypeptide, alpha polypeptide, phosphatidylinositol 4-kinase, catalytic, alpha polypeptide, phosphatidylinositol 4-kinase, catalytic, beta polypeptide, phosphoinositide-3-kinase, catalytic, gamma polypeptide.
847	217,16,	217-16 AI012221	a, n, o, x, z, kk	EST X83352, ESTs, Weakly similar to intracellular chloride ion channel protein p64H1 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 5730531E12 gene, chloride intracellular channel 1, chloride intracellular channel 3, chloride intracellular channel 5, chloride intracellular channel 9, chloride intracellular channel 9, chloride intracellular channel protein p64H1
				EST, Highly similar to phosphatidylinositol 3-kinase, regulatory subunit, polypeptide [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to P55G_MOUSE PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY GAMMA SUBUNIT (PI3-KINASE REGULATORY GAMMA SUBUNIT (PI3-KINASE P85-GAMMA) (P55PIK)
1119	11721	11721 AI103391	ee, ff	ויייוועטטינים לפקין 3-kinase, regulatory subunit, polypeptide 2 (p85 beta), phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85
2054	10015N	10015 NM_019289	n, o, jj, kk, 11	EST, Highly similar to AR41_HUMAN ARP2/3 COMPLEX 41 KDA SUBUNIT [H.sapiens], actin related protein 2/3 complex, subunit 1B (41 kD), actin related protein 2/3 complex, subunit 1B (41 kD), actin related
2054	10016N	10016 NM_019289	a, o, jj, kk, ll	EST, Highly similar to AR41_HUMAN ARP2/3 COMPLEX 41 KDA SUBUNIT [H.sapiens], actin related protein 2/3 complex, subunit 1B (41 kD), actin related protein 2/3 complex.
				(DOW) 14 Or minors for directly the

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SEQ		GenBank Arc.		A STATE OF THE STA	** Atty. Ref. 44921-5090-01-WO/2105485
<u>≘</u>	St GC to No.	No.	Model Code Human Hor	ologous Known Gene Name	Himan Homologue Source Clieber Tale
				EST	EST, Highly similar to CCAC RAT Voltage-dependent Livre calcum channel aleba
				1Cs	16 subunit (Calcium channel, L type, alpha-1 polybeptide, isoform 1 cardiac
				osnw osnw	muscle) (RAT brain class C) (RBC) [R.norvegicus], ESTs, Highly similar to
				CCA	CCAC_HUMAN VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1C
				BUS_	SUBUNIT [H.sapiens], ESTs, Highly similar to CCAD_HUMAN VOLTAGE.
					DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1D SUBUNIT IH.Sapiens). Mus
1722		24652 M59786	:: :: ::	Snm	musculus putative ion channel protein CATSPER2 mRNA, complete cds. calcium
	1	200	1, 111, JJ, NA	chanr	nnel, voltage-dependent, L type, alpha 1C subunit
				EST,	EST, Highly similar to DPOZ_HUMAN DNA POLYMERASE ZETA CATALYTIC
				nans	SUBUNIT [H.sapiens], ESTs, Highly similar to DPOZ_HUMAN DNA POLYMERASE
				ZETA	ZETA CATALYTIC SUBUNIT [H.sapiens], ESTs, Weakly similar to DPOZ HUMAN
				DNA	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (H.sapiens), REV3-like, catalytic
				ungns.	subunit of DNA polymerase zeta (yeast), REV3-like, catalytic subunit of DNA
1583	22939	22939 AI236669	7.7.	polym	polymerase zeta RAD54 like (S. cerevisiae), expressed sequence C77370.
			7, 5, JJ, MA	expres	expressed sequence C77386
				(במין ב	ESI, Highly similar to HEMU_RAT 5-AMINOLEVULINIC ACID SYNTHASE;
				ERYT	ERYTHROID-SPECIFIC, MITOCHONDRIAL PRECURSOR (DELTA-
				AMING	AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-E)
				[R.nor	[R.norvegicus], ESTs, Highly similar to SYHUAE 5-aminolevulinate synthase
				[H.sap	[H.sapiens], aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia).
	-			amino	aminolevulinic acid synthase 1, aminolevulinic acid synthase 2, erythroid, glycine C.
1894	16448 N	16448 NM 013197	- - -	acetylt	acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase), glycine C.
		T	2 2	acetylt	acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)
				בי בי בי בי בי בי בי בי בי בי בי בי בי ב	Highly similar to HS9B MOUSE HEAT SHOCK PROTEIN HSP 90-BETA
				[M.mus	[M.musculus], EST, Weakly similar to HHMS84 heat shock protein 84 - mouse
				[M.mus	[M.musculus], ESTs, Highly similar to HS9A_HUMAN HEAT SHOCK PROTEIN
				HSP 90	HSP 90-ALPHA [H.sapiens], ESTs, Highly similar to T46243 hypothetical protein
764	15849A	15849 A1008074		DKFZp	DKFZp761K0511.1 [H.sapiens], expressed sequence C81438, heat shock 90kD
				protein	protein 1, beta, heat shock protein, 84 kDa 1, heat shock protein, 86 kDa 1

IABLE 3	3			The state of the s	
SEO		GenBank Acc.	1 .		Atty: Ref. 44921-5090-01-WO/2105485
<u>.</u>	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					EST, Highly similar to HSRT4 histone H4 - rat IR norvegicus]. EST. Moderately
				is .	similar to HSHU4 histone H4 [H.sapiens], H4 histone family, member E. Mus
				E	musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library.
				<u>~~</u>	clone:1810029H14:histone 4 protein, full insert sequence, Mus musculus adult male
83	643	643 AA946439		<b>Q</b>	tongue cDNA, RIKEN full-length enriched library, clone:2310067E17:histone 4
				<u>ia</u>	protein, full insert sequence
				<b>й</b>	EST, Highly similar to JC2234 ribosomal protein S15a, cytosolic [validated] - rat
2461	15488	15458 NM 053982	77 !! × M !	<u>2.</u>	[R.norvegicus], ESTs, Highly similar to RS1A_HUMAN 40S RIBOSOMAL PROTEIN
		70000-	1) w, v, II, nn	28	S15A [H.sapiens], ribosomal protein S15a
				<u></u>	EST, Highly similar to MYHA_RAT Myosin heavy chain, nonmuscle type B (Cellular
				( <u>m</u>	myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NIMMHC-B)
		. —		<u> </u>	[R.norvegicus], ESTs, Highly similar to MYHA_MOUSE Myosin heavy chain.
				OU.	nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy
				Ch	chain-B) (NMMHC-B) [M.musculus], Homo sapiens cDNA: FLJ23324 fis. clone
				里	HEP12482, highly similar to HUMMYOHCB Human nonmuscle myosin heavy chain-
2686	18C 11 X44554	(44551		) <u>B</u>	B (MYH10) mRNA, Myosin heavy chain 11, RIKEN cDNA 5730504C04 gene.
		1001		lan	laminin, gamma 1
				<u>S</u>	EST, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat
				<u>R</u>	[R.norvegicus], EST, Weakly similar to E54024 protein kinase [H.sapiens], ESTs.
_				PiH.	Highly similar to 60S RIBOSOMAL PROTEIN L23A [R.norvegicus]. ESTS. Highly
				sim	similar to RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [H.sapiens], Mus
1480	20845	20845 41234440	. ,	חשו	musculus, ribosomal protein L23a, clone IMAGE:4988735, mRNA, partial cds.
	2007		ν, λ	ribo	ribosomal protein L23a
				ES	EST, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat
	_			[R.	[R.norvegicus], EST, Weakly similar to E54024 protein kinase [H.sapiens], ESTs.
	_			Hig	Highly similar to 60S RIBOSOMAL PROTEIN L23A [R.norvegicus], ESTs. Highly
				Simi	similar to RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [H.sapiens]. Mus
2671	20844 X65228		7	snu.	musculus, ribosomal protein L23a, clone IMAGE:4988735, mRNA, partial cds.
3	× 2004		, g, cc, ad	oqii	ribosomal protein L23a

TABLE 3			・機能がないというから	
SEO		GenBank Acc.		The state of the s
Ω	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name
				EST, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus], EST,
				Weakly similar to JN0923 ribosomal protein L8, cytosolic [H.sapiens], ESTs, Highly
				similar to R5RTL8 ribosomal protein L8, cytosolic [validated] - rat [R.norvegicus],
	_			ESTs, Highly similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L IM.musculus],
707	45070	000000		ESTs, Moderately similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L
\$	0/00	1307074943382	g, w, x	[M.musculus], expressed sequence AL024098, ribosomal protein L8
				EST, Highly similar to S611_HUMAN Protein transport protein Sec61 alpha subunit
				isoform 1 (Sec61 alpha-1) [R.norvegicus], ESTs, Highly similar to S611_HUMAN
				Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1)
			_	[R.norvegicus], SEC61, alpha subunit (S. cerevisiae), SEC61, alpha subunit 2 (S.
7,07	7	10070014	-	cerevisiae), Sec61 alpha form 2, protein transport protein SEC61 alpha subunit
9	70107	Z1010/AIZ31Z1/	=	Isoform 1
				EST, Highly similar to SNX9_HUMAN SORTING NEXIN 9 (SH3 AND PX DOMAIN-
674	77777	00673000		CONTAINING PROTEIN 1) (SDP1 PROTEIN) [H.sapiens], Homo sapiens cDNA
5	1007	H4307 000	66	FLJ11997 fis, clone HEMBB1001458, sorting nexin 9
				EST, Highly similar to STA3_RAT Signal transducer and activator of transcription 3
1786	3/3/4	243 MIM 040747		[R.norvegicus], signal transducer and activator of transcription 3, signal transducer
3	3	14/710 INI	0,1	and activator of transcription 3 (acute-phase response factor)
				EST, Highly similar to T14106 probable GTPase-activating protein SPA-1 - rat
				[R.norvegicus], ESTs, Moderately similar to 714106 probable GTPase-activating
				protein SPA-1 - rat [R.norvegicus], KIAA0440 protein, RIKEN cDNA 2610511M17
1446	4 4 9 9 7	44997 A1400444	; -	gene, Rap1, GTPase-activating protein 1, SPA-1 like protein p1294, expressed
2 2	4557		E ', 'b'	sequence AW213287
880	15885/4	15885 AA965207	1	EST, Highly similar to 714795 hypothetical protein DKFZp434E171.1 IH.sapiens

TABLE 3	E3				
SEO		GenBank Acc.		1	-01:WO/210548
۵	GLGC ID No.	No.	Model Code Human Hon	nologous Known Gene Name Human Hömölogous Sequence Cluster Tille	
				ESI, Moderately similar to HLA-B-associated transcript 1A; DINA segment, Chr 17,	agment, Chr 17,
				human D6S81E 1; nuclear RNA helicase Bat1 [Mus musculus] [M.musculus], EST,	lusculus], EST,
				Weamy similar to new Leas House to the Alb-dependent RNA helicase p47 [R.norvegicus], ESTs. Moderately similar to 1541 HI MAN ELIKABYOTTIC	se p47
				INITIATION FACTOR 4A-I [M.musculus], ESTs, Weakly similar to HE47 RAT	E47 RAT
				PROBABLE ATP-DEPENDENT RNA HELICASE P47 [R.norvegicus], HLA-B-	J. HLA-B-
				associated transcript 1A, RIKEN cDNA 2410004K13 gene, RIKEN cDNA	DINA
493		3822 AA900863	<u>*</u>	2600001H07 gene, RIKEN cDNA 2610307C23 gene, eukaryotic translation initiation	Islation initiation
				tactor 4A, isoform 1, eukaryotic translation initiation factor 4A1	
				human D6S81F 1: nindear RNA helicase Batt Information	gment, Chr 1/,
				Weakly similar to HE47 RAT Probable ATP-dependent RNA helicase A47	usculus), ESI,
				(R.norvegicus), ESTs. Moderately similar to 1641 HIMAAN ELIZADAATIO	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
				INITIATION FACTOR 4A-1 IM. musculusi. FSTs. Weakly similar to HEA7 DAT	710
				PROBABLE ATP-DEPENDENT RNA HELICASE P47 (R. norvegicus) HI A.R.	H A.P.
				associated transcript 1A, RIKEN cDNA 2410004K13 gene, RIKEN cDNA	N N
1524	_	3823 AI233147	^ >	2600001H07 gene, RIKEN cDNA 2610307C23 gene, eukaryotic translation initiation	slation initiation
				factor 4A, isoform 1, eukaryotic translation initiation factor 4A1	
				ES1, Woderately similar to RIKEN cDNA 1700113017 [Mus musculus]	[S]
				I'M.musculus], H2A histone family, member L, Homo sapiens, clone MGC:21597	IGC:21597
				IMAGE:4511035, mRNA, complete cds, Mus musculus, similar to H2A histone	A histone
122	23115/	23115 AA801165	ပ	ramily, member O, clone MGC:36202 IMAGE:5055276, mRNA, complete cds,	lete cds,
				EST Moderately cimiles to time and a sequence	
7757	15/05/8	4640E/NW 004407		Ed. ), woderately slimital to tripepudate it [Kattus norvegicus]  R.norvegicus], ESTs. Highly similar to TRIPEPTIDY! "PEPTIDASE II M musadius)	Confined M
3	100	NIM_U3113/	E	tripeptidyl peptidase II	'isninoeniii'i
				EST, Moderately similar to tripeptidy peptidase II [Rattus norvegicus]	
2257	15486 N	15486 NM_031137	w. ×	[R.norvegicus], ESTs, Highly similar to TRIPEPTIDYL-PEPTIDASE II [M.musculus],	M.musculus],
-				urpepudyi pepudase II	
		•		LS1, Woderately similar to 0/10252A histone H3 [H.sapiens], ESTs, Highly similar for 1570/19 H3 histone and 10 hours and 1	ighly similar
				histone - rat IR nonvenions I 43 histone family mambas I II	79 H3
138	145.24 AI137974	1137974	p	Gene complex 1 clone McC.9529 1880 E-301326 F-DIA COMPLEX 1 clone McC.9529 1880 E-301326 F-DIA COMPLEX 1	ns, histone
				13 COLO TILIVAY, COMPIE	cds

<u> </u>	1				
ت. د		Genbank Acc.	*	1. 「「「「「「」」」、「「」」、「「」」、「「」」、「「」、「」、「」、「」、「」	Atty. Ref. 44921-5090-01-WO/2105485
_	GLGC DN3.	S.S.	Model Code	Model Code Human Ho nologous Known Gene Name	Human Homologous Sequence Cluster Title
			·	EST, Moderately similar to 810024 cytochrome b [M.	EST, Moderately similar to 0806162B cytochrome b [M.musculus], EST, Moderately similar to 810024B cytochrome b [H.sapiens], EST, Weakly similar to 0806162B cytochrome b [M.musculus], EST, Weakly similar to 0812187A cytochrome b
	14980A	14980 AI103396	E ,	Rattus norvegicu	[Kattus norvegicus] [R.norvegicus], EST, Weakly similar to 810024M URF 6 [H.saniens]
				EST, Moderately similar to 810024i cytochrome b [M.	EST, Moderately similar to 0806/162B cytochrome b [M.musculus], EST, Moderately similar to 810024B cytochrome b [H.sapiens], EST, Weakly similar to 0806/162B cytochrome b [M.musculus], EST, Weakly similar to 0812/187A
7	14981 AI103396	1103396	Φ	[Rattus norvegious	[Rattus norvegicus] [R.norvegicus], EST, Weakly similar to 810024M URF 6
<b>∞</b>	14983 AI179150	179150	- <del> </del>	EST, Moderately a Similar to 810024E Cytochrome b [M.n. [Rattus norvegicus	EST, Moderately similar to 0806162B cytochrome b [M.musculus], EST, Moderately similar to 810024B cytochrome b [H.sapiens], EST, Weakly similar to 0806162B cytochrome b [M.musculus], EST, Weakly similar to 0812187A cytochrome b [Rattus norvegicus] [R.norvegicus], EST, Weakly similar to 810024M I IRE 6
			35 (2)	[H.sapiens]	
1129	16136 Al103983		b' d	EST, Moderately s similar to 810024C 0806162C protein COI [M.musculus], [H.sapiens], ESTs,	EST, Moderately similar to 0806162C protein COI [M.musculus], EST, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], ESTs, Weakly similar to 0806162C protein COI IM musculus].
9	16130 J01435		8	EST, Moderately si similar to 810024C 0806162C protein (COI [M.musculus], 1	EST, Moderately similar to 0806162C protein COI [M.musculus], EST, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I
				EST, Moderately sir	In.saplens), ESTS, Weakly similar to 0806162C protein COI [M.musculus] EST, Moderately similar to 0806162C protein COI [M.musculus], EST, Moderately similar to 810024C cytochrome cyldocyllus, and an extension of the cytochrome cyldocyllus and an extension of the cytochrome cyldocyllus and an extension of the cytochrome cyldocyllus and an extension of the cytochrome cyldocyllus and a cyld
2388 16	161#5 NM_053516		aa, bb	0806162C protein C COI [M.musculus], E	0806162C protein COI [M.musculus], ESTs, Moderately similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], ESTs, Weakly similar to 0806162C protein COI IM musculus).

TABLE	; ;		: ફે	The serve that the destroyed the server that the server the server that the se	and the state of t
SEO		Gen Bank Acc			Atty. Ket. 44921-5090-01-WO/2105485
<u> </u>	20.0		-		.:
2	GLGC IU NO.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					ctor 4E-binding
				<u>ā</u>	protein:ISOTYPE=1 [H.sapiens], ESTs, Weakly similar to A55258 insulin-stimulated
				10.	phosphoprotein PHAS-1 - rat [R.norvegicus], RIKEN cDNA 1110004012 gene.
				<u> </u>	eukaryotic translation initiation factor 4E binding protein 1, eukaryotic translation
7770			•		initiation factor 4E binding protein 2, eukaryotic translation initiation factor 4E
7444		15/UNN U5385/	5, t	ld	binding protein 3
					EST, Moderafely similar to 2021415A initiation factor 4E-binding
				<u>d</u>	protein:ISOTYPE=1 [H.sapiens], ESTs, Weakly similar to A55258 insulin-stimulated
					phosphoprotein PHAS-1 - rat [R.norvegicus], RIKEN cDNA 1110004012 gene.
			. <del>-</del>	ne	eukaryotic translation initiation factor 4E binding protein 1, eukaryotic translation
7,7,7			:		initiation factor 4E binding protein 2, eukaryotic translation initiation factor 4E
7444	-	15 T NM 053857	e, t, kk	bit	binding protein 3
					EST, Moderately similar to 40S RIBOSOMAL PROTEIN S25 [R.norvegicus], EST.
				W	Moderately similar to R3RT25 ribosomal protein S25, cytosolic [validated] - rat
				<u> </u>	[R.norvegicus], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S25
				<u> </u>	[R.norvegicus], EST, Weakly similar to JQ1347 ribosomal protein S25, cytosolic
2869		707407		<b>王</b>	[H.sapiens], ESTs, Highly similar to JQ1347 ribosomal protein S25, cytosolic
2000	1	199#/ V07#07	w, x	<b>E</b>	[H.sapiens], ribosomal protein S25
				<u></u>	<ol> <li>Moderately similar to A Chain A, Structure Of Human Guanylate Binding</li> </ol>
				<u> </u>	Protein-1 In Nucleotide Free Form [H.sapiens], ESTs, Weakly similar to
				.X.	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 [M.musculus], Homo
				es es	sapiens mRNA; cDNA DKFZp564C2478 (from clone DKFZp564C2478); complete
				<u> </u>	cds, guanylate binding protein 1, interferon-inducible, 67kD, guanylate binding
0504	44000	700007	_	pro	protein 2, interferon-inducible, guanylate nucleotide binding protein 1, guanylate
4507	14880	42920 MINI 032024	0	กน	nucleotide binding protein 2
				מע	ES1, Moderately similar to A25074 vimentin [H.sapiens], EST, Weakly similar to
				AZ	A25074 vimentin [H.sapiens], ESTs, Weakly similar to A25074 vimentin [H.sapiens],
2259	15185 N	15185 NM 031140	- 44 	Mu	Mus musculus, similar to FLJ00074 protein, clone MGC:36549 IMAGE:4952810,
200	1000		II, UU, II	AM.	mRNA, complete cds, desmuslin, intermediate filament-like MGC:2625, vimentin

TABLE 3		: i:					
0.3	į.	GenBank Acc.		1		The second second second	(A) (A) (A) (A) (A) (A) (A) (A) (A) (A)
1	31.60	D.N.	Model Code Human Ho	Human Ho nolog	nologous Known Gene Name	Vame	Human Homologous Sequence Cluster Title
							ES1, Moderately similar to A55146 guanine nucleotide exchange ractor elf-2B detra chain, long form - mouse [M.musculus], ESTs, Moderately similar to E2BA_HUMAN
		_					I RANSLATION INTITATION FACTOR EIF-2B ALPHA SUBUNIT [H.sapiens], ESTs, Weakly similar to 2112359A initiation factor eIF-2B [Rattus norvegicus)
							[R.norvegicus], Mus musculus, Similar to eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD), clone MGC-6458 IMAGE-2645801, months and manifest of the MGC-6458 IMAGE-2645801
							Mus musculus, Similar to eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD). clone MGC:7057 MAGE:3456532 mpMAGE:4466532 mpMAGE:4466532 mpMAGE:4466532 mpMAGE:4466532 mpMAGE:4466532 mpMAGE:4466532 mpMAGE:4466532 mpMA
933	_	23950 AI031019	s, t				2410018C20 gene, eukaryotic translation initiation factor 2B, subunit 1 (alpha,
							EST, MODERATELY SIMILAR TO CL36_HUMAN LIM DOMAIN PROTEIN CLP-36
							IH.Sapiens], ESTS, Weakly similar to A55050 enigma [H.sapiens], ESTS, Weakly similar to PDI 1 RAT PDZ and I M domain and it is
							C-terminal LIM domain protein 1) (Elfin) IR.norvegicus]. Homo saniens CDNA:
							FLJ23564 fis, clone LNG10773, Homo sapiens, Similar to enigma homolog (R.
							norvegicus), clone MGC:23807 IMAGE:4271274, mRNA, complete cds, LIM domain
7							2410002/21 gene expressed sertions AV/22856
=	77817	Z192/ Al104117	w, x			ĺ	AW123232, paxillin, transforming growth factor beta 1 included franchist 1
							EST, Moderately similar to CL36_HUMAN LIM DOMAIN PROTEIN CLP-36
							[H.sapiens], ESTs, Weakly similar to PDL1_RAT PDZ and LIM domain protein 1
							(Clim dotting protein CLP-35) (C-terminal LIM domain protein 1) (Elfin)
							Complete cds. PDZ and I M domain 1 (effe.) DDZ and I M 42
746	3700	3780 AE00000	p, u, v, ee,				protein mystique, Rattus norvegicus LIM-domain protein I MP-1 mRNA commete
2	5000		II, KK, II				cds, alpha-actinin-2-associated LIM protein
							EST, Moderately similar to COF1_HUMAN COFILIN. NON-MISCI F ISOFOR
							[H.sapiens], EST, Weakly similar to COF1_HUMAN COFILIN, NON-MUSCLE
		•					ISOFOR [H.sapiens], ESTs, Highly similar to DEST_HUMAN DESTRIN [H.sapiens],
							ESTS, Woderately Similar to COF1_HUMAN COFILIN, NON-MUSCLE ISOFOR
1291	7740 A	7740 A1175011	r, h				[n.sapiens], Homo sapiens cDNA FLJ30934 fis, clone FEBRA2007017, moderately
							Silfilliar to homo sapiens I KAF4-associated factor 2 mRNA

TABLE 3	:3			The state of the s	TO THE PARTY OF TH
SEQ		GenBank Acc.			THE POST IN THE PROPERTY OF THE POST IN TH
₽.	GLGC ID No.	No.	Model Code Human Hom	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2065		23225 NM_019360	O		EST, Moderately similar to COXI_MOUSE Cytochrome c oxidase polypeptide VIC-2 [R.norvegicus], ESTs, Moderately similar to COXH_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR [H.sapiens], cytochrome c oxidase subunit VIc.
					EST, Moderately similar to G02654 ribosomal protein L39 [H.sapiens], EST, Moderately similar to RL39_HUMAN 60S ribosomal protein L39 [R.norvegicus], ESTs, Highly similar to G02654 ribosomal protein L39 [H.sapiens], ESTs,
1812		20'45 NM_012875	cc, dd		Moderately similar to G02654 ribosomal protein L39 [H.sapiens], RIKEN cDNA 2810465016 gene, RIKEN cDNA 3930402110 gene, RIKEN cDNA 4930517K11 gene, ribosomal protein L39, ribosomal protein L39-like
532		23 73 AA925057	h, I, w, x		EST, Moderately similar to G02666 cysteine-rich protein 1 [H.sapiens], cysteine rich intestinal protein, cysteine-rich protein 1 (intestinal), expressed sequence AW743261
					EST, Moderately similar to GR75_HUMAN MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR [H.sapiens], ESTs, Highly similar to 156581 dnak-type molecular chaperone grp75 precursor - rat [R.norvegicus], ESTs, Moderately similar
2608		17w26 S78556	66		to GR73_HOWAN MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR [H.sapiens]. heat shock 70kD protein 98 (mortalin-2). heat shock protein 74 kDs. A
					EST, Moderately similar to 158311 HMG-box containing protein 1 - rat [R.norvegicus], ESTs, Highly similar to 158311 HMG-box containing protein 1 - rat [R.norvegicus], ESTs, Moderately similar to 158311 HMG-box containing protein 1 - rat [R.norvegicus], HMG-box containing protein 1 - rat [R.norvegicus], HMG-box containing protein 1, Mus musculus, Similar to protein
1901	14951	1495 NM_013221	y, z, aa, bb		kinase, Iysine deficient 4, clone IMAGE:4973225, mRNA, partial cds, RIKEN cDNA 1200010B10 gene, RIKEN cDNA 1700058005 gene
2110		22412 NM_022392	p,q		EST, Moderately similar to ISI1_RAT Insulin-induced protein 1 (Insulin-induced growth response protein CL-6) (Immediate-early protein CL-6) (R.norvegicus), RIKEN cDNA 2900053111 gene, insulin induced gene 1, insulin induced protein 2
1127	4402 A	4402 A1103874			EST, Moderately similar to JQ1522 peptidylprolyl isomerase [H.sapiens], ESTs, Moderately similar to 1613455A FK506 binding protein FKBP [H.sapiens], FK506 binding protein 3 (25kD), FK506 binding protein 7, FK506 binding protein 9 (63 kD), FK506 binding protein practices.
					soon primile process of insponsers process I Lacord

TABLE 3	3		No.		
SEQ		GenBank Acc.			Atty. Ref. 4492/1-5090-01-WO/2105485
<u>□</u>	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					DENDENT DOOTEIN V
					TYPE I-ALPHA REGULATORY CHAIN (R.norvegicus), EST, Weakly similar to
					KAP1 MOUSE CAMP-DEPENDENT PROTEIN KINASE TYPE I-BETA
					REGULATORY CHAIN [M.musculus], protein kinase, cAMP dependent regulatory,
1880		1314 NIM 013184			type I beta, protein kinase, cAMP dependent regulatory, type I, alpha, protein
3		101010 MIN			kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
					EST, MODERARIES SIMILAT TO MASZ_HUMAN MANNAN-BINDING LECTIN SERINE
					PROLEASE 2 PRECURSOR [H.sapiens], ESTs, Moderately similar to
					CRAR_HUMAN COMPLEMENT-ACTIVATING COMPONENT OF RA-REACTIVE
					FACTOR PRECURSOR [H.sapiens], Mus musculus, Similar to complement
					component 1, s subcomponent, clone MGC:19094 IMAGE:4196654, mRNA,
					complete cds, Mus musculus, Similar to complement component 1, s
					subcomponent, clone MGC:28492 IMAGE:4166254, mRNA, complete cds,
2562		18857 NIM 430000			complement component 1, r subcomponent, complement component 1, s
2002		100000 ININ	o'c		subcomponent, mannan-binding lectin serine protease 2
					EST, Moderately similar to MDHM_RAT MALATE DEHYDROGENASE,
	-				MITOCHONDRIAL PRECURSOR [R.norvegicus], EST, Weakly similar to DEMSMM
2126	1631	182 NIM 022516	;		malate dehydrogenase [M.musculus], malate dehydrogenase 2, NAD
7717	10701		۵, ر		(mitochondrial), malate dehydrogenase, mitochondrial
	·				EST, Moderately similar to PLSB MOUSE GLYCEROL-3-PHOSPHATE
					ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR [M.musculus]. EST.
					Weakly similar to PLSB_RAT GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.
					MITOCHONDRIAL PRECURSOR (GPAT) [R.norvegicus], ESTs, Weakly similar to
					GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR [M.musculus],
					ESTs, Weakly similar to PLSB MOUSE GLYCEROL-3-PHOSPHATE
1080	20284IN	20284 NM 047274			ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR [M.musculus], KIAA1560
3	110707		86		protein, glycerol-3-phosphate acyltransferase, mitochondrial

IADLES	,		The state of the s	・ 一	
SEO	-	GenBank Acc.	L		485
으	GLGC ID No.	D No.		Model Code Human Homologous Known Gene Name.	1.7
1785		1478 NM_012744	u, o	EST, Moderately similar to PYC_RAT Pyruvate carboxylase, mitochondrial precursor (Pyruvic carboxylase) (PCB) [R.norvegicus], Mus musculus, Similar to Propionyl Coenzyme A carboxylase, alpha polypeptide, clone MGC:11973 IMAGE:3601148, mRNA, complete cds, pyruvate carboxylase, pyruvate	7
				EST, Moderately Similar to RBM8_HUMAN PUTATIVE KNA-BINDING PROTEIN B   [H.sapiens], ESTs, Moderately similar to NUCLEOLIN [M.musculus], ESTs,   Moderately similar to RBM8_HUMAN PUTATIVE RNA-BINDING PROTEIN 8   H.sanians] ESTs, Modely similar to NILON 11 MAN AND COLOUR SINDING PROTEIN 8	<b>x</b>
				Homo sapiens, done MGC:22221 IMAGE:4687764, mRNA, complete cds, Mus musculus, Similar to fusion, derived from t(12;16) malignant liposarcoma, clone MGC:153860, mRNA, complete cds Mus MGC:18917 IMAGE:3153860, mRNA, complete cds Nucleolin RNA binding matter	
1193	1	18206 AI145282	a, jj, kk	protein 8A, TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68 kDa, eukaryotic translation initiation factor 3, subunit 4 (delta, 44 kDa),	- 70
				ES1, Moderately similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17 [H.sapiens], EST, Weakly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17 [R.norvegicus], EST, Weakly similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17 [H.sapiens], ESTs, Highly similar to R5HU22 ribosomal protein L17, cytosolic	7
1852		17174 NM_013030	E,	Incaplers, Ed. 8, rights similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17 [R.norvegicus], ESTs, Weakly similar to R5HU22 ribosomal protein L17, cytosolic [H.sapiens], Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600029015:hexokinase 1, full insert sequence, ribosomal protein L17	73
				EST, Moderately similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17 [H.sapiens], EST, Weakly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17 [R.norvegicus], EST, Weakly similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17 [H.sapiens], ESTs, Highly similar to R5HU22 ribosomal protein L17, cytosolic [H.sapiens], ESTs, Highly similar to R5HU22 ribosomal protein L17, cytosolic [H.sapiens], ESTs, Highly similar to R17 RAT 60S RIBOSOMAL PROTEIN L17	
2662	171*6 X60212	×60212	<b></b>	[R.norvegicus], ESTs, Weakly similar to R5HU22 ribosomal protein L17, cytosolic [H.sapiens], Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600029O15:hexokinase 1, full insert sequence, ribosomal protein L17	

TABIL			1 00		
<u> </u>	. 0	GenBank Acc.	. •	The second secon	Atty. Ref. 4492;;5090-01-WO/2105485
1	GLGC ID No.	No.	Model Code	Model Code Human He mologous Known Gene Name	ince Cluster Title.
				EST, Moderately similar to F	EST, Moderately similar to RL35_HUMAN 60S RIBOSOMAL PROTEIN L3
				[H.Sapiens], EST, Moderate	H.Sapiens], EST, Moderately similar to RL35_RAT 60S RIBOSOMAL PROTEIN
46	Ť	17212 AA799571	_=	L35 [R.norvegicus], Homo s	L35 [R.norvegicus], Homo sapiens, clone IMAGE:4183312, mRNA, partial cds,
				Indosomal protein L35	OF HIMAN SOC BIRDS
				I'M Sanjana' EST Madanata	EST, Would ately Similar to RL35_HUMAN 60S RIBOSOMAL PROTEIN L3
				insapiens, moderate	in Septembly, EST, Woderately Similar to RL35_RAT 60S RIBOSOMAL PROTEIN
1716		17211 M34331		L35 [K.norvegicus], Homo s;	L35 [K.norvegicus], Homo sapiens, clone IMAGE:4183312, mRNA, partial cds,
				indosomal protein L35	
				ES1, Moderately similar to R	ES I, Moderately similar to RL35_HUMAN 60S RIBOSOMAL PROTEIN L3
				[H.sapiens], EST, Moderatel	[H.sapiens], EST, Moderately similar to RL35_RAT 60S RIBOSOMAL PROTEIN
1716	26030 M3/334	1434334		L35 [R.norvegicus], Homo sa	L35 [R.norvegicus], Homo sapiens, clone IMAGE:4183312, mRNA, partial cds.
	70000	W04001	5	ribosomal protein L35	
				EST, Moderately similar to R	EST, Moderately similar to RS12_HUMAN 40S RIBOSOMAL PROTEIN S1
				H.sapiens], ESTs, Moderate	[H.sapiens], ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic
2318	16918	16918 NIM 031700	2	[H.sapiens], ESTs, Moderate	[H.sapiens], ESTs, Moderately similar to RS12 MOUSE 40S RIBOSOMAL
2	202	100 11 00 IV	X 'M '1 'B	PROTEIN S12 [M.musculus], ribosomal protein S12	ribosomal protein S12
	<del>-</del> -				
				EST, Moderately Similar to R.	E.S.I., INCUREIALERY SIMILIAR TO RISZ MOUSE 40S RIBOSOMAL PROTEIN S2
		-		[M.musculus], EST, Weakly s	[M.musculus], EST, Weakly similar to ribosomal protein S2; 40S ribosomal protein
				SZ [Homo sapiens] [H.sapien	S2 [Homo sapiens] [H.sapiens], EST, Weakly similar to RS2_HUMAN 40S
				RIBOSOMAL PROTEIN S2 [I	RIBOSOMAL PROTEIN S2 [H.sapiens], EST, Weakly similar to RS2_RAT 40S
				RIBOSOMAL PROTEIN S2 [F	RIBOSOMAL PROTEIN S2 [R.norvegicus], ESTs, Highly similar to ribosomal
				protein S2; 40S ribosomal pro	protein S2; 40S ribosomal protein S2 [Homo sapiens] [H.sapiens], ESTs, Highly
2338	10269 N	10269 NM 031838	, A	similar to ribosomal protein S	similar to ribosomal protein S2; repeat family 3 gene [Mus musculus] [M.musculus],
			11, 1, 17, 1	Homo sapiens, clone IMAGE:	Homo sapiens, clone IMAGE:4816496, mRNA, partial cds. ribosomal protein S2
2244	19162 NI	19162 NM 031111		EST, Moderately similar to RS	EST, Moderately similar to RS21_RAT 40S RIBOSOMAL PROTEIN S21
	70.0	7	11, 1	[R.norvegicus], ribosomal protein S21	lein S21

TABLE 3	က	:: ::.		The second section is a second section of the second section of the second section is a second section of the second section of the second section sec	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code Human Hom	iologous Known Gene Name	01-WO/2105485
788		10820 A1009411	_ 		R.norvegicus], orvegicus], orvegicus], ein S ein S PROTEIN S3
1555	11644	11644 AI235282	0, 0	inositol 1-phosphate synthase A1, ribosomal protein S3 EST, Moderately similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus], ESTs, Highly similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus], ESTs, Weakly similar to S25111 alpha-2- macroglobulin receptor precursor - mouse [M.musculus], low density lipoprotein receptor-related protein 1, low density lipoprotein-related protein 1 (alpha-2- macroglobulin receptor)	recursor - globulin 25111 alpha-2- lipoprotein pha-2-
383	13647.	13647 AA892367	w, x, cc, dd	EST, Moderately similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], EST, Weakly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs, Highly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs, Moderately similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus], ESTs, Weakly similar to RL3_MOUSE 60S RIBOSOMAL PROTEIN L3 [M.musculus], RIKEN cDNA 1110057H16 gene, ribosomal protein L3, ribosomal protein L3-like	sapiens], EST, ESTs, Highly foderately is], ESTs, isculus], ein L3-like
2667	13646)	3646 X62166	n, o, w, x, kk,	EST, Moderately similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], EST, Weakly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs, Highly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs, Moderately similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus], ESTs, Weakly similar to RL3 MOUSE 60S RIBOSOMAL PROTEIN L3 [M.musculus], RIKEN cDNA 1110057H16 gene, ribosomal protein L3, ribosomal protein L3, 2 libosomal L3, 2 libosomal protein L3, 2 libosomal protein L3, 2 libosomal p	sapiens], EST, ESTs, Highly oderately s], ESTs, sculus],
520	18251	18251 AA924548	jj, kk	EST, Moderately similar to S65792 ribosomal protein L9, robosomal protein L9, robosomal protein L9, robosomal protein L9, robosomal, EST, Weakly similar to R19_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L9 [M.musculus], RIKEN cDNA 4930401811 gene, ribosomal protein L9	apiensj, EST, icusj, ESTs, V cDNA

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عد ري		GenBank Acc		(語) ないない	-01-WO/210548F
	8	No.	Model Code		
<b>■</b> ₽*					, ESTs. Highly
				similar to SMHU1B metallothionein 1B [H.sapiens], H.sapiens mRNA for	A for
				metallothionein isoform 1R, Homo sapiens metallothionein 1H-like protein mRNA,	rotein mRNA,
				COmplete cds, Homo sapiens unknown mRNA, Homo sapiens, Similar to RNA	lar to RNA
				helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds,	complete cds,
1082	15192	15192 AI101099	٠.	Mus musculus, metallothionein 2A, clone MGC:30400 IMAGE:4501155, mRNA,	155, mRNA,
$\vdash$				Complete cds, metallothionein 1H, metallothionein 1X, metallothi	in 2
				ES1, Woderately Similar to SMHU1E metallothionein 1E [H.sapiens], ESTS, Highly	, ESTS, Highly
<u>-</u>				Similar to SMHU1B metallothionein 1B [H.sapiens], H.sapiens mRNA for	A for
				metallothionein isoform 1R, Homo sapiens metallothionein 1H-like protein mRNA,	rotein mRNA.
_				complete cds, Homo sapiens unknown mRNA, Homo sapiens, Similar to RNA	ar to RNA
				helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds.	complete cds.
1330	15191	15191 A1176456	11, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	Mus musculus, metallothionein 24, clone MGC:30400 IMAGE:4501155, mRNA.	55, mRNA.
-			1, 00, 11, MA	complete cds, metallothionein 1H, metallothionein 1X, metallothionein 2	12
				Edt, Weakly Sililiar to Camiumeracyicamiume uansiocase, minoc	апагсаппипе-
				acylcamitne translocase gene [Mus musculus] [M.musculus], ESTs, Weakly similar	Weakly similar
_	···			to solute carrier family 25 (carritine/acylcarritine translocase), member 20 [Rattus	ber 20 [Rattus
	•			norvegicus] [R.norvegicus], ESTs, Weakly similar to MCAT_HUMAN	
		-	· .	MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN IH.sapiens],	IN [H.sapiens],
				Homo sapiens, similar to solute carrier family 25 (carnitine/acylcarnitine	ie .
				translocase), member 20, clone MGC:35539 IMAGE:5200129, mRNA, complete	A, complete
				cds, Mus musculus, Similar to CG4995 gene product, clone MGC:7958	. 85
		-		IMAGE:3584570, mRNA, complete cds, expressed sequence AW491445,	445,
	•	-		expressed sequence W51672, ornithine transporter 2, solute carrier family 25	amily 25
				(carnitine/acylcarnitine translocase), member 20, solute carrier family 25	25
-				(mitochondrial carnitine/acylcarnitine translocase), member 20, solute carrier family	carrier family
2456	16546 N	16546 NM 053965 h	4	25 (mitochondrial carrier; adenine nucleotide translocator), member 3, solute carrier	solute carrier
	2	7		family 25 (mitochondrial carrier, ornithine transporter) member 15	

Human, Homologous Sequence Clust  Est, Weakly similar to Camminetary acylcamitine translocase gene [Mus to solute carrier family 25 (camtinue) acylcamitine translocase gene [Mus to solute carrier family 25 (camtinue) norvegicus] [R. norvegicus], ESTs, We MITOCHONDRIAL CARNITINEACYI Homo sapiens, similar to solute carrier family 25 (camtinue) acylcassed, member 20, clone MGC cds, Mus musculus, Similar to solute carrier translocase), in (mitochondrial carrier) adenine nuc family 25 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuc family 26 (mitochondrial carrier) adenine nuckarrier) adenine nuckarriery adenine dependent kinase 6  EST, Weakly similar to histone HZA-FZ WEST, Weakly similar to histone HZA-FZ WEST, Neckly similar to histone HZA-FZ WEST, Neckly similar to histone nuckarriery adenine convenional (Mitopheriery) associanovegicus) [Romosegicus], Romos	ITABLE	ç			( ) 在新州县 ( ) 《清水	
GLGC ID   No:   Model Code   Plumain Homologous Known Gene Native   Humain Homologous Sequence Clyst	SEO		IGenBank Acc		「から、1 できない。 これでは、1 できないできない。 これでは、1 できないできない。 これでは、1 できないできない。 これでは、1 できないできない。 これできないできないできない。 これできないできないできない。 これできないできないできない。 これできないできないできない。 これできないできないできないできないできないできないできないできないでき	Control of the Contro
16: 47 NM_053965 hh 20:902 NM_053593 r 16:42 AA395270 e 16:42 AA798520 e 1	<u>_</u>	GLGC ID	No.		Oppolie Known Gene Name	
166 47 NM 0536965 hh 663965 hh 663920 NM 053593 r 6642 AA892470 e 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6					oggads Miowil Gelie Naille	rluman rlomotogous Sequence Cluster Title
16: 47/NM_053965 hh						EST, Weakly Sittlifa to Carminieracylcarmine bansiocase, milochoriorial carminie-
3 16: 47 NM 053965 hh						acylcamitine translocase gene [Mus musculus] [M.musculus], ESTs, Weakly similar
3 16: 17 INM_053965 hh						to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 [Rattus
3 16: 47 NM 053965 hh					<u>u</u>	norvegicus] [R.norvegicus], ESTs, Weakly similar to MCAT_HUMAN
166 47 NM_053965 hh 20902 NM_053593 r 9254 AA892470 e 16942 AA799520 e 16942 AA799520 e 16942 AA799520 p 16942 AA799520 p						MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN [H.sapiens],
5 16£ 47 NM_053965 hh 20902 NM_053593 r 9254 AA892470 e 16942 AA799520 e			_		<u> </u>	Homo sapiens, similar to solute carrier family 25 (carnitine/acylcarnitine
5 16£ 47 NM_053965 hh 20902 NM_053593 г 9254 AA892470 е 16942 AA799520 е					-	translocase), member 20, clone MGC:35539 IMAGE:5200129, mRNA, complete
5 168 47 NM_053965 hh 20902 NM_053593 r 9254 AA892470 e 16942 AA799520 e					0	ds, Mus musculus, Similar to CG4995 gene product, clone MGC:7958
5 16: 47 NM_053965 hh 5 20902 NM_053593 r 6 9254 AA892470 e 7 16942 AA799520 e 904 NM_019620 p						MAGE:3584570, mRNA, complete cds, expressed sequence AW491445.
3 16: 47 NM_053965 hh 20902 NM_053593 г 9254 AA892470 е 16942 AA799520 е					<u>a</u>	expressed sequence W51672, ornithine transporter 2, solute carrier family 25
5 16£ 47 NM_053965 hh 20902 NM_053593 r 9254 AA892470 e 16942 AA799520 e					<u>)</u>	(camitine/acylcamitine translocase), member 20, solute carrier family 25
5 16 <sup>8</sup> 47 NM_053965 hh  20902 NM_053593 r  9254 AA892470 e  16942 AA799520 e			•		<u></u>	(mitochondrial carnitine/acylcamitine translocase), member 20, solute carrier family
20902 NM_053593	2/56				Ö	25 (mitochondrial carrier; adenine nucleotide translocator), member 3, solute carrier
9254 AA892470 e 16942 AA799520 e	2100			E	fa fa	imily 25 (mitochondrial carrier, ornithine transporter) member 15
9254 AA892470 e 16942 AA799520 e 904 NM_019620 p					<u> </u>	EST, Weakly similar to cyclin-dependent kinase 4 [Rattus norvegicus]
9254 AA892470 e 16942 AA799520 e					<u>u</u> .	[R.norvegicus], ESTs, Moderately similar to cyclin-dependent kinase 4 [Rattus
20902 NM_053593					<u>ਪ</u> ੂ	norvegicus] [R.norvegicus], ESTs, Moderately similar to CDK4 MOUSE CELL
9254 AA892470 e 16942 AA799520 e	2405	20902 N	VM 053593			IVISION PROTEIN KINASE 4 [M.musculus], cyclin-dependent kinase 4, cyclin-
9254 AA892470 e 16942 AA799520 e 904 NM_019620 p		4			de de	spendent kinase 6
9254 AA892470 e 16942 AA799520 e 904 NM_019620 p					<u>ű</u>	EST, Weakly similar to histone H2A.F/Z variant [Homo sapiens] [H.sapiens], ESTs,
9254 AA892470 e 16942 AA799520 e 904 NM_019620 p					<u> </u>	Weakly similar to H2AZ_HUMAN HISTONE H2A [H.sapiens], H2A histone family,
16942 AA799520 e e 904 NM_019620 p	390	9254			Ē	ember Z, Homo sapiens cDNA FLJ32241 fis, clone PLACE6005231, RIKEN cDNA
16942 AA799520 e 904 NM_019620 p	3	7		<b>D</b>	<u>ಪ</u>	530002L11 gene, histone H2A.F/Z variant
904 NM_019620   p	30	16942			<u>ш</u>	EST, Weakly similar to integral membrane protein 2B [Homo sapiens] [H.sapiens],
904 NM_019620 p	3	72.001		ם		egral membrane protein 2B
904 NM_019620 p	•				<u>ш</u>	51, Weakly similar to Kruppel associated box (KRAB) zinc finger 1 [Rattus
904 NM_019620 p	•				00	norvegicus] [R.norvegicus], EST, Weakly similar to ZINC FINGER PROTEIN 91
904 NM_019620 p	_				<u>E.</u>	.sapiens], ESTs, Moderately similar to DNA-binding protein; zinc finger protein
904 NM_019620 p				-	725	3 [Homo sapiens] [H.sapiens], ESTs, Moderately similar to ZINC FINGER
904 NM_019620 p				-	T.	ROTEIN 91 [H.sapiens], Mus musculus, Similar to RIKEN cDNA 2610036F08
904 NM_019620 p					19.6°	ne, clone MGC:28645 IMAGE:4224834, mRNA, complete cds, expressed
	2072	90.74 NI			Sec	sequence AI790734, expressed sequence AU021768, zinc finger protein 386
			1		(Kr	uppel-like), zinc finger protein 91 (HPF7, HTF10)

TABL	F 3		The Ast of the State of the	
SEO		I Gen Bank Acc		Ath@Ref. 44921-5090-01-1WO/2408-01-2
Q	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name Himan Homologous Serries Chiefer Tills
2645		20810 X14181	f, g, w, x	
CHC				EST, Weakly similar to SC65 synaptonemal complex protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to SC65 synaptonemal complex protein [Rattus norvegicus] [R.norvegicus], SC65 synaptonemal complex protein associated protein, growth suppressor 1, nucleolar autoantinan (55kn) similar to part
47		18209/AA691769 6917/AA019709	ی د	Synaptonemal complex protein  EST, Weakly similar to splicing factor 3b, subunit 1, 155 kDa [Mus musculus]  [M.musculus], ESTs, Weakly similar to S3B1_HUMAN Splicing factor 3B subunit 1  (Spliceosome associated protein 155) (SAP 155) (SF3b155) (Pre-mRNA splicing factor SF3b 155 kDa subunit 1, 155 kDa.
				Splicing factor 3b, subunit 1, 155kD  EST, Weakly similar to transforming growth factor-beta (TGF-beta) masking protein large subunit [Rattus norvegicus] [R.norvegicus], ESTs, Highly similar to FIBRILLIN 2 PRECURSOR [M.musculus], ESTs, Weakly similar to A57293 latent transforming
1368	_	22691 A1177967	r, aa, bb	growth factor beta-binding protein 3 precursor - mouse [M.musculus], RIKEN cDNA 2310046A13 gene, latent transforming growth factor beta binding protein 1,
2487	181221	18122 NM_057208	l, i	EST, Weakly similar to tropomyosin 3, gamma [Rattus norvegicus] [R.norvegicus], ESTs, Highly similar to TPMN_HUMAN TROPOMYOSIN, CYTOSKELETAL TYPE [H.sapiens], ESTs, Moderately similar to TROPOMYOSIN 5, CYTOSKELETAL TYPE
2458	15135	15135 NM_053971	h, l, n, o, w, x	EST, Weakly similar to 60S RIBOSOMAL PROTEIN L6 [M.musculus], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L6 [M.musculus], ribosomal protein 1.6
2458	15136 N	15136 NM_053971	h, I, w, ii	EST, Weakly similar to 60S RIBOSOMAL PROTEIN L6 [M.musculus], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L6 [M.musculus], ribosomal protein L6
200	22026 A	22026 AA850060	oʻu	EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746, RIKEN cDNA 3830414F09 gene

SEO Θ		GenBank Acc.	:		Atty. Ref. 44921-5090-01-WO/2105485
	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	
200	22028	22028 AA850060	99 99	EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fs, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA	mo sapiens cDNA FLJ10784 ns mRNA; cDNA
278	16029	16029 AA874803	<u> </u>	EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA	mo sapiens cDNA FLJ10784 ns mRNA; cDNA
278	16030 4	16030 AA874803	,	EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA FLJ10784 DIXEN 202044150	mo sapiens cDNA FLJ10784 ns mRNA; cDNA
ည	22030 A	22030 AI011177	h, I	EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKF766690748, RIKEN CDNA 3930414500 2000	no sapiens cDNA FLJ10784 ns mRNA; cDNA
				EST, Weakly similar to AZZ940 Keratin, 67K type II cytoskeletal [H.sapiens], EST, Weakly similar to FORMIN 4 [M.musculus], ESTs, Weakly similar to FMN2_MOUSE Formin 2 [M.musculus], ESTs, Weakly similar to FORMIN 4 [M.musculus], ESTs, Weakly similar to FORMIN 4 [M.musculus], ESTs, Weakly similar to LORI MOUSE LORICRIN [M.musculus], RIKEN cDNA	ikeletal [H.sapiens], EST, ly similar to FMN2_MOUSE N 4 [M.musculus], ESTs,
2591	1760 N	1760 NM_147211	d, kk	A330103N21 gene, expressed sequence AI854843, expressed sequence AW742646, formin 2, hypothetical protein BC012775, hypothetical protein FLJ20584, similar to Wiskott-Aldrich syndrome protein interacting protein, uridine-	ressed sequence pothetical protein teracting protein, uridine-
2215	1540 NI	1540 NM_031012	c	EST, Weakly similar to A32852 membrane alanyl aminopeptidase (EC 3.4.11.2) - rat [R.norvegicus], ESTs, Weakly similar to AMPN MOUSE AMINOPEPTIDASE N [M.musculus], RIKEN cDNA 2010111101 gene, RIKEN cDNA 4833403115 gene, alanyl (membrane) aminopeptidase	Peptidase (EC 3.4.11.2) - SE AMINOPEPTIDASE N NA 4833403115 gene, aminopeptidase
1863	1529 NA	1529 NM_013082	hh	EST, Weakly similar to A33880 syndecan 2 [H.sapiens], Mus musculus, clone   IMAGE:4983756, mRNA, partial cds, syndecan 2, syndecan 2 (heparan sulfate	opeptidase, CD13, p150)  Aus musculus, clone an 2 (heparan sulfate
646	175:40 AA955914	1955914	ø	EST, Weakly similar to A38712 fibrillarin [H.sapiens], EST, Weakly similar to FBRL MOUSE FIBRILLARIN [M.musculus], ESTs, Moderately similar to FIBRILLARIN [M.musculus], ESTs, Moderately similar to FIBRILLARIN [M.musculus], ESTs, Moderately similar to FIBRILLARIN	, Weakly similar to FBRL imilar to FIBRILLARIN
1248 2	224 32 A1171263		a, z	EST, Weakly similar to A38712 fibrillarin [H.sapiens], ESTs, Moderately similar to FIBRILLARIN [M.musculus], fibrillarin	s, Moderately similar to

TABL	~		*.	ķ.
2		GenBank Acc.		Attv. Ref. 44921-5090-01-WOI2105-488
21	GLGC II	GLGC ID No.	Model Code Human Ht n	Glogous Known Gene Name. Human Homologous Semience Christer Titl
			,	EST, Weakly similar to A45377 transcription factor ATF4 [H.sapiens], ESTs, Highly similar to A45377 transcription factor ATF4 II septens], and incline to A45377 transcription factor ATF4 II septens], and incline to A45377 transcription factor ATF4 II septens].
2197	- 1	13633 NM_024403	e, p, q, y, z	factor 4, activating transcription factor 4 (tax-responsive enhancer element B67),
				EST, Weakly similar to A45377 transcription factor ATF4 (H caniene) ESTs. Lichtiv
			. i.	similar to A45377 transcription factor ATF4 [H.sapiens], activating transcription
2197		13634 NM_024403	γ, γ τ'' τ' τ' γ'	factor 4, activating transcription factor 4 (tax-responsive enhancer element B67),
				activating transcription factor 5
0,01				Highly similar to A48045 ribosomal protein SZ/, cytosolic [H.sapiens], ESTs,
740/		2103 NM_053597	g	Drofein S77 (metallonanefimulin 1) ribosomi (H.sapiens), ribosomal
				EST, Weakly similar to AACT HUMAN ALPHA-1-ANTICHYMOTRYPSIN
2278	3202	3292 NM 031531	د.	PRECURSOR [H.sapiens], RIKEN cDNA 4833409F13 oene, serine protease
	70.70	TOO TOO TAIN	a, J, K	inhibitor 2-2
				EST, Weakly similar to AACT_HUMAN ALPHA-1-ANTICHYMOTRYPSIN
				PRECURSOR [H.sapiens], serine (or cysteine) proteinase inhibitor. clade F (alpha-2)
1719	17145	17145 M38566	56	antiplasmin, pigment epithelium derived factor), member 2, serine protease inhibitor
				EST. Weakly similar to AACT HI MAAN AI BUA 1 ANTICHIYAACTEVED
				PRECIPEOR IN control of control o
2689	17446	17446 V07534		antiplasmin, pigment epithelium derived factor), member 2 serine anxioses inhibitation
			25	2-2
				EST, Weakly similar to B36298 proline-non protein PRB3S [H.Sapiens], EST,
				weakly similar to CGHU3B collagen alpha 3(IV) chain precursor, long splice form
				In Saplens), EST, Weakly similar to D40750 proline-rich protein PRB1/2S
				In Saprens, EST, Weakly Similar to PIHUB6 salivary proline-rich protein precursor
			-	PRB1 [H.sapiens], EST, Weakly similar to PRP1_HUMAN SALIVARY PROLINE-
				AND FIGURE OF THE CURSOR [H.sapiens], Mus musculus adult male tongue
				CDINA, KIKEN tull-length enriched library, clone:2310039K21:SRY-box containing
				gene 7, full insert sequence, SRY (sex determining region Y)-box 17, SRY (sex
932	22614 A	22614 AI031004 t	-	determining region Y)-box 18, SRY (sex determining region Y)-box 7, SRY-box
				Containing gene 17

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SEO.		GenBank Acc.	L		Atty, Ref. 44921-5090-01-WO/210548F
₽	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	
				ES1, Weakly similar to B47222 uniquitin—protein ligase IH.sabiensi. ES1s. Hinhiv	ansi ests Highly
				similar to ubiquitin conjugating enzyme [Rattus norvegious] [R.norvegious], ESTs.	norvegicus), ESTs.
				Highly similar to A41222 ubiquitinprotein ligase [H.sapiens], ESTs, Moderately	STs, Moderately
				Similar to B41222 ubiquitinprotein ligase [H.sapiens], ESTs, Weakly similar to	eakly similar to
				UBCZ_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus],	D [M.musculus],
				RIKEN cDNA 2610301N02 gene, expressed sequence Al327276, ubiquitin-	6, ubiquitin-
				conjugating enzyme E2A (RAD6 homolog), ubiquitin-conjugating enzyme E2A.	enzyme E2A.
				RAD6 homolog (S. cerevisiae), ubiquitin-conjugating enzyme E28 (RAD6 homolog)	B (RAD6 homolog)
72	Ī	17380 AA799612	> 2	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae). ubiquitin-	ae). ubjavitin-
		71000 110	w, ^	conjugating enzyme E2C	
				EST, Weakly Similar to B41ZZZ ubiquitnprotein ligase [H.sapiens], ESTS, Highly	nsi, ESTS, Highly
				similar to ubiquitin conjugating enzyme [Rattus norvegicus] [R.norvegicus]. ESTs.	orvegicus! ESTs
				Highly similar to A41222 ubiquitinprotein ligase [H.sapiens], ESTs, Moderately	Ts, Moderately
				similar to B41222 ubiquitin-protein ligase [H.sapiens], ESTs, Weakly similar to	akly similar to
				UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus].	[M.musculus].
				RIKEN cDNA 2610301N02 gene, expressed sequence Al327276, ubiquitin-	, ubiquitin-
_				conjugating enzyme E2A (RAD6 homolog), ubiquitin-conjugating enzyme E2A.	enzyme E2A.
	•			RAD6 homolog (S. cerevisiae), ubiquitin-conjugating enzyme E2B (RAD6 homolog).	3 (RAD6 homolog).
2258	173.79IN	173-79 NM 031138	r. w. x	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae), ubiquitin-	e), ubiquitin-
				conjugating enzyme E2C	•
			-	Lou, Weakly Similar to B41222 ubiquitinprotein ligase [H.sap	isj, ESTS, Highly
				Similar to A41222 ubiquitinprotein ligase [H.sapiens], ESTs, Weakly similar to	akly similar to
		-		UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus].	[M.musculus],
<u></u>				RIKEN cDNA 2610301N02 gene, expressed sequence Al327276, ubiquitin	, ubiquitin
				Conjugating enzyme, ubiquitin-conjugating enzyme E2A (RAD6 homolog), ubiquitin-	molog), ubiquitin-
				conjugating enzyme E2A, RAD6 homolog (S. cerevisiae), ubiquitin-conjugating	n-conjugating
648	23357 A	23357 AA956114	oc. dd	enzyme E2B (RAD6 homolog), ubiquitin-conjugating enzyme E2B, RAD6 homology	, RAD6 homology
		1	25 (25	(S. cerevisiae), ubiquitin-conjugating enzyme E2C	6

TABL	TABI F ?		٠ •	The state of the s
035	1 .1	GenBank Acc.	<b>_</b>	Atty. Ref. 44921,5090-01-WO/2105485
2	GLGC DINS.	N.	Model Co.	Model Code Human Ho nologous Known Gene Name Human Homologous Sequence Cluster Title
				EST, Weakly similar to beta-fibrinogen precursor [H.saplens], ESTS, Moderate similar to ANL2_MOUSE Angiopoietin-related protein 2 precursor (Angiopoieti 2) [M.musculus].
				MGC:32467 IMAGE:5049765, mRNA, complete cds, Mus musculus, Similar to fibrinogen-like 1, clone MGC:37822 IMAGE:5008806, mDNA
000		COLOR		norvegicus Sprague-Dawley fibrinogen B beta chain mRNA, complete cds, Rattus andiopoietin-like 2 andiomoietin-related protein 6
3		4230 AIU 13300	₩.	hypothetical protein FLJ11286
707				EST, Weakly similar to CATM_HUMAN CATHEPSIN L2 PRECURSOR (CATHEPSIN U) (H.sapiens), EST, Weakly similar to TES1_RAT TESTIN 1/2 PRECURSOR (CMB-22/CMB-23) (R.norvegicus), RIKEN cDNA 49304861 24 rene. Patrice noncessions facili.
2		22434 AIZ30591	=	lymphocyte-associated protein 2 alpha
				EST, Weakly similar to CBP MOUSE CREB-BINDING PROTEIN [M.musculus], ESTs, Highly similar to BRD4_HUMAN BROMODOMAIN-CONTAINING PROTEIN 4 (HUNK1 PROTEIN) [H.sapiens], ESTs, Highly similar to CBP MOUSE CREB-BINDING PROTEIN IM misculus], ESTs, Madagastics
983	2662 A	2662 AI045686	e e	BINDING PROTEIN [M.musculus], ESTs, Weakly similar to CBP MOUSE CREB-
791	9746 AI	9746 A1009555	<u> </u>	EST, Weakly similar to DYJ2_HUMAN DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC [H.sapiens], LIC-2 dynein light intermediate chain 53/55, RIKEN cDNA 1110053F02 gene, dynein light chain-A, dynein, cytoplasmic, light intermediate polypeptide 2, expressed sequence AA409702
				EST, Weakly similar to DYJ2_HUMAN DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC [H.sapiens], RIKEN cDNA 1110053F02 gene, Rattus norvegicus
2219	16210 NI	16210 NM_031026	m,'	dynein light intermediate chain 1 mRNA, complete cds, dynein light chain-A, dynein, cytoplasmic, light intermediate polypeptide 2, expressed seminary AAAnozno
2341	17734 NN	17734 NM_031970	a, o, q, ee, ff, kk	EST, Weakly similar to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Highly similar to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Moderately similar to HHHU27 heat shock protein 27 [H.sapiens], FSTs, Moderately similar to HHHU27 heat shock protein 27 [H.sapiens], heat shock 27kD protein 1, hypothetical
				profein McC1U9/4

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у С		GenBank Acc.			Atty. Ref. 44921-5090-01-WO/2105485
⊋	GLGC:ID No.	No.	Model Code Human Hom	ologous Known Gene Name	Human Homologous Seguence Cluster Title
				EST, W	EST, Weakly similar to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Highly
2244		2000	a, z, ee, ff,	SIMILAT CHHHI	Similar to HHHU2/ heat shock protein 27 [H.sapiens], ESTs, Moderately similar to HHHU27 heat shock protein 27 th socials to the control heat shock protein 27 th socials to the control heat shock protein 27 th socials to the control heat shock protein 27 th socials to the control heat shock protein 27 th socials to the control heat shock protein 27 th socials to the control heat shock protein 27 th socials to the control heat shock protein 27 th social heat shock protein 27
404		17.35 NIM_031970	축	protein	protein MGC10974
				EST, W	EST, Weakly similar to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Highly
			a, I, o, q, ee,	Similar (	Similar to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Moderately similar to
2341		17736 NM_031970	ff, 矢	Drindo Protein	nnnuz/ neat snock protein 27 [H.sapiens], heat shock 27kD protein 1, hypothetical protein MGC10974
2433		156 I5 NM 053800		EST, W	EST, Weakly similar to Human Thioredoxin [H.sapiens]. RIKEN CDNA 4930429 124
				gene, th	gene, thioredoxin, thioredoxin 1
				EST, We	EST, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II IM. musculus I FSTs
				Moderat	Moderately similar to HXK3_HUMAN HEXOKINASE TYPE III [H.sapiens] FSTs
2093		171 JO NM_022179	h, I, w. x. dd	Weakly	Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], hexokinase
				Z, hexok	2, hexokinase 3 (white cell)
				מוניים ו	denty similar to 139159 GTP-binding regulatory protein gamma-11 chain
				llusaple.	In Saplens, ES is, Moderately similar to GBGB_HUMAN Guanine nucleotide-
-				d Bulbula	binding protein G(J)/G(S)/G(O) gamma-11 subunit [R.norvegicus], ESTs, Weakly
				Similar to	Similar to GBGB_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O)
•		-		gamma-1	gamma-11 subunit [R.norvegicus], RIKEN cDNA 0610037B21 gene, guanine
-		-	<del></del> -	nceotid	nucleotide binding protein (G protein), gamma 1 subunit, guanine nucleotide binding
				protein (C	protein (G protein), gamma transducing activity polypeptide 1, guanine nucleotide
2114	23705N	23705 NM_022396	e. i. k. ii	d bulpula	binding protein (G protein), gamma transducing activity polypeptide 2, guanine
				nucleotid	nucleotide binding protein 11
			-	ייייייין יייייין יייייין יייייין יייייין יייייי	akly similar to 149636 DNA-binding protein - mouse [M.musculus], ESTs,
		<del></del>		Singing Singin Singing Singing Singing Singing Singing Singing Singing Singing	riginy similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs,
				Weakly Si	Weakly Similar to OZF MOUSE ZINC FINGER PROTEIN OZF [M.musculus], ESTs,
			-	Weakly SI	weakly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], Mus
				THEOREM	musculus, clone MGC:37070 IMAGE:4951074, mRNA, complete cds, RIKEN cDNA
2013	20232 NI	20232 NM_017364 u	u, v	962001.97	2810039B14 gene, RIKEN cDNA 2810054M15 gene, zinc finger protein 146, zinc
		1		linger prot	Inger protein 260, zinc finger protein 63

ABLE 3				The state of the s
SEG		GenBank Acc	L	THE STATE OF THE S
	GLGC ID No.	No.		J. IO soucing
				FACTOR 6 [H. sapiens], ESTs, Highly similar to IF6_HUMAN EUKARYOTIC
	-			I KANSLATION INITIATION FACTOR 6 [H.sapiens], Mus musculus 10 days
				neonate cerebellum cDNA, RIKEN full-length enriched library,
1573	22212,	22212 AI236294	茶	clone:6530402L05:integrin beta 4 binding protein, full insert sequence, integrin beta
				FST Moskly eimilier to 18,000 111,000 111,000 111
	i			Homo capione and El 1907 F. 19
<u> </u>	/414/	7414 AI137586	а	importin 4
				EST, Weakly similar to JC1241 beta-interferon-inclined protein and 10 monaging.
. >				ESTs, Moderately similar to JC1241 beta-interferon-induced protein - rat
				[R.norvegicus], Mus musculus, clone MGC;31632 IMAGE:4511454 mRNA
1591	11208	11208 41237586	3	complete cds, RIKEN cDNA 1110036C17 gene, interferon induced transmembrane
		200 1001	W.	protein 2 (1-8D)
				ES1, Weakly similar to JC2324 LIM protein [H.sapiens], ES1s, Weakly similar to
		_		Jacoba Lim protein, FHL4 - mouse [M.musculus], Homo sapiens cDNA FLJ13238
				IIIs, clone OVARC1000440, Homo sapiens cDNA FLJ31627 fis, clone
				IN 12RIZUU3338, RIKEN CDNA 2410002J21 gene, activator of cAMP-responsive
				element modulator (CREM) in testis, expressed sequence AI481106, expressed
				sequence AVZ78559, expressed sequence AW123232, hypothetical protein
288	19480 A	19480 AA94442	r, bb	FLJ10044, paxillin, testis derived transcript (3 LIM domains), transforming growth
	-			lactor beta 1 induced transcript 1
	-			ES1, Weakly Similar to JCZ324 LIM protein [H.sapiens], Homo sapiens cDNA
				FLJ 13238 118, cione OVARC1000440, RIKEN cDNA 2410002J21 gene, expressed
28	20092 AA799637	4799637		sequence AVZ/8559, expressed sequence AW/123232, hypothetical protein
				LLJ10044, paxillin, transforming growth factor beta 1 induced transcript 1
	_		-	Leal, weakly similar to Jobi 11 cyclin-dependent kinase-related protein 1b - rat
				[K.norvegicus], EST, Weakly similar to S10889 proline-rich protein [H.sapiens],
				ESIS, Highly similar to KPT1 MOUSE SERINE/THREONINE-PROTEIN KINASE
				PC1AIRE-1 [M.musculus], ESTs, Weakly similar to KPT1 MOUSE
2228	25600 NM_031077		b, I, m	SEKINE/I HREONINE-PROTEIN KINASE PCTAIRE-1 [M.musculus], PCTAIRE
				protein kinase 1, PCTAIRE-motif protein kinase 1

TABLE 3		· · ·		
SEO		GenBank Acc.	Ŀ	Ally Ref 44094-500n na Michaeles
۵	GLGC ID No.	No.		
				EST, Weakly similar to JC5111 cyclin-dependent kinase-related protein 1b - rat [R.norvegicus], EST, Weakly similar to S10889 proline-rich protein [H.sapiens], EST, Highly similar to KPT1 MOUSE SFRINE/THREONING DEOTEIN MALCE
2228		6349 NM_031077	ee, #	PCTAIRE-1 [M.musculus], ESTs, Weakly similar to KPT1 MOUSE SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 [M.musculus], PCTAIRE
				EST, Weakly similar to JC5399 dual feucine zipper kinase (EC 2.7) - rat [R.norvegicus], ESTs, Highly similar to A55318 serine/threonine protein kinase
2575		21818 NM_139342	pp	[w.inusculus], ESTS, Weakly similar to JC5399 dual leucine zipper kinase (EC 2.7) - rat [R.norvegicus], ankyrin repeat domain 3, expressed sequence C81508,
				CCT Works in 1977 Serine-threonine kinase 1
			<u> </u>	(VLDL receptor) [R.norvegicus], ESTs, Weakly similar to LDVR MOUSE VFRY
				LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR [M.musculus], ESTs, Weakly similar to I DVR RAT Very four density in the second similar to I DVR RAT Very four density in the second similar to I DVR RAT Very four density in the second seco
1881	24867	24867 NM_013155		receptor) [R.norvegicus], low density lipoprotein receptor-related protein 8.
				apolipoprotein e receptor, very low density lipoprotein receptor
316	24470 A	24470 AA875523	td td	[H.Sapiens], myosin light chain, alkali, nonmuscle, myosin. light chain 6, nonmuscle form
†			no inn	smooth muscle and non-muscle
316	V 1277C	24474 4 4 8 2 5 5 2 2		HSapiens! myosin light chain 6, nonmuscle form [H.sapiens]. myosin light chain 6, nonmuscle form
=	7 / 1	C7CC /02C0	=	smooth muscle and non-muscle
				EST, Weakly similar to MOHU6N myosin alkali light chain 6, nonmuscle form
316	24472 A	24472 AA875523	:=	[H.sapiens], myosin light chain, alkali, nonmuscle, myosin, light polypeptide 6, alkali,
				EST, Weakly similar to MOHU6N myosin alkali light chain 6, nonmuscle form
464	24473 A	24473 AA894200	Q	[H.sapiens], myosin light chain, alkali, nonmuscle, myosin, light polypeptide 6, alkali,
		•		EST, Weakly similar to MOHU6N myosin alkali linht chain 6
2606	24469 877858	77858		[H.sapiens], myosin light chain, alkali, nonmuscle, myosin light nolvnentide 6 alvair
	-			smooth muscle and non-muscle

TAP.	· ·			ı	
5		Conbon's Age		Alfv Ref 1409	Altv. Ref 44921-5090-01-WC/2105485
Ú,		Genbank Acc.			2020-01-WC/LIU3403
زء	GLGC ID No.	Ņ.	Model Code	Model Code Human Hi mologous Known Gene Mame	
				EST, Weakly similar to P2YX_RAT UDP-glucose receptor (G protein-completed	Drotein-counled
				receptor GPR105) (VTR 15-20) [R.norvegicus], ESTs. Weakly similar to	similar to
				GPRY_MOUSE PROBABLE G PROTEIN-COUPLED RECEPTOR GPR34	TOR GPR34
				[M.musculus], ESTs, Weakly similar to P2YX_RAT UDP-glucose receptor (G protein	se receptor (G protein
				coupled receptor GPR105) (VTR 15-20) [R.norvegicus], G protein-coupled receptor	tein-coupled receptor
				105, G protein-coupled receptor 34, G protein-coupled receptor 86, G protein-	or 86, G protein-
2633		17296/1176206	2	coupled receptor 87, Purinergic receptor P2Y, G protein-coupled, 12, platelet	ed, 12, platelet
		010200	JJ. NA	activating receptor homolog	
				EST, Weakly similar to PRO1 MOUSE PROFILIN I IM. musculus), EST, Weakly	us), EST, Weakly
21.72		OBOO MIN OCCEA	1	similar to PRO2_HUMAN PROFILIN II [H.sapiens], ESTs, Weakly similar to	akly similar to
717		I I CZZO MINI	n, o, w, x	PRO2_HUMAN PROFILIN II IH.sapiens], Mk1 profein. profilin 1	
				EST, Weakly similar to PRS7 MOUSE 26S PROTEASE REGULATORY SUBLINIT 7	LATORY SUBUNIT 7
2357		SK77 MM 022226		[M.musculus], RIKEN cDNA 2300001E01 gene, proteasome (prosome, macropain)	rosome, macropain)
3		4IM_035230	-	26S subunit, ATPase 2, syntaxin 8	-
				EST, Weakly similar to PRSB MOUSE 26S PROTEASE REGULATORY SUBUNIT 8	LATORY SUBUNIT 8
				[M.musculus], Homo sapiens mRNA; cDNA DKFZp586I1420 (from clone	rom clone
				DKFZp5861420); partial cds, YME1-like 1 (S. cerevisiae), hypothetical protein	othetical protein
				DKFZp667C165, protease (prosome, macropain) 26S subunit, ATPase 5,	ATPase 5,
2263	1.00.1	1291 NM 031140		proteasome (prosome, macropain) 26S subunit, ATPase, 5, proteasome (prosome,	oteasome (prosome,
		OF LOOP	5	macropain) 26S subunit, ATPase, 6	
				LS1, Weakly similar to R6HUP1 acidic ribosomal protein P1, cytosolic [H.sapiens],	rosolic [H.sapiens],
		_		ESTS, Highly similar to R6HUP1 acidic ribosomal protein P1, cytosolic [H.sapiens],	rtosolic [H.sapiens],
909	24521 4	24521 44945636	-5	ESTs, Weakly similar to RLA1 MOUSE 60S ACIDIC RIBOSOMAL PROTEIN P1	AL PROTEIN P1
	7	000000	1, 1,	[M.musculus], expressed sequence AI255964, ribosomal pro	n, large, P1
				EST, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL.A	IN RAL-A
				[M.musculus], ESTs, Weakly similar to Crystal Structure Of The Small G Protein	Small G Protein
				Rap2a With Gdp (SUB 1-167 [H.sapiens], ESTs, Weakly similar to RALA MOUSE	to RALA MOUSE
2232	15201 N	15201 NM 031093	- -	RAS-RELATED PROTEIN RAL-A [M.musculus], v-ral simian leukemia viral	rkemia viral
			11, 1, W	oncogene homolog A (ras related)	

TABLE 3	E 3		. :	The state of the s
SEO	,	GenBank Acc.		
	GLGC ID No.	No.	Model Code Human Hom	duman Homologous Known Gene Name Human Homologous Sequence Cluster Title
				EST, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL-A
				[M.musculus], ESTs, Weakly similar to Crystal Structure Of The Small G Protein
-			f, w, x, cc,	RAS-REI ATED PROTEIN DATA AND CONTRIBUTED RALA MOUSE
7737		15202 NM_031093	용	oncogene homolog A (ras related)
				EST, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL-A
				[M.musoulus], ESTs, Weakly similar to Crystal Structure Of The Small G Protein
				Rap2a With Gdp (SUB 1-167 [H.sapiens], ESTs, Weakly similar to RALA MOUSE
2232		15203 NM_031093	aa, bb	RAS-RELATED PROTEIN RAL-A [M.musculus], v-ral simian leukemia viral
				FST. Weakly similar to RB6K MOLISE BARKINESIN & M
1200		A144E0C0	-	similar to RB6K MOUSE RABKINESIN-6 IM. musculus   RABK interaction vinacia
3		1637 71143900	E 'i	like (rabkinesin6), Rab6, kinesin-like
				EST, Weakly similar to RL12_HUMAN 60S RIBOSOMAL PROTEIN 112
2654	18606	18606 X53504	>	[H.sapiens], ESTs, Weakly similar to RL12_HUMAN 60S RIBOSOMAL PROTEIN
			× 'a'	L12 [H.sapiens], ribosomal protein L12
2647	192 44	192 td X15013	f, a, w, x	EST, Weakly similar to RL7A MOUSE 60S RIBOSOMAL PROTEIN L7A
-				Im.musculus], RIKEN cDNA 4632404N19 gene, ribosomal protein L7a
				ES1, Weakly similar to RS11_HUMAN 40S ribosomal protein S11 [R.norvegicus],
2243	108 /8	108 /8 NM_031110	g, j, k	Homo sapiens mrNA; cDNA DKFZp434A0326 (from clone DKFZp434A0326),
				EST. Weakly similar to S210ts francision control of the second of the se
				IR nonvenious   ESTE Highly eimiter to ECUIA feed 11.5.
				alpha-1 Chain IH. Saniens! FSTs Weakly similar to C21055 translation action eEF-1
	-v		·	factor eEF-1 alpha chain - rat [R.norvegicus], G1 to S phase transition 1 G1 to
7362	2//40			phase transition 1, G1 to phase transition 2, eukarvotic translation elementary
7007	121	SCCCCO MINING 1447	E, KK	1 alpha 1
-	_			EST, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens], ESTs, Weakly
1422	13673 A	13673 AI227763		Similar to S26650 DNA-binding protein 5 [H.sapiens], hypothetical protein
				Let Month circles 2010 6
9	0010		:	RIKEN cDNA 1810012810 dene expressed segions a MK29900 binde den
1038	165% AI102486		ee, ff, kk	gene MGC1127

IABLES	į		,-A. 14. N. F.	Service Control of th	
e 19 €	٠ ز	GenBank Acc.			怒
		. (A)	Wodel Code	Model Code Human Hemologous Known Gene Name Human Homologous Sequence Cluster Title	
				EST, Weakly similar to S37583 RING finger protein rfp - mouse [M.musculus],	1
1253		16599/AI171366	ee, ff, jj, kk	gene MGC1127	
				EST, Weakly similar to S46992 protein p130 - rat [R.norvegicus], ESTs, Weakly	1
				Similar to A59300 myosin-If - mouse [M.musculus], ESTs, Weakly similar to CASL	
				4634403DD3 2000 DIVEN CANA OCCUPATION 1 [M.musculus], RIKEN CDNA	
				1403 1403F to gene, RIKEN cDNA G30006B10 Gene, RIKEN cDNA C330006B10	
433		21652 AA893267	u, v	factor 13 proline-serine threating theory of the factor is the factor of the factor is	
1213		11550 AH69591		EST, Weakly similar to S57447 HPBRIL-7 protein I'll sanions and	_
	1	1000011		polyadenylation specific factor 6, 68kD subunit, hypothetical profein FI 112529	
				EST, Weakly similar to S71929 cytochrome-c oxidase (EC 1.9.3.1) chain VIII	_
1100		11953 AI102505	듄	precursor, hepatic - mouse [M.musculus], cytochrome c oxidase, subunit VIIIa,	
				Heme-regulated initiation factor 2-alpha kinase	_
				ES1, Weakly similar to S71929 cytochrome-c oxidase (EC 1.9.3.1) chain VIII	_
<del>-</del>		11954 AI102505	重	predutsor, nepatic - mouse [M.musculus], cytochrome c oxidase, subunit VIIIa,	
				Instituted initiation factor 2-alpha kinase	
				E31, weakly similar to S/1929 cytochrome-c oxidase (EC 1.9.3.1) chain VIII	_
1703	11955L48209	48209	듄	precursor, nepatic - mouse [M.musculus], cytochrome c oxidase, subunit VIIIa,	
				Infilierre-regulated intration factor 2-alpha kinase	
	<del></del> .			Lot, weakly similar to secreted cyclophilin-like protein [H.sapiens], ESTs, Weakly	<del>,</del>
	_			Similiar to cyclophillin B [Rattus norvegicus] [R.norvegicus], RIKEN cDNA	
				37.324 IUE 19 gene, peptidylprolyl isomerase (cyclophilin)-like 1, peptidylprolyl	
2135	8097 N	8097 NM_022536		Isomerase B, peptidylprolyl isomerase B (cyclophilin B), peptidylprolyl isomerase C.	
				peptidylprolyl isomerase C (cyclophilin C)	
				EST, Weakly Similar to secreted cyclophilin-like protein [H.sapiens], ESTs, Weakly	
				Similar to Cyclophilin B [Rattus norvegicus] [R.norvegicus], RIKEN cDNA	_
				3/3/2410E19 gene, peptidylprolyl isomerase (cyclophilin)-like 1, peptidylprolyl	
2135	N 808	8098 NM_022536		Isomerase B, peptidylprolyl isomerase B (cyclophilin B), peptidylprolyl isomerase C,	
				(pepudylprolyl isomerase C (cyclophilin C)	

TABLE 3	33				TO COMPANY OF THE PROPERTY OF
SEO		GenBank Acc.			Atty: Ket: 44921-5090-01-WO/2105485
<u>۵</u>	GLGC ID No.	No.	Model Code	Model Code Human Homologous, Known Gene Name Human Homologous Sequence Cluster Title	
				EST, Weakly similar to SYFB_MOUS	EST, Weakly similar to SYFB_MOUSE PHENYLALANYL-TRNA SYNTHETASE RETA CHAIN (PHENYLA) ALANIMIE TEMA LICASE BETA CHAIN (PHENYLA)
				[M.musculus], Homo sapiens cDNA F	M. musculus), Homo sapiens cDNA FLJ30727 fis. clone FEBRA2000007 highly
				similar to Homo sapiens putative phe	similar to Homo sapiens putative phenylalanyl-tRNA synthetase beta-subunit
				mRNA, KIAA1185 protein, RIKEN cD	mRNA, KIAA1185 protein, RIKEN cDNA 2900010D03 gene, expressed sequence
1376		6502 AI178283		C76708, phenylalanine-tRNA synthet	C76708, phenylalanine-tRNA synthetase-like, phenylalanyi-tRNA synthetase beta-
				EST, Weakly similar to T00051 hypot	EST, Weakly similar to T00051 hypothetical protein KIAA0404 fH sapiens I Homo
730		0.2000.4		sapiens, clone IMAGE:4657824, mRN	sapiens, clone IMAGE:4657824, mRNA, KIAA0404 protein, hypothetical protein
3		40 TO PARABOBI 8	۵,۷	FLJ10242	
				EST, Weakly similar to 700357 hypot	EST, Weakly similar to T00357 hypothetical protein KIAA0685 [H.sapiens], Homo
861		230 15 41012621	د.	sapiens mRNA for KIAA1558 protein,	sapiens mRNA for KIAA1558 protein, partial cds, KIAA0685 gene product,
3	L	17071011	۱, ۸	KIAA1115 protein, chromosome 11 op	pen reading frame 23
832		040 101 A1014474	# # # # # # # # # # # # # # # # # # #	EST, Weakly similar to T00637 hypoti	EST, Weakly similar to T00637 hypothetical protein H_GS541B18.1 [H.sapiens],
7	1	14/4	a, ee, II, II	golgi phosphoprotein 2	
				EST, Weakly similar to T12456 hypoth	EST, Weakly similar to T12456 hypothetical protein DKFZp564M2423.1 [H.sapiens],
				ESTs, Highly similar to T12456 hypott	ESTs, Highly similar to T12456 hypothetical protein DKFZp564M2423.1 [H.sapiens],
436	22345	22345 A A R 0 2 2 2 8	=======================================	PAL-1 mRNA-binding protein, RIKEN of	PAI-1 mRNA-binding protein, RIKEN cDNA 1200009K13 gene, intracellular
3	3	T	, u, v	hyaluronan-binding protein	
				EST, Weakly similar to 712482 hypott	EST, Weakly similar to T12482 hypothetical protein DKFZp564P0662.1 [H.sapiens],
				ESTs, Weakly similar to T12482 hypothetical protein DKFZp564P0662.1	thetical protein DKFZp564P0662.1
				[H.sapiens], Homo sapiens cDNA FLJ	[H.sapiens], Homo sapiens cDNA FLJ32000 fis, clone NT2RP7009370, weakly
990	70007	7000 00000		similar to PUTATIVE SERINE/THREO	similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1),
000	13251	HI044040	cc, aa, gg	echinoderm microtubule associated pr	echinoderm microtubule associated protein like 2
				EST, Weakly similar to T13963 formin	related protein, lymphocyte specific - mouse
				[M.musculus], ESTs, Highly similar to '	[M.musculus], ESTs, Highly similar to T13963 formin related protein, lymphocyte
		-		specific - mouse [M.musculus], ESTs,	specific - mouse [M.musculus], ESTs, Moderately similar to T13963 formin related
				protein, lymphocyte specific - mouse (P	protein, lymphocyte specific - mouse [M.musculus], Homo sapiens mRNA; cDNA
1373	6050	6050 41178745		DKFZp762B245 (from clone DKFZp76	DKFZp762B245 (from clone DKFZp762B245); partial cds, formin homology 2
212	Joseph Land		3	domain containing 1, formin-like	

Cit.GC   D No.   Another Acc.   Auth Ref. 4482-5580-0-1-NO/2105-88	I ADLE S	?		•		
St. GC   D   No.   Model Code   Human Homologous Known Gerie Name   EST, Wealdy Smillar to MYH9_RAT Mymoral Rest   Wealdy Smillar to MYH9_RAT Mymoral Rest   Wealdy Smillar to MYH9_RAT Mymoral Rest   Wealdy Smillar to MYH9_RAT Mymoral Rest   Wealdy Smillar to Informace   Wea	SEO		GenBank Acc		The second secon	-5090-01-WO/210548
2882 AA789423	ا ۾	GLGC ID	No.		ologous Known Gene Name Human Homologous Sequence Cluster	
2881 AF056034 b, d, u, v b b d, u, v b b d, u, v b b d, u, v b b d, u, v b b d, u, v b b d, u, v b b d, u, v b b d, u, v b b d, u, v b b d, u, v b					EST, Weakly similar to 142637 hypotnetical protein 162K - ESTs, Highly similar to MYH9_RAT Myosin heavy chain, no	ouse [M.musculus], nuscle type A (Cellula
2882 AA799423  II 2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 f, s, t tt th					myosin heavy chain, type A) (Nonmuscle myosin heavy chain the serve the myosin heavy chain to the myosin heavy chain the myosin heavy cha	-A) (NMMHC-A)
2882 AA799423					יייין איז	eavy chain,
2882 AA799423					chain-A) (NMMHC-A) [R.norvegicus], Mus musculus, clone	GC:7530
2882 AA789423					IMAGE:3492114, mRNA, complete cds, Myosin, heavy poly	ptide 9, non-muscle,
2881 AF056034 b, d, u, v  16566 NM_054004 hh  17159 J00797 hh, II  17158 NM_022298 f, s, t  17160 NM_022298 b, 1, m, aa					RIKEN cDNA 3110050K21 gene, eukaryotic translation initi	on factor 3, myosin
2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 b, I, m, aa	82		AA799423	_	heavy chain IX, myosin, heavy polypeptide 9, non-muscle, r	opharyngeal
2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, ll 17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa					epithelium specific protein 1	
2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, II 17159 JM_022298 f, s, t 17160 NM_022298 b, l, m, aa					E31, Weakly Similar to 14263/ hypotheucal protein 162K-1 ESTs. Highly similar to MYH9_RAT Munsin beaut shair and	use [M.musculus],
2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, II 17159 J00797 hh, II 17160 NM_022298 f, s, t EE					myosin heavy chain tyne A\ (Nonmissle myosin heavy chain tyne A\ (Nonmissle myosin han a	iuscie type A (Ceilular
2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa	,				IRA NONDANIAL ESTE MANARA AMAIN DATES.	A) (INMINITION)
2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa					It will yell any very search similar to MY HALL KALL MYOSIN	eavy chain,
2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa					nominascie type A (Celiular myosin heavy chain, type A) (No	nuscle myosin heavy
2881 AF056034 b, d, u, v 16566 NM_054004 hh 17159 J00797 hh, il 17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa					Chialin-A) (NinimHC-A) [K.norvegicus], Mus musculus, clone I	C:7530
2881 AF056034 b, d, u, v  16566 NM_054004 hh  17159 J00797 hh, II  17158 NM_022298 f, s, t  17160 NM_022298 b, l, m, aa					IIMAGE:3492114, mRNA, complete cds, Myosin, heavy polyr	otide 9, non-muscle,
2881 AF056034 b, d, u, v  16566 NIM_054004 hh  17159 J00797 hh, II  17158 NIM_022298 f, s, t  17160 NIM_022298 b, l, m, aa					RIKEN cDNA 3110050K21 gene, eukaryotic translation initia	n factor 3, myosin
16566 NM_054004 hh 17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa	751	2881	1F056034	; ;	heavy chain IX, myosin, heavy polypeptide 9, non-muscle, n	pharyngeal
16566 NM_054004 hh  17159 J00797 hh, II  17158 NM_022298 f, s, t  17160 NM_022298 b, l, m, aa	+		100000	o, u, u, v	epithelium specific protein 1	
16566 NM_054004 hh 17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa					EST, Weakly similar to T42735 TBP-Interacting protein TIP1.	- rat [R.norvegicus].
17159 J00797 w, x, aa, bb, hh, II 17158 NM_022298 f, s, t	2468	16566 N	JM 054004	4	Homo sapiens cDNA FLJ14877 fis, clone PLACE1003044, T	-interacting protein,
17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa			Looton III		expressed sequence Al195005	•
17159 J00797 hh, II 17158 NM_022298 f, s, t 17160 NM_022298 b, I, m, aa				* × **	EST, Weakly similar to TBA1 MOUSE TUBULIN ALPHA-1 CI	IN [M.musculus],
17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa	1686	17150	70707	14, 4, 44, UU,	tubulin, alpha 1, tubulin, alpha 2, tubulin, alpha 3, tubulin, alp	6, tubulin, alpha 7.
17158 NM_022298 f, s, t 17160 NM_022298 b, l, m, aa		3	10100	# 'III	tubulin, alpha, ubiquitous	
17158 NM_022298 f, s, t 17160 NM_022298 b, I, m, aa					EST, Weakly similar to TBA1 MOUSE TUBULIN ALPHA-1 Ch	IN [M.musculus],
17160 NM_022298 b, l, m, aa	2105	17158 N	80000 MI	÷	tubulin, alpha 1, tubulin, alpha 2, tubulin, alpha 3, tubulin, alp	6, tubulin, alpha 7.
17160 NM_022298   b, l, m, aa			05550	1, 9, 1	tubulin, alpha, ubiquitous	
17160 NM_022298 b, I, m, aa					EST, Weakly similar to TBA1 MOUSE TUBULIN ALPHA-1 CF	N [M.musculus],
יייטן יייין עבבבטט ויין ווון ממ	2105	17160 NI	M 022298	8	tubulin, alpha 1, tubulin, alpha 1, tubulin, alpha 2, tubulin, alpha 3, tubulin, alph	6, tubulin, atoha 7.
			111 055500	U, I, III, aa	tubulin, alpha, ubiquitous	

<b>TABLE 3</b>	E3		に指すられ	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
SEQ		GenBank Acc.		The second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the section of the second section of the section of
₽	GLGC ID No.	No.	Model Code Human Hom	ologous Known Gene Name
2105		17161 NM_022298	a, z, kk	
265		13974 AA860030	x m 0 0	EST, Weakly similar to TBB5 MOUSE TUBULIN BETA-5 CHAIN [M.musculus], RIKEN cDNA 2310061K05 gene, RIKEN cDNA 2410129E14 gene, RIKEN cDNA 4930542G03 gene, tubulin, beta 5, tubulin, beta polypeptide, tubulin, beta, 2,
1444		13977 AI229707		tubulin, beta, 5 EST, Weakly similar to TBB5 MOUSE TUBULIN BETA-5 CHAIN [M.musculus], RIKEN cDNA 2310061K05 gene, RIKEN cDNA 2410129E14 gene, RIKEN cDNA 4930542G03 gene, tubulin, beta 5, tubulin, beta polypeptide, tubulin, beta, 2,
1046		9604 AI071230	ee, ff, gg	EST, Weakly similar to TESTIN 2 [M.musculus], Homo sapiens cDNA FLJ31627 fis,
2266	15273	15273 NM_031237	aa, bb	EST, Weakly similar to UB5C_HUMAN Ubiquitin-conjugating enzyme E2-17 kDa 3 (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2(17)KB 3) [R.norvegicus], ESTs, Weakly similar to S53358 ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus], Homo sapiens EST from clone 37208, full insert, RIKEN cDNA 1100001F19 gene, RIKEN cDNA 160002817 gene, prefoldin 5, ubiquitin-
2266	15277IN	15277 NM 031237		Conjugating enzyme EZD 3 (UBC4/5 homolog, yeast) EST, Weakly similar to UB5C_HUMAN Ubiquitin-conjugating enzyme E2-17 kDa 3 (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2(17)KB 3) [R.norvegicus], ESTs, Weakly similar to S53358 ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus], Homo sapiens EST from clone 37208, full insert, RIKEN cDNA 1100001F19 gene, RIKEN cDNA 160002817 gene, prefoldin 5, ubiquitin-
1292	17679 A		늄	EST, Weakly similar to WS3_HUMAN WS-3 PROTEIN [H.sapiens], novel RGD-
1174	15660		7	EST, Weakly similar to ZF37_RAT Zinc finger protein 37 (Zfp-37) [R.norvegicus], ESTs, Weakly similar to ZF29 MOUSE ZINC FINGER PROTEIN 29 [M.musculus], ESTs, Weakly similar to ZF93_MOUSE ZINC FINGER PROTEIN 93 (ZFp-93) [M.musculus], expressed sequence AW557864, zinc finger protein 29, zinc finger
<u>F</u>	Algorici Tigorici	13803/A1137302 (C	cc, dd	protein 37, zinc finger protein 37 homolog (mouse)

TABI 5.2		· «,	こうない	
¥		RenBank Acc.		AttyRef. 44921-5090-01-WOI210548F
3	GLGC ID No.	Ŋ.	Model Code	Omologous Seguience Chiefer Title
	ς,			
				musculus, Similar to aminopeptidase B, clone MGC:29229 IMAGE:5041005
2234		1295 NM 031097		mRNA, complete cds, RIKEN cDNA 2010111101 gene, expressed sequence
			1 1/4 (1)	Al894167, hypothetical protein FLJ14675, leukotriene A4 hydrolase
				ESTs, Highly similar to eukaryotic translation elongation factor 1 beta 2: eukaryotic
1302		18507 AI175551	4 × ×	translation elongation factor 1 beta 1 [Homo sapiens] [H.sapiens]. enkanyotic
			11, 1, W, A, AA	translation elongation factor 1 beta 2
				ESTs, Highly similar to Glutamate receptor interacting protein IRathus porvening
				[R.norvegicus], Glutamate receptor interacting protein, RIKEN cDNA 493140nEn3
2548		5283 NM 138535	5	gene, channel-interacting PDZ domain protein, multiple PDZ domain protein
		00000	66	Syntrophin, alpha 1 (dystrophin-associated notein A1 50kD oxidio company)
38		15%03 AA799518	>	ESTs, Highly similar to hypothetical protein FLJ13725; KIAA1930 protein IHomo
		01000 50	W, ^	Sapiens] [H.sapiens]
				ESTs, Highly similar to lymphocyte activation-associated protein [Homo saniens]
				[H.sapiens], ESTs, Weakly similar to KEAP_RAT Kelch-like ECH-associated protein
				1 (Cytosolic inhibitor of Nrf2) (INrf2) [R.norvegicus], Kelch-like ECH-associated
				protein 1, Mus musculus, Similar to KIAA0952 protein, clone MGC:25591
43	17599/	17599 AA799539		IMAGE:4011475, mRNA, complete cds, RIKEN cDNA 2700038B03 gene, kelch-like
			,	ECH-associated protein 1
		•		ES1S, Highly similar to MAP-kinase activating death domain; Rab3 GDP/GTP
			_	exchange protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to MAP-
				Kinase activating death domain; Rab3 GDP/GTP exchange protein [Rattus
			_	norvegicus] [R.norvegicus], MAP-kinase activating death domain, Mus musculus.
				Similar to MAP-kinase activating death domain, clone MGC:7838 IMAGE:3500720
2402	21170N	21170 NM 053585	+	mRNA, complete cds, RIKEN cDNA 2010004M01 gene, suppression of
		T	1	tumorigenicity 5
			_	ESTs, Highly similar to Matrix metalloproteinase 23 [Rattus norvegious]
2408	11794 N	11794 NM 053606 III		[R.norvegicus], matrix metalloproteinase 23, matrix metalloproteinase 23A, matrix
		1		metalloproteinase 23B

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SHO		GenBank Acc.		The state of the s	WO/2105485
<u>₽</u>	GLGC ID No.	D No.			
					dicus
				[R.norvegicus], ESTs, Moderately similar to microtubule-associated protein 1a	tein 1a
_				[Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to microtubule-associated	9-associated
				protein 1a [Rattus norvegious] [R.norvegious], ESTs, Weakly similar to	
				MAPA_MOUSE Microtubule-associated protein 1A (MAP 1A) [M.musculus].	ns]
2211		1991 NM 030995	_ 	chromatin assembly factor 1, subunit A (p150), expressed sequence Al853608.	53608.
			-	microtubule-associated protein 1A	
				ESTs, Highly similar to multiple PDZ domain protein [Mus musculus] [M.musculus]	musculus
				Homo sapiens cDNA FLJ25282 fis, clone STM06685, highly similar to Raffus	affirs
1158		144 34 AI112291		norvegicus mRNA for multi PDZ domain protein, ligand of numb-protein X 1	× 1
			=	multiple PDZ domain protein	
				ESTs, Highly similar to NF-E2-related factor 2 (Rattus norvegicus) (R. norvegicus)	Overright)
	<u> </u>			ESTs, Weakly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus]	Nenicus]
2328		1139 NM 031789		nuclear factor (erythroid-derived 2)-like 2, nuclear factor, erythroid derived 2, like 3	d 2. like 3
Γ		200	,	nuclear, factor, erythroid derived 2, like 2	
				ESTs, Highly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus]	Vegicus
				ESTs, Weakly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus]	regicus).
2328		11 70 NM 031789	d   m   kk	nuclear factor (erythroid-derived 2)-like 2, nuclear factor, erythroid derived 2, like 3.	12, like 3.
Γ			Wy off true is to	nuclear, factor, erythroid derived 2, like 2	
				FSTe Highly eimilar to accept a transfer of the Highly eight and the	
8	16215	16215 AA874999	h, l, n, o	SECRI hata sulvinit II ansional II ansional protein transport protein	ort protein
				ESTs, Highly similar to proteoglycan 3 (megakaryocyte simulating factor articular	nplex beta
				Superficial zone protein) [Mus musculus] [M.musculus]. protectiven 4	
	·			(megakaryocyte stimulating factor, articular superficial zone protein), proteogivcan	soalvcan
1162	4959	4959 AI113008	l, k, n, o	4, (megakaryocyte stimulating factor, articular superficial zone protein,	 }
				Leaniptodaciyiy, artnroparny, coxa vara, pericarditis syndrome), vitronectin	

Human Homologous Sequence ESI's, Highly similar to ribosomal protein, ribosomal protein, ribosomal protein, ribosomal protein L36a [Homologous Sequence in the seman protein L36a [Homologous Sequence in the seman protein L36a [Homologous Protein L	707	•	•			
Cl. GC   D   No.   Model   Code   Human Honologous Known Gene Name   ESI S. Highly similar to hosomal protein; those the protein; those the protein; those the protein; those the protein; those the protein; those the protein; those the protein; those the protein; those the protein; those the protein; those those those minute; the protein; those those those minute; the protein; those tha	, 10 10 10 10 10 10 10 10 10 10 10 10 10		GenBank Acc			The second second
23307 NM_ 057119	- 1	0.00 0.00 1.00 1.00 1.00 1.00 1.00 1.00	No.			Human Homologou's Seguence: Cluster Title
23307 NM_057119 e c, d d limii						ESTs, Highly similar to ribosomal protein L36a; 60S ribosomal protein L44; L44-like
233X7/NM_057119						ribosomal protein; ribosomal protein L44; ribosomal protein L36a homologue; 60S ribosomal protein L36a IHomo saniene; IH saniene; ESTS MAASSELS STREET
23307 NM_057119						ribosomal protein L36a; 60S ribosomal protein L44. L44-like ribosomal protein:
17298 NIM_057119 6 . s, t	·-					ribosomal protein L44; ribosomal protein L36a homologue; 60S ribosomal protein
23310 NIM_057119	2240		NM_031105	q		L36a [Homo sapiens] [H.sapiens], RIKEN cDNA 2410038A03 gene, ribosomal
23370 NIM_057119						inclain Loga-like, ribosomal protein L44
2337 NM_057119 e	2202		01010	:		ESTS, Fighty Similar to synaptogyrin 2 (Rattus norvegicus) (R.norvegicus), Mus musculus 18 days embro whole hody Ana Ana Ana Ana Ana Ana Ana Ana Ana Ana
23310 NM_057119 e	2030		NIM UDSDDS	용 8	0	clone:1110032G03:synaptogyrin 2, full insert sequence, synaptogyrin 2
23307 NM_057119 e						Till Bridge Complete
23307 NM_057119 e					щ (	ES1s, Fighly similar to ILS-associated serine-arginine protein 1, isoform 1; TLS-
23307 NM_057119 e					מ ב	associated senne-arginine protein 1; TLS-associated protein TASR [Homo sapiens]
23310 NM_057119 e, s, t  20082 Al639488 d  17350 AA892240 I, m, ii					<b>.</b>	ansformer 2 December 6 per 12 of 12
23310 NIM_057119 e   P   P   P   P   P   P   P   P   P						usculus hexaribonicleotide binding profess 2 / /
23310 NIM_057119 e, s, t  20082 Al639488 d  17350 AA892240 I, m, ii	0770	10000		•	70	DNA 1500010G04 dana mairral calicat prairie (activity) minuta, partial cds, RIKEN
23310 NIM_057119 e, s, t 20082 AI639488 d 17350 AA892240 I, m, ii	24/3	7330/	NM_057119	9	4	1, Splicing factor, arginine/serine-rich 10 (transformer 2 homology December 1).
23310 NIM_057119 e, s, t 20082 A1639488 d 17350 AA892240 l, m, ii						Sample of the spinish
23310 NIM_057119 e, s, t 20082 Al639488 d 17350 AA892240 l, m, ii					ŭ	ESTs, Highly similar to TLS-associated serine-arginine protein 1, isoform 1: TLS-
23310 NIM_057119 e, s, t 20082 A1639488 d 17350 AA892240 l, m, ii		_			SG :	associated serine-arginine protein 1; TLS-associated protein TASR [Homo sapiens]
23310 NM_057119 e, s, t 20082 A1639488 d 17350 AA892240 l, m, ii		-			<u> </u>	sapiens), ESTs, Weakly similar to splicing factor, arginine/serine-rich
23310 NM_057119 e, s, t 20082 Al639488 d 17350 AA892240 l, m, ii					in)	(transformer 2 Drosophila homolog) 10 [Rattus norvegicus] [R.norvegicus], Mus
23310 NIM_057119 e, s, t 20082 AI639488 d 17350 AA892240 l, m, ii	<del></del> -				Ē	musculus hexaribonucleotide binding protein 3 (Hmbp3) mRNA, partial cds, RIKEN
20082 A1639488 d 17350 AA892240 l, m, ii	2479	23310N	IM 057119		3	INA 1500010G04 gene, neural-salient serine/arginine-rich, silica-induced gene
20082 Al639488 d 17350 AA892240 l, m, ii					41	41, splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
20082 Al639488 d 17350 AA892240 l, m, ii						1s, Highly similar to 1814460A p53-associated protein [H.sapiens], Mdm2,
17350 AA892240 (, m, ii	1641	20082 A		٠	Train and a second	nstormed 313 cell double minute 2, p53 binding protein (mouse), transformed
17350 AA892240 l, m, ii	-				Ш	use 373 cell double minute 2
17350 AA892240 (1, m, ii						ES1s, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus]
	377	17350A				1s, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], SET
					lra	translocation, SET translocation (myeloid leukemia-associated)

WO 2004/063334 PCT/US2004/000240

TABLE 3	E3.	The state of the state of	in the second second	をおいて 後 送すし	* 1985.Be	
S 6		GenBank Acc.				Atty. Ref. 44921-5090-01-WQ/2105485
2	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Name	Human Homologous Sequence Cluster Title
			<del>-</del>			ESTs, Highly similar to 40S RIBOSOMAL PROTEIN S23 [H.sapiens], Mus
1529		23296/AI233316	<u>.</u>			indesculus, Similar to mitochondrial ribosomal protein S12, clone MGC:13892 IMAGE:4209358, mRNA, complete cds. mitochondrial ribosomal protein S12
						ribosomal protein S23
						ESTs, Highly similar to A37100 myosin regulatory light chain A, smooth muscle - rat
						[R.norvegicus], RIKEN cDNA 2900073G15 gene, myosin light chain,
2006	ĺ	20848 NM_017343	bb, hh, jj, kk			phosphorylatable, cardiac ventricles, myosin regulatory light chain, myosin, light
						polypeptide, regulatory, non-sarcomeric (20kD)
						ES 15, Highly similar to A37100 myosin regulatory light chain A, smooth muscle - rat
						R. norvegicusj, RIKEN cDNA 2900073G15 gene, myosin light chain,
2006		201 49 NM_017343	60			phosphorylatable, cardiac ventricles, myosin regulatory light chain, myosin, light
						polypeptide, regulatory, non-sarcomeric (20kD)
						ESTS, Highly similar to A38351 phosphoprotein phosphatase 2-alpha regulatory
175	16: 71	16: 71 AA819691				chain [H.sapiens], RIKEN cDNA 2410004D02 gene, protein phosphatase 2
	<del>  -</del> 					(formerly 2A), regulatory subunit B (PR 52), alpha isoform
					<del></del>	ESTs, Highly similar to A38351 phosphoprotein phosphatase 2-alpha regulatory
2466	16! 62 N	16: 62 NM 053999	η. ν			chain [H.sapiens], RIKEN cDNA 2410004D02 gene, protein phosphatase 2
	<del> </del>					(formerly 2A), regulatory subunit B (PR 52), alpha isoform
					<u> </u>	ESTs, Highly similar to A45445 janusin precursor, long form - rat IR norvenirus
			_		<u></u>	ESTs, Weakly similar to JQ1322 tenascin precursor - mouse IM musculural
2474	17709 N	17709 NM 057101			_	Tenascin-R (Restrictin, janusin, J1-160/180), tenascin R (restrictin janusin)
	<del>  -</del> 					(enascin XB
					ш <u>:</u>	ESTs, Highly similar to A54602 microtubule-associated serine/threonine protein
			_		<u> </u>	kinase MAS1205 - mouse [M.musculus], ESTs, Moderately similar to A54602
						microtubule-associated serine/threonine protein kinase MAST205 - mouse
					<u> </u>	Ilwmusculus], Homo sapiens cDNA: FLJ21699 fis, clone COL09829, KIAA0303
					<u>5.</u> T	Protein, KIAAU361 protein, KIAA0807 protein, Mus musculus adult male cecum
-					3 8	CONT., RINEIN Juli-length enriched library, clone:9130026D18:syntrophin associated
797	15884 AA866276		d, f, g, r		<u> </u>	serimentine kinase, full insert sequence, microtubule associated testis specific
					86	sering un conne protein kinase, syntrophin associated serine/threonine kinase

TABLE 3	رب س		1.24	the state of the s
SEQ		GenBank Acc.		100 July Ref. 44921-5090-01-WOIZINEER
<u>.</u>	GLGC ID No.	No.		
				chain - rat [R.norvegicus], ESTs, Weakly similar to A56011 transcription factor IIIC alpha
2525		1791 NM_133541	=	alpha chain - rat [R.norvegicus], general transcription factor III C 1, general
				LESTS, Highly Similar to A59252 myosin heavy chain parameter to
				[H.sapiens], ESTs, Weakly similar to neuronal thread protein IHomo saniens]
				[H.sapiens], ESTs, Weakly similar to LORICRIN [M.musculus], Homo sapiens
				mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227), Homo sapiens, clone
-				IMAGE:4111094, mRNA, partial cds, KIAA0638 protein, Mus musculus, Similar to
				hypothetical protein MGC2705, clone MGC:36471 IMAGE:5359433, mRNA.
				complete cds, Mus musculus, clone MGC:32394 IMAGE:5037534, mRNA, complete
2542		1530 NM_134397	a, e, ji, kk	cds, expressed sequence Al036317, expressed sequence AV253284, expressed
				Sequence C/7/080, loricrin
· <u>-</u> -				Similar to ANK1 MOUSE ANKYRIN 1 [M.musculus], ESTS, Weakly
				CDNA FLU25053 fis clone CRI Marchine Culus, GASZ, Gasz, Homo sapiens
				Containing COCE by and the containing anklytin repeat domain-
				Contraining Social Asp-16 mRNA, complete cds, Mus musculus, Similar
				The hypotrieural protein DKFZp5640043, clone MGC:36949 IMAGE:4946879,
				III/N/A, Complete cas, RIKEN cDNA 1110058D09 gene, RIKEN cDNA 4933400N19
				gene, nypotnetical protein similar to ankyrin repeat-containing priotein AKR1, likely
2431	11606N	11606 NM 053795	- 00	nomolog of rat kinase D-interacting substance of 220 kDa, regulatory factor X-
-			200	associated ankyrin-containing protein
				ESTS, Highly Similar to B Chain B, Peptide-In-Groove Interactions Link Target
				Proteins to The B-Propeller Of Clathrin [R.norvegicus], RIKEN cDNA 1700034F02
2057	17507 NI	17507 NM_019299	يئو ن	gene, clathrin, heavy polypeptide (Hc), clathrin, heavy polypeptide-like 1, expressed
				sequence K/4/32
831	13787 AI011462	1011462	8. dd	ESTS, Highly similar to C259_HUMAN PROTEIN C210RF59 [H.sapiens],
				Chromosome 21 open reading frame 59

TABLE 3				- 11-7
SEO		Bank Acc	122	7,000
	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name
2627	20386	20386 U68562	cc, dd	[M.musculus], ESTs, Weakly similar to CH60_HUMAN 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR [H.sapiens], heat shock 60kD protein 1 (chaperonin), heat shock protein 60 kDa
				ESTs, Highly similar to CIA1_HUMAN WD40-REPEAT CONTAINING PROTEIN CIAO 1 [H.sapiens], ESTs, Weakly similar to LIS1_MOUSE Platelet-activating factor
				acetylinydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH 45 kDa subunit) (LIS-1) kDa subunit) (LIS-1) kDa and WD-40 domain protein 7 (archinelase boxelia)
				Drosophila), Homo sapiens cDNA FLJ31861 fis, clone NT2RP7001319, Homo sapiens, clone MGC:4710 IMAGE:3534806, mRNA complete cds, Milo and the cds, Milo and the cds, M
				box-WD40 repeat protein 6 (Fbxw6) mRNA, complete cds, Mus musculus, Similar to RIKEN cDNA 1500041N16 gene, clone MGC:12066 IMAGE:3708188 mRNA
				complete cds, nuclear receptor co-repressor/HDAC3 complex subunit, platelet-lactivating factor acethylydrolase help subunit (DAE ALLEAS)
644	12426A	12426 AA955760	n, v	factor acetylhydrolase, isoform 1b, beta1 subunit, platelet-activating factor
				acetylhydrolase, isoform lb, alpha subunit (45kD), transducin (beta)-like 1 ESTS, Highly similar to DDR1 neitx-destabilizing Droien - Partik notvemener est e
				Highly similar to ROA3_HUMAN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3 14 sanians1 ESTs Linkly Strates of Strates
				protein A1 [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle
				protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear
				HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/81 (M.musculins)
				Mus musculus, similar to heterogeneous nuclear ribonucleoprotein A3 (H. sapiens), clone MGC:37309 IMAGE:4975085 mRNA complete add pictor and control a
				2610510D13 gene, RIKEN cDNA 3010025E17 gene, heterogeneous nuclear
1359	17570 AI177683		n, o, hh	ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A2/B1,
1			-	neterogeneous nuclear ribonucleoprotein A3, hypothetical protein 23851

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YOU A	·			1		( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( )	1	A section
ر د 'ا		GenBank Acc.	_				The state of the s	Affy Ref. 44921-5090-01-WO/2105485
	GLGC DINO	No.		Model Code Human Hc	nologous Kno	nologous Knovin Gene Name		n Homologous Sequence Cluster
37		17612 AA799511	. =	•				ory NG Sy
								ESTs, Highly similar to DDRT helix-destabilizing protein - rat [R.norvegicus], ESTs, Highly similar to S12520 core protein A1 [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to ROA2 MOUSE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 [M.musculus].
181		17614 AA848306	а					A3 (H. sapiens), done MGC:37309 IMAGE:4975085, mRNA, complete cds, RIKEN cDNA 2610510D13 gene, RIKEN cDNA 3010025E17 gene, heterogeneous nuclear
192	2075	2075, A & 840204						ESTS, Highly similar to DDRT helix-destabilizing protein -rat [R.norvegicus], ESTS, Highly similar to DDRT helix-destabilizing protein -rat [R.norvegicus], ESTS, Highly similar to S12520 core protein A1 [H.sapiens], ESTS, Highly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTS, Moderately similar to S38384 SEB4 protein - mouse [M.musculus], ESTS, Moderately similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTS, Weakly similar to S38384 SEB4 protein - mouse [M.musculus] heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTS, Weakly similar to
1062	5740A		μ', Ε				- H	ribonucleoprotein A1, seb4-like (Xenopus laevis) ESTs, Highly similar to DYNC_HUMAN DYNACTIN, 50 KD ISOFORM [H.sapiens], dynactin 2 (p50)
421	16482 AA892940		56				БVE	ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], U5 small nuclear ribonucleoprotein 116 kDa, eukaryotic translation elongation factor 2

TABLES	2			
		L Carbert A		The same record of the same reco
)		Gelibank Acc.		
<u>a</u>	GLGC ID No.	No.	Model Code Human Hom	Human Homologous Known Gene Name Human Homologous Sequence Chister Title
		-		ESTs, Highly similar to ERR3_HUMAN ESTROGEN-RELATED RECEPTOR
28		6581 AA799412	ө	GAMMA (H.Sapiens), estrogen related receptor, alpha, estrogen-related receptor
				ESTS, Highly similar to H33 HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family
8		15644 AI010256	芝	1810027010 gene
				ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family
1167		24212 AI136747	cc, dd	3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA
				ESTS, Highly similar to H33 HUMAN HISTONE H3 3 IH canienci U2 histone for its
2462		156 12 NIM 053985		3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA
				1810027O10 gene
			-	ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family
2462		15645 NM_053985	q	3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA
				ESTS Hinbly similar to Hinb Unitative National Contraction Contrac
				hippocalcin (P23K) (Calcium-hinding protein
				Moderately similar to VIS3 MOUSE VISININ-LIKE PROTEIN 3 IM miscentus   Muse
				musculus, clone MGC:21424 IMAGE:4500919, mRNA, complete cds. expressed
	-			sequence Al848120, guanylate cyclase activator 1A (retina), guanylate cyclase
2010	24428 N	24428 NM_017356	=	activator 1B (retina), guanylate cyclase activator 1C, guanylate cyclase activator 1a
	<del> </del>			(reuna), hippocalcin-like 1, hypothetical protein FLJ11767, neurocalcin delta
			_	[Ronadicula Pote Highly cimilar to Tabada Long Protein HSP 90-beta (HSP 84)
		-		DKFZp761K0511 1 IH canione] Mus musculus class 1140 Crosses
2	100			Dartial Cds expressed socious O84429 hour Dartis Co. Co. Co. Co. Co. Co. Co. Co. Co. Co.
Š	V CM/07	ZU/W5 AA944397	e, ee	shock protein, 84 kDa 1, heaf shock protein, 86 kDa 1
				ESTs, Highly similar to HS9B_RAT Heaf shock protein HSP 90-beta (HSP 84)
				[R.norvegicus], ESTs, Highly similar to 746243 hypothetical protein
			d, ee, ff, jj.	UKF-Zp761K0511.1 [H.sapiens], Mus musculus, clone IMAGE:3584589, mRNA,
1335	16548 AI176546		圣	partial cds, expressed sequence C81438, heat shock 90kD protein 1, beta, heat
				Sirioxk protein, 84 kDa 1

TABLE	en i		11 17 17		
25	·	GenBank Avc		1000人人 自然計算し、	Atty: Ref: 44921-5090-01-WO/2105485
₽	G. GC D No.	N.	Model Code	Model Code Human Ho notogous Known Gene Name	minno Cheta Titla
	-				protein HSP 90-bet
				[R.norvegicus], ESTs, Hi	R.norvegicus], ESTs, Highly similar to T46243 hypothetical protein
				Sequence CR1438 heat	DNT-2p761R0311.1 [H.sapiens], KIKEN cDNA 1810014B01 gene, expressed
=		25104 AA685903	d, e, r	tumor rejection anticen (	codecies octros, reactations and protein 1, beta, neat snock protein, 84 kDa 1, tumor rejection anticen (no.96) 1 htmor rejection anticen
·				ESTs, Highly similar to H	ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84)
				[R.norvegicus], ESTs, Hi	R.norvegicus], ESTs, Highly similar to T46243 hypothetical protein
				DKFZp761K0511.1 [H.sa	DKFZp761K0511.1 [H.sapiens], RIKEN cDNA 1810014B01 gene, expressed
2603		18647 \$69316	٥	sequence C81438, heat	sequence C81438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1,
			5	tumor rejection antigen (c	tumor rejection antigen (gp96) 1, tumor rejection antigen gp96
				ESTs, Highly similar to H	ESTs, Highly similar to Human Translation Initiation Factor Eif1, Nmr, 29 Structures
1003		19093 AID58869	E	[H.sapiens], putative tran.	[H.sapiens], putative translation initiation factor, suppressor of initiator codon
			, ,,,	mutations, related sequence 1 (S. cerevisiae)	nce 1 (S. cerevisiae)
				ESTs, Highly similar to H	ESTs, Highly similar to Human Translation Initiation Factor Eiff, Nmr. 29 Structures
1504		19094 41232024		[H.sapiens], putative trans	[H.sapiens], putative translation initiation factor, suppressor of initiator codon
			S	mutations, related sequence 1 (S. cerevisiae)	nce 1 (S. cerevisiae)
		-		ESTS, Figniy similar to 14	ESTS, Fighry Similar to 148722 zinc finger protein - mouse [M.musculus], ESTS,
				Moderately similar to S47/	Moderately similar to S47073 finger protein HZF2, Krueppel-related [H.sapiens],
				Homo sapiens cDNA FLJ3	Homo sapiens cDNA FLJ31843 fis, clone NT2RP7000271, moderately similar to
				Mus musculus zinc finger	Mus musculus zinc finger protein 276 C2H2 type (Zfp276) mRNA, Homo sapiens
				cDNA: FLJ22829 fis, clone	cDNA: FLJ22829 fis, clone KAIA4075, highly similar to HSCH16FAA Homo sapiens
387	22868 A	22868 AA892391	<u>ئ</u>	mRNA for FAA protein, cili	mRNA for FAA protein, ciliary neurotropic factor, hypothetical protein BC016816,
			= 123	hypothetical protein FLJ20	hypothetical protein FLJ20531, zinc finger protein 354A, zinc finger protein 354B
				ESTS, Highly similar to 149	ESTS, Highly similar to 149523 Mouse primary response gene B94 mRNA, 3'end -
1105	22487	22487 41102578		mouse [M.musculus], RIKR	mouse [M.musculus], RIKEN cDNA 1600013K19 gene, hypothetical protein
	1017	מוסקסות		MGC16332, tumor necrosi	MGC16332, tumor necrosis factor, alpha-induced protein 2

TABLE 3	:3	) ;;	į.		AM AM TO SECURE
SEO		GenBank Acc			S Auy. Ket: 449Z1-5030-01-W0/Z105485
₽	CC ID	No.	Model Code Human Hom	ologous Known Gene Name	Human Homologous Sequence Cluster Title
				ESTs, Highly similar to I49	ESTs, Highly similar to 149636 DNA-binding protein - mouse [M.musculus], ESTs,
				Highly similar to OZF_HUN	Highly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs,
				Moderately similar to 1496.	Moderately similar to 149636 DNA-binding protein - mouse [M.musculus], ESTs,
				Weakly similar to OZF_HU	Weakly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs,
				Weakly similar to 2177_HL	Weakly similar to 2177_HUMAN ZINC FINGER PROTEIN 177 [H.sapiens], Homo
				sapiens mRNA, cDNA DKF	sapiens mRNA; cDNA DKFZp547C146 (from clone DKFZp547C146), Mus
				musculus, Similar to zinc fil	musculus, Similar to zinc finger protein 97, clone MGC:6111 IMAGE:3494875,
1410		A1480087		mRNA, complete cds, Panc	mRNA, complete cds, Pancreas zinc finger protein, see also D1Bda10/2, zinc finger
707	1	8. 86 A AODEODS	2 T	protein 177, zinc finger pro	protein 177, zinc finger protein 260, zinc finger protein 63, zinc finger protein 97
3	$\perp$	AASSOSSS	D	ESTs, Highly similar to 1584	ESTs, Highly similar to 158408 IK factor [H.sapiens], IK cytokine
				ESTs, Highly similar to 163	ESTs, Highly similar to 163168 gene Ube1x protein - rat (fragment) [R.norvegicus],
				ubiquitin-activating enzyme	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity
070		00707014		complementing), ubiquitin-	complementing), ubiquitin-activating enzyme E1, Chr X, ubiquitin-activating enzyme
0/0		101 80 AIU13160	n, v	E1, Chr Y 1, ubiquitin-activating enzyme E1-like	ating enzyme E1-like
2/0		7003607		ESTs, Highly similar to 1674	ESTs, Highly similar to 167428 retinoic acid receptor homolog - rat (fragment)
2		10,040,040,000	II, KK	(R.norvegicus), refinoid X re	R.norvegicus], retinoid X receptor gamma, retinoid X receptor, gamma
7/18		40850 AE046207	13	ESTs, Highly similar to 1674	ESTs, Highly similar to 167428 retinoic acid receptor homolog - rat (fragment)
7			J), KK	[R.norvegicus], retinoid X re	[R.norvegicus], retinoid X receptor gamma, retinoid X receptor, gamma
				ESUS, FIIGUIL SIMILATION SIMILATI	S_HUMAN I KANSFORMATION-SENSITIVE PROTEIN
				IEF SSP 3521 [H.sapiens],	IEF SSP 3521 [H.sapiens], ESTs, Weakly similar to small glutamine-rich
				tetratricopeptide repeat (TP)	tetratricopeptide repeat (TPR) containing protein (SGT) [Rattus norvegicus]
				I'K.norvegicusj, Mus muscul	IK.norvegicus), Mus musculus, clone MGC:27660 IMAGE:4527683, mRNA,
				complete cds, RIKEN cDNA	complete cds, RIKEN cDNA 5330427H01 gene, hypothetical protein FLJ12788,
		-		small glutamine-rich tetratric	small glutamine-rich tetratricopeptide repeat (TPR) containing protein (SGT), small
				glutamine-rich tetratricopept	glutamine-rich tetratricopeptide repeat (TPR)-containing, stress-induced
25.52	44040	44000 MM 420044		phosphoprotein 1, stress-inc	phosphoprotein 1, stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing
2000	1040	1	20	(protein)	
				ESTs, Highly similar to IF4E	ESTS, Highly similar to IF4E_HUMAN EUKARYOTIC TRANSLATION INITIATION
		<del></del>		racion 4E [H.sapiens], Ki	TACTOR 4E [H.sapiens], RIKEN CUNA 1300018P11 gene, RIKEN CDNA
1386	18848 A	18848 AI178816	C	Z/UUU9EU9 gene, eukaryoi initiafian fontan III.a	Z/ ՍՍՍԵՑԵՍՑ Gene, eukaryouc translation initiation factor 4E, eukaryotic translation
				IIIIIIIIIIII I AE-IIKE 3	

TABLI			a myan ariya	The state of the s		
SEO		GenBank Acc	上		**************************************	Atty. Ref. 44921-5090-01-WG/2105485
₽	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name		Human Homologous Sequence Cluster Title
						ESTs, Highly similar to IFM3_HUMAN INTERFERON-INDUCED TRANSMEMBRANE PROTEIN 3 [H.sapiens], ESTs, Highly similar to S17182
1218		21660 AI169751	e, K			interferon-induced protein 1-8U [H.sapiens], RIKEN cDNA 1110004C05 gene, interferon induced transmembrane protein 1 (9-27), interferon induced
						transmembrane protein 3 (1-8U) ESTs, Highly similar to IFM3_HUMAN INTERFERON-INDUCED
						TRANSMEMBRANE PROTEIN 3 [H.sapiens], ESTs, Highly similar to S17182 interferon-induced protein 1-811ft saniens). BIKEN AND 444000405
2665		21657 X61381	d, j, k, m, y, z, kk		- <b>!</b> - <b>!</b>	interferon induced transmembrane protein 1 (9-27), interferon induced
						transmembrane protein 3 (1-8U) ESTs, Highly similar to JC4577 transcription elongation factor 11 IH sanions   ESTs
	_					Highly similar to Transcriptional Elongation Factor Sii [H.sapiens], ESTs, Weakly
					<u> </u>	similar to JC5430 transcription elongation factor S-II-T1, testis-specific - mouse
4076	7	0500571				Iwnusculusi, Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFIISH Homo sapiens mRNA for transcription elonoation factor TEIIS - DHD
12/0	70417	Z140 A11/22/2	u u		fi	iger protein 3, transcription elongation factor A (SII). 3
					בל הל	ESTs, Highly similar to JE0190 polyubiquitin unit [H.sapiens], ESTs, Highly similar to UQHUC polyubiquitin 9 [H.sapiens], Homo sapiens, Similar to orosomucoid 1
2560	3015N	3015 NM_138895	aa, bb		0 <	clone MGC:24263 IMAGE:3934516, mRNA, complete cds, expressed sequence
					<b>4</b>	ALUSSZ68, ubiquitin B, ubiquitin C
	-				ш :	ESTs, Highly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-
					<u> </u>	HYDROXYDEHYDROGENASE [H.sapiens], ESTs, Weakly similar to
					ix	HYDROXYDEHYDROGENASE IH. sapiens]. Homo sapiens, clone IMAGE-4793702
322	2846 A	2846 AA875639	, co		E	mRNA, Mus musculus, clone MGC:32469 IMAGE:5050433, mRNA, complete cds,
					5 ŭi	Gystallin, zeta, tatty acid synthase, quinone oxidoreductase homolog ESTs. Highly similar to I CK MOUSE PROTO ONCOCENE TYBOSINE BROTEN
					<u>X</u>	KINASE LCK [M.musculus], RIKEN cDNA 8430404F20 gene, hemopojetic cell
	-				<u> </u>	kinase, lymphocyte protein tyrosine kinase, lymphocyte-specific protein tyrosine
1890	1258N	1258 NM 013185			<u>X</u>	kinase, src-related kinase lacking C-terminal regulatory tyrosine and N-terminal
						III) Signation sites

TABLE3	щ Э		3 . (4	TO THE PARTY OF TH
SEO		GenBank Acc.		1
Ω	GEGC ID No.	No.	Model Code Human Hom	luman Homologous Known Gene Name Human Homologous Sequence Chister Title
				ESTs, Highly similar to MEM2 RAT MEMBRANE-ASSOCIATED PROTEIN HEM-2
				[R.norvegicus], ESTs, Highly similar to NCP1_RAT Nck-associated protein 1 (NAP 1) (0125Nap1) (Membrang-associated protein HEM. 9) to represent the new protein
1014		8729 AI059485	w, x	associated protein 1
				ESTs, Highly similar to MXI1_RAT MAX interacting protein 1 (MXI1 protein)
				[R.norvegicus], ESTs, Moderately similar to MXI1_RAT MAX interacting protein 1
				(MX11 protein) [R.norvegicus], Homo sapiens cDNA FLJ32472 fis, clone
				SKNMC2000356, highly similar to Mus musculus Max-interacting transcriptional
2583		335 NM 145773	_ =	repressor (Mad3) mRNA, MAX interacting protein 1, Max interacting protein 1, likely
			2 2	ortholog of mouse Max dimerization protein 3
				ESTs, Highly similar to MX/1_RAT MAX interacting protein 1 (MXI1 protein)
				[R.norvegicus], ESTs, Weakly similar to MXI1_RAT MAX interacting protein 1 (MXI1
1884		3465 NM 013160	-	protein) [R.norvegicus], MAX dimerization protein, MAX interacting protein 1, Max
		001010	- (=)	interacting protein 1
				ESTS, TIGITIY SIMILIATIO INTERPENATI INVOSIMMEANY CHAIM, TICHTIMUSCIE TYPE A (CEITURA)
				myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A)
				I'K.norvegicus), ESTs, Highly similar to MYHA_MOUSE Myosin heavy chain,
				nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy
				Chain-B) (NMMHC-B) [M.musculus], ESTs, Weakly similar to MYH9_RAT Myosin
				heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle
				(myosin heavy chain-A) (NMMHC-A) [R.norvegicus], ESTs, Weakly similar to
				MYHA_MOUSE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy
				Chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B) [M.musculus],
				RIKEN cDNA 2400004E04 gene, RIKEN cDNA 5730504C04 gene, TGFB1-induced
				anti-apoptotic factor 1, myosin heavy chain IX, myosin, heavy polypeptide 9, non-
1892		1970 MM 042404		muscle, protein tyrosine phosphatase, receptor-type, F interacting protein, binding
700		1414 015134	66	protein 2
· <u> </u>				ESTs, Highly similar to NTC1_RAT Neurogenic locus notch homolog protein 1
				precursor (Notch 1) [R.norvegicus], Homo sapiens cDNA FLJ25053 fis, clone
		-		CBL04266, Notch gene homolog 1, (Drosophila), Notch homolog 1, translocation-
228	13802 A	13802 AAR58853	E	associated (Drosophila), hypothetical protein similar to ankyrin repeat-containing
		1	11 11 12	priotein AKR1, likely homolog of rat kinase D-interacting substance of 220 kDa

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Ų.		RanBank Acc		一、一、一、一、一、一、一、一、一、一、一、一、一、一、一、一、一、一、一、	Atty Bef 44024 5000 04 WOJ9465425
, 	SLGC DINO	No.	Model Cool Unast	1. 「「「「「「」」」「「」」「「」」「「」」「「」」「「」」「「」」「「」」「	
1			anon lanoivi	nologous Known Gene Name	9
	-			ESTS, Highly similar to P2CB_HUMAN PROTEIN PHOSPHATASE 2C BETA	OTEIN PHOSPHATASE 2C BETA
				ISOFORM [H.sapiens], ESTs, Weakly similar to P2CB_HUMAN PROTEIN	lar to P2CB_HUMAN PROTEIN
				PHOSPHATASE 2C BETA ISOFORM [H.sapiens], Homo sapiens cDNA FLJ30553	apiens], Homo sapiens cDNA FLJ30553
				its, clone BRAWH2003689, highly similar to Mus musculus clone mouse1-9 putative	o Mus musculus clone mouse1-9 putative
				protein phosphatase type 2C mRNA, protein phosphatase 1B (formerly 2C),	in phosphatase 1B (formerly 2C),
2355		25529 NM 033096	c	magnesium-dependent, beta isoform, protein phosphatase 1B, magnesium	in phosphatase 1B, magnesium
				dependent, beta isoform	
				ESTs, Highly similar to PZCB_HUMAN PROTEIN PHOSPHATASE 2C BETA	OTEIN PHOSPHATASE 2C BETA
				ISOFORM [H.sapiens], ESTs, Weakly similar to P2CB_HUMAN PROTEIN	ar to P2CB_HUMAN PROTEIN
				PHOSPHATASE 2C BETA ISOFORM [H.sapiens], Homo sapiens con Fi 130553	apiens], Homo sapiens cDNA FI (30553
			_	fis, clone BRAWH2003689, highly similar to Mus musculus clone mouse1-9 purative	Mus musculus clone mouse1-9 putative
				protein phosphatase type 2C mRNA, protein phosphatase 1B (formerly 2C)	n phosphatase 1B (formerly 2C)
2355		25569 NM 033096		magnesium-dependent, beta isoform, protein phosphatase 1B. magnesium	in phosphatase 1B. magnesium
	1			dependent, beta isoform	
				ESTs, Highly similar to PZCB_HUMAN PROTEIN PHOSPHATASE 2C BETA	TEIN PHOSPHATASE 2C BETA
				ISOFORM [H.sapiens], ESTs, Weakly similar to P2CB_HUMAN PROTEIN	ir to P2CB_HUMAN PROTEIN
				PHOSPHATASE 2C BETA ISOFORM [H.sapiens], Homo sapiens cDNA FLJ30553	piens], Homo sapiens cDNA FLJ30553
				fis, done BRAWH2003689, highly similar to Mus musculus done mouse1-9 putative	Mus musculus clone mouse1-9 putative
				protein phosphatase type 2C mRNA, protein phosphatase 1B (formerly 2C),	phosphatase 1B (formerly 2C),
2355		19148 NM_033096		magnesium-dependent, beta isoform, protein phosphatase 1B, magnesium	n phosphatase 1B, magnesium
				Uependent, beta isotom ESTs Hinhly similar to Dyda Dydan Dydan	
-				I'll sanions   ESTS Moderately STEEN OF A DENYTRIE-BINDING PROTEIN	ADENYLA! E-BINDING PROTEIN 1
				It is adviced by it is not be in the interest of the interest	CLEOLIN [M.musculus], ESTs,
				Woderately similar to PAB1 MOUSE POLYADENYLATE-BINDING PROTEIN 1	DENYLATE-BINDING PROTEIN 1
				[M.musculus], ESTs, Weakly similar to NUCL_HUMAN NUCLEOLIN [H.sapiens],	HUMAN NUCLEOLIN [H.sapiens],
				ESTS, Weakly similar to PAB1 MOUSE POLYADENYLATE-BINDING PROTEIN 1	YADENYLATE-BINDING PROTEIN 1
				[M.musculus], Nucleolin, RIKEN cDNA 4932702K14 gene, nucleolin, pigpen, poly A	702K14 gene, nucleolin, pigpen, poly A
2540	19840N	19840 NM_134353   I		Dinding Protein, cytoplasmic 1, poly(A) binding protein, cytoplasmic 3, poly(A)	g protein, cytoplasmic 3, poly(A)
				Dinding protein, cytoplasmic, pseudogene 2	
			_	ES18, Highly similar to PAB1_HUMAN POLYADENYLATE-BINDING PROTEIN 1	ADENYLATE-BINDING PROTEIN 1
2464	18025 N	18025 NM 053989 W	×××	[IH.sapiens], RIKEN cDNA 2810411E22 gene, RIKEN cDNA 4432411E13 gene.	, RIKEN cDNA 4432411E13 gene.
		1		KIKEN cDNA 4930431E10 gene	

TABLE 3	3		The Marie Co.	は特別の任何を持ち、	AND PAINT AND PAINT AND AND AND AND AND AND AND AND AND AND
SEO		GenBank Acc			
	GLGC.ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2235		12638 NM_031099	е		ESTs, Highly similar to PC4210 ribosomal protein L5 [H.sapiens], ribosomal protein L5
2235		12639 NM_031099	g		ESTs, Highly similar to PC4210 ribosomal protein L5 [H.sapiens], ribosomal protein L5
					ESTs, Highly similar to PMX1_MOUSE Paired mesoderm homeobox protein 1 (PRX 1) (Paired related homeobox protein 1) (Homeobox protein MhoX) (Homeobox
					protein K-2) (Rhox) [R.norvegicus], ESTs, Weakly similar to PMX1_MOUSE Paired mesoderm homeobox protein 1 (PRX-1) (Paired related homeobox protein 1)
					(Homeobox protein MhoX) (Homeobox protein K-2) (Rhox) [R.norvegicus], paired
896		72 12 A1014065	85		mesoderm homeo box 1, paired related homeobox 1, paired related homeobox protein
					ESTs, Highly similar to RASH_RAT TRANSFORMING PROTEIN P21/H-RAS-1 (C-H-DAS) ID propositional Language Communications of the communic
					sarcoma virus oncogene, mayer nat sarcoma oncogene, subgroup n, marvey rat sarcoma
					viral oncogene homolog, clone MGC:19390 IMAGE:3152667, mRNA, complete cds,
1300	4445	4445 AH75466			related RAS viral (r-ras) oncogene homolog, v-Ha-ras Harvey rat sarcoma viral
					ESTs, Highly similar to RL26_HUMAN 60S RIBOSOMAL PROTEIN L26
	· <del>-</del> ······				[H.sapiens], ESTs, Highly similar to S33713 ribosomal protein L26, cytosolic
438	185.42	185.42 4803.403			[H.sapiens], ESTs, Moderately similar to RL26_HUMAN 60S RIBOSOMAL
3	7	20000	מ		ESTs, Highly similar to RL26 HUMAN 60S RIBOSOMAL PROTEIN 1.26
					[H.sapiens], ESTs, Highly similar to S33713 ribosomal protein L26, cytosolic
					[H.sapiens], ESTs, Moderately similar to RL26_HUMAN 60S RIBOSOMAL
2646	18:41 X14671	X14671	9		PROTEIN L26 [H.sapiens], ribosomal protein L26, ribosomal protein L26-like 1
					ESTs, Highly similar to RS26_HUMAN 40S RIBOSOMAL PROTEIN S26
00,	3		•		[H.sapiens], Homo sapiens, clone IMAGE:4100953, mRNA, polymerase (RNA) II
1803	CLS	4775L0 MNICL8	lg, h, l, w, x		(DNA directed) polypeptide D, ribosomal protein S26

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ָרָר מָרָרָ		GenBank Acc.		The second secon	Atty. Ref: 44921-5090-01-WO/2105485
9	GLGC ID No.	No.	Model Code	nologous Segmence Cluster	
	-			ESTs, Highly similar to S12520 core protein A1 [H.s. heterodeneous ribonuclear particle protein A1 III 200	ESTs, Highly similar to
		,		to heterogeneous ribonuclear particle protein A1 [H.sapiens]. Mis misculus Similar	Sols, Moderately similar Mis misculus Similar
				to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437, mRNA, complete	6437, mRNA, complete
				cds, RIKEN cDNA 2610510D13 gene, RIKEN cDNA 4930547K05 gene,	7K05 gene,
81	15011	15011 AA799893	뫄	neterogeneous nuclear ribonucleoprotein A1, heterogeneous nuclear	s nuclear
				ESTs, Highly similar to S57449 fusca protein homolog - rat IR norveoloris   ESTs	Ruorveolous Este
				Weakly similar to S57449 fusca protein homolog - rat IR.norvegicus]. G protein	vegicus). G profein
				pathway suppressor 1, Mus musculus, Similar to G protein pathway suppressor 1.	athway suppressor 1.
2457	6357	6357 NM_053969	<b>o</b>	clone MGC:7191 IMAGE:3481979, mRNA, complete cds, RIKEN cDNA	KEN cDNA
				Z4VUVUDATB gene	
				Construction of the second of	s, Weakly similar to
				Socios trin protein (H.sapiens), Homo sapiens cDNA FLJ31994 fis, clone	994 fis, clone
817	18691	18691 AI010605	Q	N12RP/009215, Homo sapiens, Similar to RIKEN cDNA 1810054013 gene, clone	0054O13 gene, clone
				IMAGE: 3845933, mRNA, partial cds	
				ES18, Highly similar to S68215 Mas 20 protein [H.sapiens], Homo sapiens cDNA	lomo sapiens cDNA
				rLJ3U361 fis, clone BRACE2007764, RIKEN cDNA 1810060K07 gene, RIKEN	K07 gene, RIKEN
2592	10544	10544 NM 152935	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	CDNA 4930553D19 gene, translocase of outer mitochondrial membrane 20 (yeast)	membrane 20 (yeast)
-		1	a la la la	Bolomon	•
			_	ESTs, Highly similar to S68418 protein phosphatase 1M chain M110 isoform - rat	n M110 isoform - rat
				[R.norvegicus], ESTs, Weakly similar to S68418 protein phosphatase 1M chain	phatase 1M chain
				M110 isoform - rat (fragment) [R.norvegicus], expressed sequence Al449786.	lence Al449786.
		-		expressed sequence AI746547, leukocyte receptor cluster (LRC) member 3 myosin	3C) member 3. myosin
8	20982 A	20982 AA799657	:: ''e '''	phosphatase, target subunit 1, protein phosphatase 1, regulatory (inhibitor) subunit	ory (inhibitor) subunit
				124	

<b>ITABLE 3</b>	65	1,	Section Assets	The state of the s	
CHO		Conbont Ago		から 一般の 一般の 一般の 一般の 一般の 一般の 一般の 一般の 一般の 一般の	Ath Ref 44091-5000-04 MOINGINE AND
	GLGC ID No.	No.		OMO	10403 I-WO/Z 103463
				ESTS, Highly similar to S70642 ubiquitin ligase Nedd4 - rat (tragment)	at (tragment)
				[R.norvegicus], ESTs, Moderately similar to S70642 ubiquitin ligase Nedd4 - rat	uitin ligase Nedd4 - rat
				(fragment) [R.norvegicus], Mus musculus, clone MGC:12070 IMAGE:3708271,	070 IMAGE:3708271,
-				mRNA, complete cds, RIKEN cDNA 1700056O17 gene, RIKEN cDNA 5830462N02	RIKEN cDNA 5830462N02
				gene, expressed sequence AW212605, neural precursor cell expressed,	cell expressed,
				developmentally down-regulated 4, neural precursor cell expressed	expressed,
1388		23043 41178968	٠.4	developmentally down-regulated gene 4a, thyroid hormone receptor interactor 12	le receptor inferactor 12
		0000	2	ubiquitin profein ligase E3A	Ī
				ESIS, Highly similar to SL56_KAT SODIOM-DEPENDENT MOLTIVITAMIN	LIMOLITYITAMIN
				I KANSPORTER (NA(+)-DEPENDENT MULTIVITAMIN TRANSPORTER)	RANSPORTER)
				[R.norvegicus], ESTs, Highly similar to SL56_RAT Sodium-dependent multivitamin	n-dependent multivitamin
	<del>.</del>	•		transporter (Na(+)-dependent multivitamin transporter) [R.norvegicus]. Homo	norvegicus], Homo
				sapiens cDNA FLJ14949 fis, clone PLACE2000341, highly similar to Homo sapiens	similar to Homo sapiens
	_			sodium-dependent multivitamin transporter (SMVT) mRNA, Homo sapiens mRNA.	V. Homo sapiens mRNA:
				cDNA DKFZp434F152 (from clone DKFZp434F152), solute carrier family 5 (sodium	e carrier family 5 (sodium
2508	15 12 1	15 12 NW 130746		iodide symporter), member 5, solute carrier family 5 (sodium-dependent vitamin	m-dependent vitamin
T		T	3	transporter), member 6	
				ESIS, Highly similar to SLSE_KAT SODIOM-DEPENDENT MOLTIVITAMIN	MOLITVITAMIN
				I RANSPORTER (NA(+)-DEPENDENT MULTIVITAMIN TRANSPORTER)	(ANSPORTER)
				[R.norvegicus], ESTs, Highly similar to SL56_RAT Sodium-dependent multivitamin	-dependent multivitamin
		-		transporter (Na(+)-dependent multivitamin transporter) [R.norvegicus], Homo	norvegicus], Homo
				sapiens cDNA FLJ14949 fis, clone PLACE2000341, highly similar to Homo sapiens	similar to Homo sapiens
				Sodium-dependent multivitamin transporter (SMVT) mRNA, Homo sapiens mRNA,	, Homo sapiens mRNA;
				CDNA DKFZp434F152 (from clone DKFZp434F152), solute carrier family 5 (sodium	carrier family 5 (sodium
2508	1503 N	1503 NM 130746	7	iodide symporter), member 5, solute carrier family 5 (sodium-dependent vitamin	n-dependent vitamin
3	2	T		transporter), member 6	
				ECT. Linkly similar to TOOTOO.	
	_			to Teed, but I than the property of the chain [H.sapiens], ESTs, Highly similar	is), ESTs, Highly similar
				12410129E14 GENE CINE AGADAZKOS GENE DELATION (I BETATATO) [K.norvegicus], RIKEN CONA	egicus), RIKEN cDNA
707	0.000			gene, Rat mRNA for beta-tubulin T beta 15 expressed segmence A1454500	4 CDIVA 4350342GU3
2007	ZZAZINI	22972 NM_145/78   e		expressed sequence C79445, tubulin, heta 3 tubulin gamma 1	GIICE AI401302,
				F. Company Carrier Community Communi	_

TABIL	20			
יאפרני א	2			7. 公共等に対し、 このはない
ე □ □	GLGC ID No.	GenBank Acc.	Model Code Human Hom	tuman Homologous Known Gene Name. Himian Homologous Secuence Chiefer THG
				ESTs, Highly similar to T42/31 atrophin-1 related Weakly similar to dentatoruhral nallidoluwsian atro
2449		385 NM_053885	b, o, u, v, ee, ff. kk	glutamic acid dipeptide (RE) repeats, dentatorubral pallidoluysian atrophy,
1201		11346 Al145991	Ę; K	ESTS, Highly similar to T46266 hypothetical protein DKFZp761A179.1 [H.sapiens],
446		19411 AA893667	cc, dd	ESTS, Highly similar to T46904 hypothetical protein DKFZp761D081.1 [H.sapiens], Homo sapiens cDNA: FLJ21587 fis, clone COL06946, likely ortholog of mouse
489		16753 AA900474	w, x	ESTs, Highly similar to T50619 hypothetical protein DKFZp762M136.1 [H.sapiens], hypothetical protein DKFZp762M136.1 [H.sapiens],
2192		11628 NM_024383	q	ESTs, Highly similar to TRANSCRIPTION FACTOR HES-5 [M.musculus], hairy and enhancer of solid (Drosonhila) hampled 2 hairy and carbonacters.
				ESTs, Highly similar to TVR/UR1 transforming protein rap1b [H.sapiens], ESTs, Weakly similar to GTP-binding protein ROC2 [M.musculus], Mus musculus, Similar to AS-like settons conjuded county.
2536		16456 NM_134346	:=	MAGE:4483442, mRNA, complete cds, RAP1B, member of RAS oncogene family, RAP2B, member of RAS-like, estrogen-regulated, growth-inhibitar
2256	15052	15052 NM_031136	c, w, x, aa, bb	ESTS, Highly similar to TYB4 MOUSE THYMOSIN BETA-4 [M.musculus], ESTs, Moderately similar to PC4259 ferritin associated protein [H.sapiens], Homo sapiens cDNA FLJ31414 fis, clone NT2NE2000260, weakly similar to THYMOSIN BETA-4, thumosin beta 4 X chamasana
1202	11363/	11363 A1145997	ų.	ESTs, Highly similar to UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B [M.musculus], RAD23 homolog B (S. cerevisiae), RAD23b homolog (S. cerevisiae)
2428	14015 N	14015 NM_053770	lh	ÈSTS, Moderately similar to Arg/AbI-interacting protein ArgBP2 [Rattus norvegicus] [R.norvegicus], ESTS, Weakly similar to Arg/AbI-interacting protein ArgBP2 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 2010203003 gene, SH3-domain protein 5 (ponsin), sorbin and SH3 domain containing 1

<b>TABLE 3</b>	: :	٠.	Š	7 Trans.	
SEO	L	GenBank Acc.			15.48F
<u>e</u>	GLGC ID No.	No.	Model Code Human Hon	iologous Kriown Gene Name	3
2428		14017 NM_053770	돌		cus] Ittus ein 5
1693		381 L00124	b, l, m	ESTs, Moderately similar to elastase 3B, pancreatic [Mus musculus] [M.musculus], ESTs, Weakly similar to EL2 MOUSE ELASTASE 2 PRECURSOR [M.musculus], ESTs, Weakly similar to EL2_RAT Elastase 2 precursor [R.norvegicus], elastase 2, elastase 2A, elastase 3A, pancreatic (professor E), elastase 2A.	us],
2222		17727 NM_031043	O	ESTs, Moderately similar to glycogenin 2 [Homo sapiens] [H.sapiens], glycogenin, glycogenin, 2 [Homo sapiens] [H.sapiens], glycogenin, glycogenin, 2 [Homo sapiens], glycogenin, glycogeni	Ė,
2138		9541 NM_022542	Ď	ESTs, Moderately similar to rhoB gene [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to rhoB gene [Rattus norvegicus] [R.norvegicus], Mus musculus, clone MGC:29297 IMAGE:5003249, mRNA, complete cds, RIKEN cDNA 5830400A04 gene, ras homology B (RhoR), ras homology can formally manner than the contraction of	s,
782	21596	21596 Al009168	j, K	ESTs, Moderately similar to rhoB gene [Rattus norvegicus] [R.norvegicus], member B musculus, clone MGC:29297 IMAGE:5003249, mRNA, complete cds, RIKEN cDNA 5830400A04 gene, cell division cycle 42 homolog (S. cerevisiae), ras homolog B (RhoB), ras homolog gene family, member B, ras homolog gene family, member U,	ă j
2348	18898 N	18898 NM_031985	:=	ESTs, Moderately similar to ribosomal protein S6 kinase, 70kD, polypeptide 2; S6 kinase 270kD, polypeptide 2; S6 kinase 2 [Mus musculus] [M.musculus], RIKEN cDNA 2610318115 gene, ribosomal protein S6 kinase, 70kD, polypeptide 1, ribosomal protein S6 kinase, 70kD, polypeptide 1, ribosomal protein S6 kinase, 70kD,	क छ
2348	18899 N	18899 NM_031985	66	ESTs, Moderately similar to ribosomal protein S6 kinase, 70kD, polypeptide 2; S6 kinase, 70kD, polypeptide 2; S6 kinase 2 [Mus musculus] [M.musculus], RIKEN cDNA 2610318115 gene, ribosomal protein S6 kinase, 70kD, polypeptide 1, ribosomal protein S6 kinase, 70kD, polypeptide 1, ribosomal protein S6 kinase, 70kD,	(C) #
215	16934A	16934 AA851403	a	ESTs, Moderately similar to RIKEN cDNA 2900010i05 [Mus musculus] [M.musculus], NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI), RIKEN cDNA 2900010i05 gene	1

TABLE 3		A 3.		一般なるできるとはない こうかん かんしょう かんかん こうかん	STATE OF THE PROPERTY OF THE P
SEO		GenBank Acc.			8
₽	00 00 00 00 00 00 00 00 00 00 00 00 00	No.	Model Code	Model Code Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
		!			ESTs, Moderately similar to CO1B_RAT Coronin 1B (Coronin 2) [R.norvegicus],
					Mus musculus, Similar to coronin, actin binding protein, 2A, clone IMAGE:4984475,
1323		13339 AI176308	ψ. •		mRNA, partial cds, coronin, actin binding protein 1B, coronin, actin binding protein
	1				IC, Ilypouleucal protein DNF29/62/166 ESTs Moderately similar to DID UTIMAN PID PROTEIN 111
					dene product RIKEN CONA 0810000114 cm. DIVEN ENV 484000109
					gone product, ranch control of tought forth they gene, Rincin control 18100433112 gene, TSC-29-like transforming grount forth they did included tought for they are
1179		17402 AI137553	ee, ff		growth factor beta-stimulated protein TSC-22
					ESTs, Moderately similar to DIP HUMAN DIP PROTEIN IH saniens! KIAAN669
					gene product, RIKEN cDNA 0610009M14 gene, RIKEN cDNA 1810043.112 gene.
			a, p, q, z,		TSC-22-like, transforming growth factor beta 1 induced transcript 4. transforming
1854	174.31	174.31 NM_013043	ee, ff, kk		growth factor beta-stimulated protein TSC-22
					ESTS, Moderately similar to HB2D_RAT RT1 CLASS II HISTOCOMPATIBILITY
					ANTIGEN, D-1 BETA CHAIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to
					HB2D_RAT RT1 CLASS II HISTOCOMPATIBILITY ANTIGEN, D-1 BETA CHAIN
					PRECURSOR [R.norvegicus], Rattus norvegicus Class II MHC RT1.D(a) beta chain
				-	precursor (RT1.D(a)) mRNA, complete cds, Rattus norvegicus Class II MHC
2652	4E 4E VESOE4	/E00E4	= = = = = = = = = = = = = = = = = = = =		RT1.D(n) beta chain precursor (RT1.D(n)) mRNA, complete cds, major
7007		V33034	CC, dd, II		histocompatibility complex, class II, DR beta 5
					ES IS, Moderately similar to HB2D_RAT RT1 CLASS II HISTOCOMPATIBILITY
					ANTIGEN, D-1 BETA CHAIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to
	-				HB2D_RAT RT1 CLASS II HISTOCOMPATIBILITY ANTIGEN, D-1 BETA CHAIN
					PRECURSOR [R.norvegicus], Rattus norvegicus Class II MHC RT1.D(a) beta chain
		_			precursor (RT1.D(a)) mRNA, complete cds, Rattus norvegicus Class II MHC
0300	707607	,,,			RT1.D(n) beta chain precursor (RT1.D(n)) mRNA, complete cds, major
7007	PCUSCY OI /OI	4202C	S		histocompatibility complex, class II, DR beta 5
					ESTs, Moderately similar to JC7220 nuclear protein SR-25 [H.sapiens], HSVI
ç	00007				binding protein, SRp25 nuclear protein, expressed sequence AA408210, expressed
302	187791	162US AA892318	s, t		sequence AA408365

TABLE 3	١.				107 10701011100
03	ŀ	GenBank Aug		· · · · · · · · · · · · · · · · · · ·	J-01-W0/Z105485
Œ	ည	D N,	Model Code	Model Code Human Ho nologous Known Gene Name Human Homologous Sequence Cluster Title	
					ij, ESTs, Weakly ulusj, ESTs,
				Weakly similar to JE0343 terf protein - rat [R.norvegicus], butyrophilin, subfamily 1, Imember A1. expressed sequence AA414909 expressed sequence AW538801 rat	ilin, subfamily 1,
854		7120 AI012393	>	finger protein, tripartite motif protein 17, tripartite motif-containing 17	7
				ESTs, Moderately similar to KHL1_MOUSE Ketch-like protein 1 [M.musculus],	.musculus],
				ESIS, Weakly Similar to ENCI_MOUSE ECTODERM-NEURAL CORTEX-1 [DROTEIN (ENCI 1) M minorities ESTS Models similar to 1995 1 M minorities 1 ESTS Models similar to 1995 1 M minorities 1 ESTS MODELS 1995 1 M M M M M M M M M M M M M M M M M M	ORTEX-1
				nrofelin (Krollike profein 23) (Sermein) 18 popuenius (VA 446) matri Maria (Krollike profein 23) (Sermein) 18 popuenius (VA 446) matri Maria	VAI Keich-related
				musculus, clone MGC:28950 IMAGE:4235202, mRNA, complete cds. RIKFN cDNA	proteint, mus
9			;	1300013C10 gene, expressed sequence AL022703, kelch-like 1 (Drosophila),	rosophila),
2463		13460 MM 05/191	d, ee, ff	sarcomeric muscle protein, speckle-type POZ protein	
				ESTs, Moderately similar to KHL1_MOUSE Kelch-like protein 1 [M.musculus],	musculus],
				ESTs, Weakly similar to ENC1_MOUSE ECTODERM-NEURAL CORTEX-1	RTEX-1
				PROTEIN (ENC-1) [M.musculus], ESTs, Weakly similar to KRP1_RAT Kelch-related	AT Kelch-related
				protein 1 (Kel-like protein 23) (Sarcosin) [R.norvegicus], KIAA1842 protein, Mus	protein, Mus
				musculus, clone MGC:28950 IMAGE:4235202, mRNA, complete cds, RIKEN cDNA	ls, RIKEN cDNA
2000		114 057404	5	1300013C10 gene, expressed sequence AL022703, kelch-like 1 (Drosophila),	rosophila),
7400		TRL/CO WININGSCI	ee, π	sarcomeric muscle protein, speckle-type POZ protein	
				ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE	XIDASE
				PRECURSOR [H.sapiens], ESTs, Moderately similar to LYOX_RAT Protein-lysine 6-	Protein-lysine 6-
1115	2100	8190 41490353	4	oxidase precursor (Lysyl oxidase) [R.norvegicus], Lysyl oxidase, lysyl oxidase, lysyl	yl oxidase, lysyl
2	0 0			oxidase-like 2, lysyl oxidase-like 4	
				ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE	XIDASE
				PRECURSOR [H.sapiens], ESTs, Weakly similar to LYOX_RAT Protein-lysine 6-	tein-lysine 6-
777	20200			oxidase precursor (Lysyl oxidase) [R.norvegicus], Lysyl oxidase, lysyl oxidase, lysyl	yl oxidase, lysyl
1	700077	22300 AAGUU844	6	oxidase-like, lysyl oxidase-like 1, lysyl oxidase-like 2	
				ESTS, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE	XIDASE
				PRECURSOR [H.sapiens], ESTs, Weakly similar to LYOX_RAT Protein-lysine 6-	tein-lysine 6-
252	22385 A	22385 AA859805		oxidase precursor (Lysyl oxidase) [R.norvegicus], Lysyl oxidase, lysyl oxidase, lysyl	yl oxidase, lysyl
		]	3 6 6	OXIGASE-IIKE, IYSYI OXIGASE-IIKE 1, IYSYI OXIGASE-IIKE 2	

TABLE	3		The state of the s	The state of the s	
SEO		IGenBarik Acc.	_	大き 一大き 一大き 一大き 一大き 一大き 一大き 一大き 一大き 一大き 一	Atty, Ret, 44921-5090-01-WO/2105485
<u>.</u>	GLGC ID No.	No.	Model Code Human Hom	ologous Known Gene Name	· · · · · · · · · · · · · · · · · · ·
				ESTs, Moderately similar to NUCLEOLIN [M.muscutus], ESTs, Weakly similar to A35804 nucleolin [H.sapiens], ESTs, Weakly similar to NUCL_HUMAN NUCLEOLIN	sculus), ESTs, Weakly similar to iliar to NUCL_HUMAN NUCLEOLIN
1787		8820 NIM 042740		It is apticible, ESTS, weakly similar to NOCL_RAT Nucleotin (Protein C23) [R.norvegicus], RIKEN cDNA 1200009A02 gene, eukaryotic translation initiation	Nucleolin (Protein C23) eukaryotic translation initiation
2		64/710 NIN	J, K, IIII, KK	factor 3, subunit 4 (defta, 44 kDa), nucleolin, pigpen   ES1s, Moderately similar to P4H1_RA1 Prolyf 4-hydroxylase alpha-1 subunit	ven hydroxylase alpha-1 subunit
				precursor (4-PH alpha-1) (Procollagen-proline, 2-oxoglutarate-4-dioxygenase alpha-	oxoglutarate-4-dioxygenase alpha-
				i subunit) įk.norvegicusį, homo sapiens, done iMAGE:3162218, mRNA, partial cds, RIKEN cDNA 4933406E20 gene, procollagen-proline, 2-oxoglutarate 4-	MAGE:3162218, mRNA, partial n-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide, procollagen-proline, 2-	ypeptide, procollagen-proline, 2-
				Oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide,	e), alpha II polypeptide,
				proceilageir-proline, z-oxogiutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I, proceilagen-proline, 2-oxogiutarate 4-dioxygenase (proline 4-	e (proline 4-hydroxylase), alpha 4-dioxygenase (proline 4-
1483		233-04 AI231310	ee, ff	hydroxylase), alpha polypeptide II	
				ESTs, Moderately similar to PAB1 MOUSE POLYADENYLATE-BINDING PROTEIN	ADENYLATE-BINDING PROTEIN
				1 [M.musculus], ESTs, Weakly similar to PAB1 MOUSE POLYADENYLATE-	OUSE POLYADENYLATE-
				BINDING PROTEIN 1 [M.musculus], RIKEN cDNA 4932702K14 gene, poly A	4 4932702K14 gene, poly A
1536	i	15485 AI233870	hh h	binding protein, cytoplasmic 1, poly(A) binding protein, cytoplasmic 4 (inducible (form)	otein, cytoplasmic 4 (inducible
				ESTS, Moderately similar to PRS6_HUMAN 26S PROTEASE REGULATORY	PROTEASE REGULATORY
1663		1884 D50695	si si	SUBUNIT 6B [H.sapiens], proteasome (prosome, macropain) 26S subunit, ATPase,	macropain) 26S subunit, ATPase,
				ESTS, Moderately similar to RBMA_RAT RNA-BINDING PROTEIN 107RNA	ADING PROTEIN 10 (RNA
				BINDING MOTIF PROTEIN 10) (S1-1 PROTEIN) [R.norvegicus], Homo sapiens	(R.norvegicus), Homo sapiens
				cDNA FLJ10100 fis, clone HEMBA1002469, moderately similar to DXS8237E	erately similar to DXS8237E
				PROTEIN, Mus musculus, Similar to RNA binding motif protein 10, clone MGC:7826	motif protein 10, clone MGC:7826
862	6489	6489 AI012636		IMAGE:3500403, mRNA, complete cds, RNA binding motif protein 10, S1-1 protein	ing motif protein 10, S1-1 protein
		0007		TOM INCE	77.10.10
				chain precursor - rat [R.norvegicus], histocompatibility 2, O region aloha locus.	ompatibility antigen K11-B alpha lility 2, O region alpha locus.
<u>a</u>	14968 K02815		S	major histocompatibility complex, class II, DO alpha	

	TABLE 3	m		ter set in the		
CLGC ID   No.   Model Code   Human Homologous Knöwn, Gene Namie   Human Hemologous Sequeince	SEO		GenBank' Acc		Service Control of th	ath : Athy. Ref. 44921-5090-01-WO/2105485
3903 AA699966 w, x  3906 A1103403 a  3906 NM_022516 s, t  7861 A1044042 l, m  22596 AA955298 y, z  first		arec ID	No.			man Homolónous Comissión Chasta Talla
3905 A1103403 a B B B B B B B B B B B B B B B B B B						T. W. I while your acquestion of the constant
3903 AA899986 w, x  3900 NM_022516 s, t  3900 NM_022516 aa, bb, II  7961 Al044042 i, m  22568 AA955298 y, z					2	i s, iwoderately similar to S15552 polypyrimidine tract-binding protein 1 - rat
3903/AA6999866 w, x  3905/A1103403 a  3905/A1103403 a  3906/NM_022516 s, t  10					<u>Y.</u>	norvegicus), ESTs, Weakly similar to S15552 polypyrimidine tract-binding protein
3905 A103403 a 3905 A1103403 a 3900 NM_022516 s, t 3904 NM_022516 aa, bb,				_	-	rat [R.norvegicus], Mus musculus, Similar to regulator of differentiation (in S.
3905 A103403 a a i i i i i i i i i i i i i i i i i					od.	mbe) 1, clone MGC:11742 IMAGE:3969488, mRNA, complete cds, RIKEN cDNA
3905 A103403 a a B B B B B B B B B B B B B B B B B	483		A A 80008 <i>B</i>	,	28	10036L13 gene, heferogeneous nuclear ribonucleoprotein L, polypyrimidine tract
3905 AI103403 a a 1 E E E E E E E E E E E E E E E E E	3		00000000	w, X	hin	ding protein 1, polypyrimidine tract binding protein 2
3905 A1103403 a 3900 NM_022516 s, t 3904 NM_022516 aa, bb, II 7961 A044042 I, m 22596 AA855298 y, z	-				ES.	1s, Moderately similar to S15552 polypyrimidine tract-binding protein 1 - rat
3905 A1103403 a 3900 NM_022516 s, t 3904 NM_022516 aa, bb, II 7961 A044042 I, m 62256 AA855298 y, z						norvegicus], ESTs, Weakly similar to S15552 polypyrimidine tract-binding protein
3905 A1103403 a a 3900 NM_022516 s, t b   1   2   22596 AA955298 y, z   1   1   1   2   2   2   2   2   2   2				_	<u></u>	rat [R.norvegicus], Mus musculus, Similar to regulator of differentiation (in S.
3905 A1103403 a a 3900 NM 022516 s, t a b, ll		uod	nbe) 1, clone MGC:11742 IMAGE:3969488, mRNA, complete cds. RIKEN cDNA			
3900 NM_022516 s, t 3904 NM_022516 aa, bb, II 7961 A1044042 l, m 622596 AA955298 ly, z	1100	3000	707707		281	0036L13 gene, heterogeneous nuclear ribonucleoprotein L. polypyrimidine fract
3900 NM_022516 s, t  3904 NM_022516 aa, bb, II  7961 A1044042 I, m  22596 AA955298 y, z	3	COSC	AI 103403	m	bind	Jing protein 1, polypyrimidine tract binding protein 2
3900 NM_022516 s, t 3904 NM_022516 aa, bb, II 7961 A1044042 I, m					ES	s, Moderately similar to S15552 polypyrimidine tract-binding protein 1 - rat
3900 NIM_022516 s, t 3904 NIM_022516 aa, bb, II 7961 AI044042 I, m 1022596 AA955298 y, z					Rr	orvegicus), ESTs, Weakly similar to S15552 polypyrimidine tract-binding protein
3900 NM_022516 s, t  3904 NM_022516 aa, bb, II  7961 Al044042 l, m					-	at [R.norvegicus], Mus musculus, Similar to regulator of differentiation (in S.
3900 NM_022516 s, t 3904 NM_022516 aa, bb, II 7961 Al044042 I, m					hod	ibe) 1, done MGC:11742 IMAGE:3969488, mRNA, complete cds, RIKEN cDNA
3904 NM_022516 aa, bb, II		281	0036L13 gene, heterogeneous nuclear ribonucleoprotein L, polypyrimidine tract			
3904 NM_022516 aa, bb, II 7961 Al044042 I, m 8 22596 AA955298 y, z	7	10000	01 CZZ0 MIN	2, 1	bind	ling protein 1, polypyrimidine tract binding protein 2
3904 NM_022516 aa, bb, II 7961 Al044042 I, m					ESI	s, Moderately similar to S15552 polypyrimidine tract-binding protein 1 - rat
3904 NM_022516 aa, bb, II		[R <sub>n</sub>	orvegicus], ESTs, Weakly similar to S15552 polypyrimidine tract-binding protein			
3904 NM_022516 aa, bb, II 7961 A1044042 I, m					i-	at [R.norvegicus], Mus musculus, Similar to regulator of differentiation (in S.
3904 NM_022516 aa, bb, il 7961 Al044042 l, m 22596 AA955298 y, z		•			mod	lbe) 1, clone MGC:11742 IMAGE:3969488, mRNA, complete cds, RIKEN cDNA
7961 A1044042 I, m 22596 AA955298 y, z	2126	3904	IM DOSEAR	44	2810	3036L13 gene, heterogeneous nuclear ribonucleoprotein L, polypyrimidine tract
7961 A1044042 I, m	1	1	111 V250 10	aa, UD, 11	bind	ing protein 1, polypyrimidine tract binding protein 2
7961 A1044042 I, m				-	EST	s, Moderately similar to S47073 finger protein HZF2, Krueppel-related
22596 AA955298 y, z	970	7064	1044040		[H.St	apiens], zinc finger protein 191, zinc finger protein 354A, zinc finger protein
22596 AA955298 y, z	3	V 1061	24044		354	
22596 AA955298 y, z					ESI	s, Moderately similar to 746637 transcription factor 1, neural - rat
22596 AA955298 y, z					[R.nc	pregicus], ESTs, Weakly similar to A35804 nucleolin [H.sapiens], Homo
22596 AA955298 y, z		_,_			sapit	ans mRNA; cDNA DKFZp434E0922 (from clone DKFZp434E0922), Mus
22596 AA955298 y, z					Snw	culus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library,
1) 7	638	22596 A	A955298		Clone	3:2810003118:myelin transcription factor 1-like, full insert sequence, myelin
		1,53	TOO TOO	17, 4	trans	cription factor 1-like, nucleolin

TABLE 3	က		1 12.00	多
SEO		GenBank Acc.	1,11	
으	GEGC ID No.	No.	Model Code	Model Gode Human Homologous Known Gene: Name
				ESTs, Moderately similar to T46637 transcription factor 1, neural - rat
				[R.norvegicus], Homo sapiens mRNA; cDNA DKFZp434E0922 (from clone
				DKFZp434E0922), Mus musculus 10, 11 days embryo whole body cDNA, RIKEN
2520		NIM 499499	17	full-length enriched library, clone:2810003118:myelin transcription factor 1-like, full
6262	-	1000U NIVI 133423	e, cc, aa	insert sequence, myelin transcription factor 1-like
_				ESTs, Moderately similar to 747137 hypothetical protein DKFZp761K2213.1
				[H.sapiens], myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog
7				(Drosophila), myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,
1020	- {	10277/AI059925	u, v	Drosophila); transfocated to, 4
-		!		ESTs, Moderately similar to T47183 hypothetical protein DKFZp434K1822.1
834		/050/AI011547	۵	[H.sapiens], ubiquitin specific protease 22
				ESTs, Moderately similar to T50638 synaptic glycoprotein SC2 [H.sapiens], ESTs.
				Weakly similar to T50638 synaptic glycoprotein SC2 [H.sapiens], expressed
				sequence AI173355, glycoprotein, synaptic 2, steroid 5 alpha-reductase 2, steroid 5
07.70	OF TOO	071007		alpha-reductase 2-like, steroid 5-alpha-reductase 2, steroid-5-alpha-reductase,
2767	27473	23479 NM 138549	Ž,	alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)
				ESTs, Moderately similar to TALIN [M.musculus], Mus musculus, Similar to
770	07770			hypothetical protein MGC11134, clone MGC:41710 IMAGE:1364225, mRNA,
2	71410	Z1410 AA80096Z	E	complete cds, talin, talin 2
į				ESTs, Moderately similar to TROPOMYOSIN 5, CYTOSKELETAL TYPE
4/4	1514	1514 NM 0126/8	ga	[M.musculus], tropomyosin 4

	ABI	الله ا	٠.	,	600 Th	
CLIGG   Div.   Model Code   Human Hc minggous Known Gene Name   Flumath Homologous Saquence Cluster Title	<u>ر</u>		GenBank Acc.	-	では、 一般の	DANKABE
2 4858 AA901238 W, x (Feb. 23300 NM_022398 Jj. kk	2	· O-	N.		iologolis Kraum Gene Mamo	2017
25 4858 AA901238 W, x  25 23300 NM_ 022398 Jj, kk  1845 NM_ 031010 c, v  19667 NM_ 021690 ji  19667 NM_ 021690 ji  19667 NM_ 021690 ji  19667 NM_ 021690 ji						
2 4858 AA901238 W, X (C) FE (C		-			ES IS, IMODERATELY SIMILAR OBUS THUMAN UBILUTING CONTRACTING FINA	- Nu V / 1
2 4858 AA901238 W, x   0   0   0   0   0   0   0   0   0		-			E2-21 KD UBCH6 [H.sapiens], ESTs, Weakly similar to S53358 uhimitin-	i   
2 4858 AA901238 W, X   1					Conjugating enzyme E2.17kB - rat IR norvenicus Homo sanions and a runor	
2 4858 AAB01238 w, x ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) (			<del>-</del>		fis, clone CBR08008, highly similar to HBIOLITIAL CONTINCT FILES	70107
2 4858 AA901238 w, x  5 23300 NM_022398 jj, kk  1845 NM_031010 c, v  19667 NM_021690 ji					KDA (FC & 3.219) Mingray Constitution Consti	EZ-73
2 23300 NM_ 022398					Account of the control of the contro	.ZE3
25517 NM_031010 c, v E E E E E E E E E E E E E E E E E E					(Incinologous to yeast UBC4/5), clone MGC:28917 IMAGE:4923869, mRNA.	
2 25517 NM_031010 c, v E E E E E E E E E E E E E E E E E E			-		Complete cds, RIKEN cDNA 1100001F19 gene. RIKEN cDNA 160001F19	- 6
2 4858 AA901238 W, x 5 23300 NM_022398 jj, kk 1845 NM_031010 c, v 1842 NM_138531 gg 19667 NM_021690 ji			·		RIKEN cDNA 6130401104 dene, hynothetical protein El 141014 usticalities	ב <u>י</u>
2 4858 AA901238 w, x  5 23300 NM_022398 jj, kk  1845 NM_031010 c, v  1845 NM_138531 gg  4422 NM_138531 gg  6 6 66					Conjugating enzyme F2D 3 (HBC4/F hamales)   Conjugating enzyme F	
2 4858 AA901238 w, x 5 23300 NM_022398 jj, kk 1845 NM_031010 c, v 4422 NM_138531 gg					F2D 3 (homologuis to vesse) in Start in	nzyme
2 4858 AA901238 w, x 5 23300 NM_022398 jj, kk 1845 NM_031010 c, v 4422 NM_138531 gg					Lesson of Jeast Up (1974), upidulun-conjugating enzyme E2E 1	
5 23300 NM_022398 jj. kk 25517 NM_031010 c, v 1845 NM_031010 c, v 4422 NM_138531 gg	202		AA901238	w, x	(UBC4/5 homolog, yeast), ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homol	olog,
5 23300 NIM_022398 jj, kk 25517 NIM_031010 c, v 1845 NIM_031010 c, v 4422 NIM_138531 gg					yeast)	 5
5 23300 NM_022398 jj, kk 25517 NM_031010 c, v 1845 NM_031010 c, v 4422 NM_138531 gg		•			ESTS, Weakly similar to 2-oxoglutarate carrier [Rattus norveoicus] IR norveoicus	1010
5 23300 NM_022398 jj, kk 3 25517 NM_031010 c, v 1845 NM_031010 c, v 4422 NM_138531 gg					Solute carrier family 25 (mitochondrial carrier adenine nindextite transferences)	 (5)
25517 NM_031010 c, v 1845 NM_031010 c, v 4422 NM_138531 gg	2115	23300	NIM 022208	3	member 10, solute carrier family 25 (mitnehandrial carrier oxygatisticated),	
3 25517 NM_031010 c, v 1845 NM_031010 c, v 4422 NM_138531 gg			02200	JJ, AA	member 11	
3 25517 NM_031010 c, v 1845 NM_031010 c, v 4422 NM_138531 gg					ESTs, Weakly similar to arachidonate 12 linowingers (Partice 11)	T
1845 NM_031010 c, v 4422 NM_138531 gg	200				IR populations and included the	
1845 NM_031010 G, v 4422 NM_138531 gg	27.13	71007	NM_031010	ر, د	in the second of	
1845 NM_031010 c, v  4422 NM_138531 gg					pseudogene 2, arachidonate 15-lipoxygenase	
1845 NM_031010 c, v  4422 NM_138531 gg					ESTS, Weakly similar to arachidonate 12-lipoxygenase [Rattus norvegicus]	T
4422 NM_138531 gg	2213	1845 N		ر ن ک	[R.norvegicus], arachidonate 12-lipoxygenase, arachidonate 12-lipoxygenase	
4422 NM_138531 gg		<del>  -</del> 			pseudogene 2, arachidonate 15-lipoxygenase	
4422 NM_138531 gg					ESTS, Weakly similar to associated molecule with the SH3 domain of STAM THA	owo.
19667 NM_021690 ii	2547	4422N			sapiens] [H.sapiens], RIKEN cDNA 1700095N21 gene, associated molecula with	- ±
19667 NM_021690 ii		-		000	the SH3 domain of STAM	
19667 NM_021690 ii					ESTS, Weakly similar to Cgetz-pending; cAMP-dependent Rap1 quanine-	T
19667 NM_021690 ii					nucleotide exchange factor; cAMP-GEFII [Mus musculus] [M.musculus]. Mus	
19667 NM_021690 ii					musculus, Similar to cAMP-regulated guanine nucleotide exchange factor I (cAM)	Mp.
19667 NM_021690 ii					GEFI), clone MGC:19192 IMAGE:4236136, mRNA, complete cds. RIKFN chwa	
19667 NM_021690 ii					4921517L17 gene, Rap1 guanine-nucleotide-exchange factor directly activated h	
	2084	19667 NI	M 021690		CAMP-regulated guanine nucleotide exchange factor II. chromosome 30	<u> </u>
					Open reading frame 152, expressed sequence C86120	

TABLE 3		- 25.00	6.000		
SEO		GenBank Acc		A STATE OF THE STA	THE AMOUNT AND THE PROPERTY OF THE AMOUNT AND THE PROPERTY OF
<u>.</u>	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	CONTROL TOWN TOWN TOWN TOWN TOWN TOWN TOWN TOWN
					ESTs. Weakly similar to CXC chemokina recently floating according
611		20619 AA945737	d. r. aa. bb		[R.norvegicus], G protein-coupled receptor, chemokine (C-X-C motif), receptor 4
			20 tm (; (;		(fusin), chemokine (C-X-C) receptor 4
					ES1s, Weakly similar to CXC chemokine receptor [Rattus norvegicus]
2097		20249 NM_022205	=		(C-X-C motif), receptor 4 (fusin), chemokine (C-X-C motif), receptor 4
					ESTs, Weakly similar to 91-related zinc finger protein IMus musculus
1223		6969 AI170244	ļų	-	[M.musculus], Homo sapiens, clone IMAGE:3956746, mRNA, partial cds, g1-related
					Zinc finger protein, similar to RIKEN cDNA 1300002C13
					ESTS, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside
					expression factor 2 [Rattus norvegicus] [R.norvegicus], GABA(A) receptor-
					associated protein, GABA(A) receptor-associated protein like 1, GABA(A) recentor-
		_	- H		associated protein like 2, GABA(A) receptor-associated protein-like 2. GABA(A)
1102		5989 A1102520	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\		receptors associated protein like 3, gamma-aminobutyric acid (GABA(A)) receptor-
					associated protein-like 1, gamma-aminobutyric acid receptor associated protein
					ESTS, Weakly similar to L1 cell adhesion molecule [Mus musculus] [M.musculus].
			- 1		ESTS, Weakly similar to A41060 neural cell adhesion molecule L1 precursor
					[H.Sapiens], ESTs, Weakly similar to S36126 neural cell adhesion molecule L1 - rat
					[R.norvegicus], L1 cell adhesion molecule, L1 cell adhesion molecule
					(hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation,
895	15904 A	15904 AI013971	E <u>'</u>		aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraplegia 1),
	<del> -</del> 				close homolog of L1, neuronal cell adhesion molecule
		_			ESTS, weakly similar to mitochondrial processing peptidase beta [Rattus
					norvegicus] [R.norvegicus], RIKEN cDNA 3110004018 gene, mitochondrial
-					processing peptidase beta, peptidase (mitochondrial processing) beta, ubiquinol-
2113	18221 N	18221 NM_022395	S, G,		cytochrome c reductase core protein 1, ubiquinol-cytochrome c reductase core
					Protein   ESTs World: initial to page 1:
					introcellulor coldinar to 5100 calcium-binding protein A9 (calgranulin B);
			a, e, y, z,		Intracellular calcium-binding protein (MRP14) [Raftus norvegicus] [R.norvegicus],
2403	21445NI	21445 NM 053587	ee, ff		S100 calcium binding protein A13, S100 calcium binding protein A7 (psoriasin 1),
					Caron cardining protein AB (calgrandin B)

ABL	:	**: *** *** *** *** *** *** *** *** ***	1	
2. C	! 8	GenBank Acc.		Atty. Ref. 44921-5090-01-WO/2105485
2	GEGC ID No.	No.	Model Code	ā
			·	ESTs, Weakly similar to Ser/Arg-related nuclear matrix protein; plenty-of-prolines-
				101; serine/arginine repetitive matrix protein 1 [Mus musculus] [M.musculus], Mus
				IMAGE:5257666 mRNA complete out brain characterine MGC13125, clone MGC:38070
2108		18246 NIM 020200		Drotein 1. expressed seminance Attanesses all and a property of the property o
3		1414 022300	E .	Serine/arginine repetitive matrix 1
				ESTs, Weakly similar to syntenin [Rattus norvegicus] IR.norvegicus]. syndecan
2349		19768 NM_031986	f, g, cc, dd	binding protein, syndecan binding protein (syntenin), syndecan binding protein
				FSTs Moskly similar to 1. 2012
				related) (Postus noncessus) to a similar leukemia viral oncogene homolog B (ras
2426				homolog R (ras rafatad) was simian feukemia viral oncogene
7420		20421 NM 053821	=	related: GTP binding and in leukemia viral oncogene homolog B (ras
				ESTS, Weakly similar to 1607338A transcription factor BTE22 rules and transcription f
			_	musculus, basic transcription factor 3, clone MGC:6799 IMAGE:7848048 PNA
187	7749	7749 AA848804	<u>*</u>	complete cds, RIKEN cDNA 1700054E11 gene, RIKEN cDNA 5730434f03 gene
				basic transcription factor 3
				ESIS, Weakly similar to 2019405A upstream regulator element-binding protein
				[Rattus norvegicus] [R.norvegicus], Mus musculus, clone MGC:12070
	_			IIMAGE:3708271, mRNA, complete cds, RIKEN cDNA 1110018G07 gene, RIKEN
				CDINA 2810411E22 gene, RIKEN cDNA 4432411E13 gene, RIKEN cDNA
1562	2687 A	2687 AI235877	s, t	4930431E10 gene, expressed sequence AW212605, upstream regulatory element
2540				ESTs. Weakly circling to 2422250A 1
277	00	LEGUEU MINICIOO	aa, bb	1, RIKEN cDNA 1200007021 gene
			<del></del>	ESTs, Weakly similar to 2204387A peroxisome assembly factor 2 Rathus
	_	-		norvegicus] [R.norvegicus], ESTs, Weakly similar to TRANSITIONAL
_		·		ENDOPLASMIC RETICULUM ATPASE [M.musculus], RIKEN cDNA 4833413G10
2481	919 N	919 NM 057125	E	gene, expressed sequence Al195026, peroxisomal biogenesis factor 6, peroxisome
				biogenesis factor 1, valosin containing protein

TABLE	E3				
ე ე	GLGC ID No.	GenBank Acc.		Alomolomus Konim Cook	y. Ref. 44921-5090-01-WC
				roggous rational defile name	Hüman Homologous Sequence Cluster Title
1549		18444 AI234915	182	ESTs, Weakly si ESTs, Weakly si	ESTs, Weakly similar to A26882 plL2 hypothetical protein - raf [R.norvegicus], ESTs, Weakly similar to AF191020 1 E2IG5 [H.sapiens], RIKEN cDNA 2310056P07
				יייייייייייייייייייייייייייייייייייייי	gene, mixture of 2007 3NU6 gene, hypothetical protein, estradiol-induced
				Clathrin coat ass	ES1s, Weakly similar to A2M1_HUMAN Clathrin coat assembly protein AP50 (Clathrin coat associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa
				protein) (HAZ 50 (AP-2 mu 2 chain	protein) (HAZ 50 kDa subunit) (Clathrin assembly protein complex 2 medium chain) (AP-2 mu 2 chain) (R.norvegicus), adantor protein complex AD 4
				adaptor protein or	adaptor protein complex AP-2, mu1, adaptor-related protein complex 1, mu 2
2439		160 J9 NM_053837	f, r, cc, dd	Subunit, adaptor-	subunit, adaptor-related protein complex 2, mu 1 subunit, adaptor-related protein
106		179w7 AA800671	n	ESTs, Weakly sim	ESTs, Weakly similar to A54854 Ras GTPase activating protein-related protein
				ESTS, Weakly sim	milar to A55190 transitional endonlasmic retroitum A 1 Bass 1/77
				3.6.1) [validated]	3.6.1) [validated] - rat [R.norvegicus], ESTs, Weakly similar to TRANSITIONAL
				spermatogenesis s	Spermatogenesis associated factor (SPAF) mRNA complete At RIKEN ADMA
	-			4833413G10 gene	4833413G10 gene, RIKEN cDNA 4933439B08 gene, expressed sequence
				A1195026, katanin	Al195026, katanin p60 (ATPase-containing) subunit A1, nuclear VCP-like,
2445	18357 N	18357 NM_053864	n, 0	peroxisome bioger containing profein	peroxisome biogenesis factor 1, spermatogenesis associated factor, valosin containing profein valosin-containing poetsis
				ESTs, Weakly simi	ESTs, Weakly similar to A55571 chloride conductance inducer Mat-8 IH saniens
2108	N 969	695 NM_022388	۱۵, ۷	FXYD domain-con	FXYD domain-containing ion transport regulator 3, FXYD domain-containing ion
				transport regulator 4	14
				ESTs, Weakly simi	ESTs, Weakly similar to A55817 cyclin-dependent kinase n130 BITS! BE
				[M.musculus], RIKE	[M.musculus], RIKEN cDNA 2600011L02 gene, RIKEN cDNA A930036K24 gene
2112	23061 NA	23061 NM_022394	s, t	aldehyde dehydrog	aldehyde dehydrogenase family 5, subfamily A1, cell division cycle 2 homolog (S.
				pompe)-like 2, expr	pomoe)-like 2, expressed sequence Al255170, scaffold attachment factor B

TABLE 3	60	<i>2</i> .		
SEO		GenBank Acc		THE DOOR FOOM FOR THE STATE OF
Ω	GLGC ID No.	No.	Model Code Human Hom	holorone Known Com
				יייים אינים
				EDIS, Weakly Similar to ADT1 MOUSE ADP, ATP CARRIER PROTEIN,
				THEART/SKELETAL MUSCLE ISOFORM T1 [M.musculus], Mus musculus, Similar
				TO RIKEN CDNA 1700066C05 gene, clone MGC:28125 IMAGE:3980327, mRNA,
				complete cds, RIKEN cDNA 1700034,06 gene, solute carrier family 25
1654		19053 D12770	aa, bb	(mitochondrial carrier, Aralar), member 12, solute carrier family 25 (mitochondrial
				(carrier, adenine nucleotide translocator), member 4
				ESTS, Weakly similar to AMPE MOUSE GLUTAMYL AMINOPEPTIDASE
2100		6263 NM_022251	jj, kk	[M.musculus], aminopeptidase puromycin sensitive, glutamyl aminopeptidase,
				Boltaniyi aniinopepitdase A), puromycin-sensitive aminopepitdase
1			j, k, p, q, y,	THE STATE OF THE S
15/5		15051 AI236332	z, ee, ff	In. Sabiensj, Kirken con 2610016A03 gene, spermidine/spermine N1-
1300	16/30	10007	•	ESTS. Weakly similar to B Chain B Cruster Of The Business
1052	02+01	10420 All /0234	S, 69	From The Himan Shan Core Domain to contain the Und Sub-Complex
				ESTs, Weakly similar to B41182 collagen alpha 1(II) chain precured Manager III
2519	19326	19326 NM 133419	74 :: ^ ::	PUMA/JFY1 protein, RIKEN cDNA 4933407C03 gene, RIKEN cDNA 5730512 in
-			Will fit to	gene, dyskeratosis congenita 1, dyskerin
				ESTs, Weakly similar to BCN1_MOUSE Beclin 1 (Colled-coll myosin-like BCl 2.
				Interacting protein) [M.musculus], RIKEN cDNA 4921513J16 gene, beclin 1 (coiled-
2422	15269 N	15269 NM_053739	ď, ť, g	(coil, myosin-like BCL2 interacting protein), beclin 1 (coiled-coil, myosin-like BCL2-
				Interacting protein)
i				ES15, Weakly Similar to C35826 hypothetical 13K protein A [H.sapiens], X-linked
23/8	160171	16017 NM_053401	o, aa	protein, brain expressed X-linked 2, nerve growth factor receptor (TNFRSF16)
		•		FSTs Weakly similar to C28926 http://www.
0220	16040	707070		Drotein. Drain expressed X-linked 2 posts grount forth and investigation of the contract of th
23	100.001	100 to 101M U034U1	o'a	associated protein 1. reduced extression 3
				ESTs, Weakly similar to casein kinase IM.musculus]. RIKEN CDNA 2810208K14
2170	23215N	23215 NM 023102	E. L.	gene, RIKEN cDNA 3300002K07 gene, VRK3 for vaccinia related kinase 3. casein
		Γ		Kinase 1, alpha 1, casein kinase 1, delta, casein kinase 1, gamma 2
158	4491 A	4491 AA818798	w, x	ESTS, Weakly similar to CATZ_HUMAN Cathepsin Z precursor (Cathepsin X) (Cathepsin D) IH saniens Cathepsin Z precursor (Cathepsin X)
				1. Carlebail 4, expressed sequence AU019819

TABL	E3				
SEO		GenBank Acc.			**************************************
<u>_</u> _	GLGC ID No.	No.		Model Code Human Homologous Known Gene Name	90-01-W0/Z103463
210		4490 AA851184	j. 0		Cathensin X)
619	2	20839 AA9460AO	=	(Cathepsin P) [H.sapiens], cathepsin Z, expressed sequence AU019819 ESTs, Weakly similar to COXG MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VIB IM. musculus]. Homo saniens, hymothetical page 1 OC435057	019819 ASE
		Otto Control	E	clone MGC:33640 IMAGE:4827471, mRNA, complete cds ESTs, Weakly similar to DHB4 MOUSE ESTRADIOL 17 BETA-DEHYDROGENASE	EHYDROGENASE
2195		25070 NM 024392	:= <u></u>	4 [M.musculus], ESTs, Weakly similar to DHB4_HUMAN ESTRADIOL 17 BETA-DEHYDROGENASE 4 [H.sapiens], RIKEN cDNA 1110029G07 gene, RIKEN cDNA 1700010M22 gene, RIKEN cDNA 3110069K09 gene, hydroxysteroid (17-heta)	DIOL 17 BETA- ene, RIKEN cDNA oid (17-heta)
				dehydrogenase 4 ESTs, Weakly similar to EGR2 MOUSE EARLY GROWTH RESPONSE PROTEIN 7	ONSE PROTEIN 2
2413		857 NM_053633	y, z, ee, ff	[M.musculus], MYC-associated zinc finger protein (purine-binding transcription factor), early growth response 2, early growth response 2 (Krox-20 homolog,	transcription homolog,
1689	17136 J04035	104035	f, aa, bb	ESTs, Weakly similar to ELS MOUSE ELASTIN PRECURSOR [M.musculus], RIKEN cDNA 4930554K12 gene, elastin, elastin (supravalvular aortic stenosis,	musculus], rtic stenosis,
				ESTs, Weakly similar to FIBULIN-1, ISOFORM C PRECURSOR [M.musculus],	/u.musculus],
670	24135 A	24135 AA957736	0 ':	FLJ32009 fis, clone NT2RP7009498, weakly similar to FIBULIN-1, ISOFORM A PRECURSOR, Mus musculus mRNA for CRTAC1-B protein (CRTAC1 gene),	s cDNA ISOFORM A 4C1 gene),
				ESTS, Weakly similar to FMOD_HUMAN FIBROMODULIN PRECURSOR Ifficial in the financial forcing the features of th	RSOR
2498	23551 N	23551 NM_080698	:=	fibronectin leucine rich transmembrane protein 1, fibronectin leucine rich transmembrane protein 1, fibronectin leucine rich transmembrane protein 2, fibronectin leucine rich transmembrane protein 3, hypothytical protein 2, fibronectin leucine rich	rotein 1, e rich
2190	15622 N	15622 NM_024369	f, g	ESTS, Weakly similar to FRP MOUSE FOLLISTATIN-RELATED PROTEIN	OTEIN
2190	15623 NI	15623 NM_024369		ESTS, Weakly similar to FRP MOUSE FOLLISTATIN-RELATED PROTEIN	OTEIN
	•	•		I TACONOON IN. MUSCALLINE, TOILISTATIN-like, Toilistatin-like, Toi	_

TABI E.2	2.5		14 · · · · · · · · · · · · · · · · · · ·		
) 	<u>, 1-4</u> -	GenBank Acc.			VO/2105485
أة	GLGC ID No.	No.		Model Code Human Ht mologous Known Gene Name Human Homologous Sequence Cluster Tifle	7
	S. T. Karling and			ESTs, Weakly similar to GPV_RAT Platelet glycoprotein V precursor (GPV) (CD42D) [R. norvegicus], Platelete glycoprotein 5, RIKEN cDNA 1300018K11 gene, RIKEN cDNA 5430427N11 nene	oV) IK11 gene,
1177		7122 Al137468	66	carboxypeptidase N, polypeptide 2, 83kD, glycoprotein 5 (platelet), glycoprotein V (platelet), hypothetical protein FLJ12568, leucine-rich alpha-2-glycoprotein	protein V in
2639		20818 X02904	:=	ESTs, Weakly similar to GTP_RAT Glutathione S-transferase P (GST 7-7) (Chain 7) (GST class-pi) [R.norvegicus], Mus musculus, clone MGC:37914 IMAGE:5102505, mRNA. complete cds. clutathione S-transferace of clutathione S-	7) (Chain 7)
		·		ESTS, Weakly similar to GUANINE NUCLEOTIDE DISSOCIATION STIMIL ATOD	ase, pr.2
				RALGDS FORM A [M.musculus], ESTs, Weakly similar to T12453 hypothetical protein DKFZp564D2123.1 [H.sapiens], RIKEN cDNA 1300003D20 gene. RIKEN	letical RIKEN
2048		18761 NM_019250	99	cDNA 4930573C08 gene, RalGDS-like gene, ral guanine nucleotide dissociation stimulator, ral guanine nucleotide dissociation	ciation
2573	9775	9775 NM_139334	O	ESTs, Weakly similar to guanine nucleotide regulatory protein [H.sapiens], Rho	, Rho
1752	1708	1708 NIM 012584		ESTs, Weakly similar to HOMEOBOX PROTEIN HOX-A2 [M.musculus], even skipped homeotic gene 2 homolog, expressed sequence Al894218 homeo hox	ven
1752	1709	1709 NM 012584	=	A11, homeo box A2, homeo box B2 ESTs, Weakly similar to HOMEOBOX PROTEIN HOX-A2 [M.musculus], even skipped homeotic gene 2 homolog, expressed sequence Al894218, homeo hox	ven
1648	7602	7503 A 1004030		A11, homeo box A2, homeo box B2 ESTs, Weakly similar to 156519 taipoxin-associated calcium binding protein-49 precursor - rat [R.norvegicus], Homo sapiens cDNA FLJ14474 fis, clone MAMMA1001256, calumenin, reticulocalbin 1. EF-hand calcium binding domain	149
	3	6761000		reticulocalbin 2, reticulocalbin 2, EF-hand calcium binding domain ESTs, Weakly similar to IM7A_RAT Mitochondrial import inner membrane	,
741	11745 A	11745 AB006450	hh, jj, kk	translocase subunit TIM17 A [R.norvegicus], translocase of inner mitochondrial membrane 17 homolog A (yeast), translocase of inner mitochondrial membrane 17 homolog B (yeast), translocase of inner mitochondrial membrane 17	drial rane 17
				Indianal Description of Indianal Description of Inner mitochondrial membrane 17 kDa, a	_

TABLE 3	ш Э	:	:;·	the paper.	
SEO		GenBank Acc		では、「は、「は、「は、「は、」では、「は、」では、「は、」では、「は、」では、「は、」では、「は、」では、「は、」では、「は、」では、「は、」では、「は、」では、「は、」では、「は、」では、「は、」	Atty. Ref. 44921-5090-01-WO/21054RF
<u></u>	GLGC ID No.	No.		5	
					misculie kanonharin
				(importin) alpha 2, karyopherin (importin) alpha 3, karyopherin (importin) alpha 4,	in (importin) alpha 4,
2385		00700		had yopherin alpha 3 (importin alpha 1), karyopherin alpha 3 (importin alpha 3) karyopherin alpha 3 (importin	pherin alpha 3 (importin
6007		13330 MINIM 053483	ž	alpha 6)	l aipila 3 (iiiipoi iii)
				ESTS, Weakly similar to JC5251 beta-galactoside alpha-2,3-sialyltransterase	sialyltransterase
				[H.sapiens], sialyltransferase, sialyltransferase 4A (beta-galactosidase alpha-2,3-	ctosidase alpha-2,3-
				sialytransferase), sialytransferase 4B (beta-galactosidase alpha-2,3-	pha-2,3-
				sialytransferase), sialyltransferase 5, sialyltransferase 7 ((alpha-N-acetylneuraminy	ha-N-acetylneuraminy
				2,3-beta-galactosyl-1,3)-N-acetyl galactosaminde alpha-2,6-sialyltransferase) A	sialv(transferase) A.
				sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-beta-galactosyl-1,3)-N-acetyl	tosvi-1.3)-N-acetvi
				galactosaminde alpha-2,6-sialyltransferase) B, sialyltransferase 7D ((alpha-N-	ise 7D ((alpha-N-
1385		16468 AI178751	:=	acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-	minide alpha-2.6-
	1			sialyltransferase)	
				ES18, Weakly similar to JC5251 beta-galactoside alpha-2,3-sialyitransterase	ialyitransterase
				I'H. Sapiens], sialyltransferase, sialyltransferase 4A (beta-galactosidase alpha-2,3-	ctosidase alpha-2,3-
	_		_	sialytransterase), sialytransferase 4B (beta-galactosidase alpha-2,3-	ha-2,3-
				Sialytransterase), sialytransferase 5, sialytransferase 7 ((alpha-N-acetylneuraminy)	na-N-acetylneuraminyt
				2,3-beta-galactosyr-1,3)-N-acetyl galactosaminde alpha-2,6-sialyltransferase) A,	ialyltransferase) A,
			_	sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-beta-galactosyl-1,3)-N-acetyl	tosyl-1,3)-N-acetyl
				galactosaminde alpha-2, 6-sialyltransferase) B, sialyltransferase 7D ((alpha-N-	se 7D ((alpha-N-
2313	16863 N	16863 NM 031695		acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-	ninide alpha-2,6-
	-			sialytransterase)	
171	6281 A	6281 AA819517	<u> </u>	ES1s, Weakly similar to JC5707 HYA22 protein [H.sapiens], hypothetical protein	ypothetical protein
-	<del>                                     </del>			BC010/36	
		-		ESTS, Weakly similar to JC7328 amino acid transporter A1 [H.sapiens], Homo	sapiens], Homo
1247	5963 A	5%53 A1171231	<i>u</i> ,	sapiens clone 24674 mRNA sequence, solute carrier family 38, member 1, solute	, member 1, solute
$\vdash$				Carrier family 38, member 2	
				ES is, Weakly similar to LANP_RAT Leucine-rich acidic nuclear protein	ir protein
				(R.norvegicus), acidic (leucine-rich) nuclear phosphoprotein 32 family, member A.	family, member A.
1817	187 N	187 NM 012903		acidic nuclear phosphoprotein 32, cerebellar ataxia 3, hypothetical gene	lical gene
	<del> </del> 			MGC16309, small nuclear ribonucleoprotein polypeptide A	

9. 年 1. 年	TABL	<u>سا</u>	•	a Cade Caritim	
31.3C D NV. Model Cgda Human Ho nologous known Gene Name  16003 NM_ 031757	0 2 3 3		GenBank Avc.		「高い地域のあっている。」は「高いないのでは、「一人」は「自然のできない。」というないでは、「一人」というない。「「一人」というない。「一人」というない。「一人」というない。「一人」というない。「一人」
1037 AF016296 64, kc, c, 1037 AF016296 64, kk  1316 NM_053656 5, t, ii  15629 NM_053551 r, aa, bb  1356 D83538 u, v pp  12700 NM_152936 h, l	آء	3.60	Ž.	Model Code	Human Homologous Sequence Cluster Title
1097 AF016286 6, t, ii  1316 INM_053656 8, t, ii  753 INM_053657 ee, ff, gg  15829 INM_053857 t, aa, bb  1356 D83538 u, v  12700 INM_152936 h, i		·····			
1037 AF016296 dd, kk  11316 NM_053656 s, t, ii  753 NM_053657 ee, ff, gg  753 NM_053551 r, aa, bb  1356 D83538 u, v  12700 NM_152936 h, I					LSTS, WEGANY SHIRING TO MININGY_MOUSE MATRIX METALLOPROTEINASE-24  PRECURSOR (MMP-24) (MEMBRANE-TYPE MATRIX METALL OPROTEINASI
1037 AF016296 dd, kk 11037 AF016296 dd, kk 7 1037 AF016296 dd, kk 7 53 MM_053897 ee, ff, gg 15829 MM_053551 r, aa, bb 1386 D83538 u, v 12700 NM_152936 h, I					(MT-MMP 5) (MEMBRANE-TYPE-5 MATRIX METALLOPROTEINASE) (MT5-M
1356 D83538	2324		3 NM 031757	ပ	(MMP-21) [M.musculus], matrix metalloproteinase 17, matrix metalloproteinase
1316 NM_053656 S, t, ii  753 NM_053656 S, t, ii  15829 NM_053551 r, aa, bb  1356 D83538 u, v  12700 NM_152936 h, 1				e, j, k, ας,	inanx metalloproteinase 24, matrix metalloproteinase 24 (membrane-inserted) ESTS. Weakly similar to NRP1 HIMAN NET IRODII IN 1 DECLIDED IT
1316 NM_053656 s, t, ii  753 NM_053897 ee, ff, gg e, n, o, p, q, 15829 NM_053551 r, aa, bb 1356 D83538 u, v pp	<b>4</b> /		7/AF016296	dd, Kk	neuropilin, neuropilin 1, platelet derived growth factor C
1356 DB3538			-		ESTs, Weakly similar to P2X6 MOUSE P2X PURINOCEPTOR 6 [M.musculus],
753 NM_053897 ee, ff, gg  15829 NM_053551 r, aa, bb  1356 D83538 u, v  12700 NM_152936 h, I	2416		NM 053656	:= - -	purinergic receptor P2X, ligand-gated ion channel, 2, purinergic receptor P2X,
753 NM_053897 ee, ff, gg  15829 NM_053551 r, aa, bb  1356 D83538 u, v  12700 NM_152936 h, 1				2 5	ligand-gated ion channel, 5
15829 NM_053897 ee, ff, gg e, n, o, p, q, 15829 NM_053551 r, aa, bb 1356 D83538 u, v					ESTs, Weakly similar to PAR3 MOUSE PROTEINASE ACTIVATED RECEPTOR
15829 NM_053551 r, aa, bb 1356 D83538 u, v	2450		NM 053897	# 00	PRECURSOR [M.musculus], coagulation factor II (thrombin) receptor-tike 1,
15829 NM_053551 r, aa, bb 1356 D83538 u, v			i coco lant	ge, 11, 9g	coagulation factor II (thrombin) receptor-like 2
15829 NM_053551 r, aa, bb 1356 D83538 u, v					ESTS, Weakly similar to PDK4_MOUSE [PYRUVATE DEHYDROGENASE
15829 NM_053551 r, aa, bb 1356 D83538 u, v				2	[LIPOAMIDE]] KINASE ISOZYME 4, MITOCHONDRIAL PRECURSOR
1356 D83538 u, v	2392	-	NM 053551	2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2	(PYRUVATE DEHYDROGENASE KINASE ISOFORM 4) [M.musculus], pyruvate
1356 D83538 u, v 12700 NM_152936 h, I		1	10000	1, aa, DD	dehydrogenase kinase 4, pyruvate dehydrogenase kinase, isoenzyme 4
1356 D83538 u, v 12700 NM_152936 h, I					ESTS, Weakly similar to PK3G_KAT Phosphatidylinositol 3-kinase C2 domain-
1356 D83538 u, v 12700 NM_152936 h, I					Containing gamma polypeptide (Phosphoinositide 3-Kinase-C2-gamma) (PtdIns-3
1356 D83538 u, v 12700 NM_152936 h, I					kinase C2 gamma) (PI3K-C2gamma) [R.norvegicus], Homo sapiens cDNA
1356 D83538 u, v 12700 NM_152936 h, I				-	FL/12591 fis, clone NT2RM4001313, moderately similar to
1356 D83538 u, v 12700 NM_152936 h, I					PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137),
1356 D83538 u, v 12700 NM_152936 h, I					phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide,
1356 D83538 u, v 12700 NM_152936 h, I					phosphatidylinositol 3-kinase, catalytic, alpha polypeptide, phosphatidylinositol 4-
12700 NM_152936 h, I	1665	1256	702520	-	kinase, catalytic, beta polypeptide, phosphoinositide-3-kinase, class 2, gamma
12700 NM_152936  h, I	3	2002	0000	n, v	polypeptide
12700 NM_152936 h, I	<del></del>				ESTs Maskly similar to DSC4 MOLINE ATTOCATATION OF ATTOCATATIO
12/00/NM_152936 h, l	- 6				GLYCOPROTEIN PRECURSOR IM musculus RIKEN CDNA 2340065D40 2000
	2562	12/00		h, l	Serine profease inhibitor. Kazal type 1. serine profease inhibitor. Kazal type 1.

GLGC   DNo.   Genbank Acc.   Model Code   Human Homologous Sequence Clusier Title   ESIs, Weeky similar to RR17, HUMAN Ras.   C44(G)   YLO)   R. Accordance Intil, RABES, mem sequence And Sequence Clusier Title   ESIs, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   Mosconal potein L37   ESIS, Weeky similar to RR137   ESIS,	ABLE				A STATE	The state of the s		11 (2008)	
CLGC   No.   Model Code   Human Homologous Known Gene Name   Human Homologous Sequence Cluster Title	Z Z Z		GenBank Acc.				į.		A CONTRACTOR OF THE PARTY OF TH
239 NM 031152		GLGC ID	No.	Model Code	Human Homologou	is Known Gene	Name		Human Homologous Seminarya Ourstey Tillo
23390 A172328									ESTs, Weakly similar to R11A_HUMAN Ras-related protein Rab-114 (RAB-11)
23350 A172328									(24KG) (YL8) [R.norvegicus], RAB11A, member RAS oncogene family, RAB11a,
23390 A172328	2264		NM_031152	9					member RAS oncogene family, RAB25, member RAS oncogene family, expressed sequence AW496496
2 77 99 AI013911 t iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii									ESTs, Weakly similar to R6RT37 ribosomal protein L37, cytosolic Ivalidated - rat
23390 A172328 6 E E E E E E E E E E E E E E E E E E	2241		NM_031106	f, g					R.norvegicus], RIKEN cDNA 1500002F19 gene, RIKEN cDNA 3110005M08 gene,
23390 A172328 , e 10070 A1058505									riousomai protein L3/ FSTs Westiv similar to DBMs WATION PRESENT BY A BENEFICIAL SIMILAR TO BENEFICIAL SIMILAR TO BENEFICIAL SIMILAR
23390 A172328									LOIS, WEARN SIMILIER TO REINS MOUSE PUTATIVE RNA-BINDING PROTEIN 3
2 77 99 A1013911 t 94 12 A1230691 f, g 23390 A172328 e 10070 A1058505 u, v 2211 AA963834 i, m									Iwinusculus, mus musculus adult male tongue cDNA, RIKEN full-length enriched
23330 A172328									ilbrary, cone:23100/4E15:RNA binding motif protein 3, full insert sequence, RNA
23390 A172328									binding motif protein 3, RNA binding motif protein, X chromosome, RNA binding
23390 A172328 , e 10070 A1058505 u, v 2211 AA963834 i, m	892		AI013911						mout protein, X chromosome retrogene, cold inducible RNA binding protein, cold
23390 A172328 . e 10070 A1058505 u, v 2211 AA963834 l, m									inducible KNA-binding protein
23390 A172328		_							ESIS, WEAKIN SIMILAR TO RE34_HUMAN 60S RIBOSOMAL PROTEIN L34
23390 A1172328 e e 10070 A1058505 u, v e 2211 AA963834 l, m	1462	9, 12,		£.,					in Saplens], ES1s, Weakly similar to RL34_RAT 60S RIBOSOMAL PROTEIN L34
23390 A172328									K.norvegicusj, KIKEN cDNA 1100001122 gene, ribosomal protein L34
23390 A172328 e e 10070 A1058505 u, v E E E E E E E E E E E E E E E E E E		-						_	Lend String of KUD_KAI Heterogeneous nuclear ribonucleoprotein DO
23390 A172328 e									nnRNP DU) (AU-rich element RNA-binding protein 1) [R.norvegicus], Mus
23390 A1172328 e e 10070 A1058505 u, v 2211 AA963834 l, m E E E E E E E E E E E E E E E E E E	-							=	nusculus, clone MGC:36467 IMAGE:5359082, mRNA, complete cds, RIKEN cDNA
23390 A172328 e e 10070 A1058505 u, v 2211 AA963834 l, m 473 A1228548 aa									933434H11 gene, heterogeneous nuclear ribonucleoprotein D, heterogeneous
23390 A172328 . e e 10070 A1058505 u, v				-				<u> </u>	inclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD),
10070 At058505 u, v  2211 AA963834 l, m  1473 A1228548 aa	282	23390	•	<b>-</b>					eterogeneous nuclear ribonucleoprotein D-like, high-glycine/fyrosine protein type I
10070 Al058505 u, v  2211 AA963834 l, m  1473 Al228548 aa	-								.5, musashi homolog 2 (Drosophila)
2211 AA963834 I, m 1473 A1228548 aa	966	10070		u. v				<u> </u>	SIS, Weakly similar to RRM1_HUMAN PUTATIVE RIBOSOMAL RNA
2211 AA963834 I, m 1473 A1228548 aa	<u> </u>	-							TELHYLI KANSFERASE 1 [H.sapiens], FtsJ homolog 2 (E. coli)
1473/A1228548 aa	681	2211 A		E				<u> </u>	S1s, Weakly similar to S105_MOUSE S100 calcium-binding protein A5 (S-100D
1473/A1228548 aa	-								Orelln) (K.norvegicus), S100 calcium binding protein A5
1473/A1228548 aa								<u>u</u>	3.5, Weakly similar to S10A MOUSE S-100 PROTEIN, ALPHA CHAIN  I.musculusi S100 calcium binding protein 44, 5400 calcium binding protein 44, 5400 calcium binding protein 44, 5400 calcium binding protein 44, 5400 calcium binding protein 44, 5400 calcium binding protein 44, 5400 calcium binding protein 54, 5400 calcium binding prot
11.0/1720010 da	433	1473						<u>.                                    </u>	alizzarin), S100 calcium binding protein P. S1002 protein. expressed serrience
	3	C		g g				V	1266795

TABLE 3	က			
SEQ ID	GLGC ID No.	GenBank Acc. No.	Model Code	ologous Knowin Gene Name
2342		1475 NM_031971	a, p, q, ee, ff	
391	11992,	11992 AA892485		ESTs, Weakly similar to S21766 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - rat (fragment) [R.norvegicus], Mus musculus, clone IMAGE:3586777, mRNA, partial cds, Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein, RIKEN cDNA 1600017E01 gene, RIKEN cDNA 4930529008 gene, dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease), dihydrolipoamide branched chain transacylase E2, pyruvate dehydrogenase complex, component X
1653	5049	5049 D10655	g, w, cc, dd, Jj, kk	ESTs, Weakly similar to S21766 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)  - rat (fragment) [R.norvegicus], Mus musculus, clone IMAGE:3586777, mRNA, partial cds, Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein, RIKEN cDNA 1600017E01 gene, RIKEN cDNA 4930529008 gene, dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex, maple syrup urine disease), dihydrolipoamide branched chain transacylase E2, pyruvate dehydrogenase complex, component X
1653	3050 D	5050 D10655	f, g, cc, dd	ESTs, Weakly similar to S21766 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - rat (fragment) [R.norvegicus], Mus musculus, clone IMAGE:3586777, mRNA, partial cds, Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein, RIKEN cDNA 1600017E01 gene, RIKEN cDNA 4930529008 gene, dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease), dihydrolipoamide branched chain fransacylase E2 pyrux purine disease), dihydrolipoamide
2225	15967 N	15967 NM_031050c	 	ESTs, Weakly similar to S52284 lumicon, secretory intersticial proteoglycan precursor - rat [R.norvegicus], dermatan sulfate proteoglycan 3, dermatan sulphate proteoglycan 3, lumican

TABLE	TABLE 3		THE PARTY OF THE P	The second secon
SEO		GenBank Acc.		The state of the s
므	GLGC ID No.	No.	Model Code Human Hom	ologous Known Gene Name Human Homologous Sequence
				ESTs, Weakly similar to S53358 ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus], RIKEN cDNA 1100001F19 gene, RIKEN cDNA 160002817 gene
				prefoldin 5, ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast), ubiquitin-
756		2947 AF099093	u, v	conjugating enzyme E2D 3 (homologous to yeast UBC4/5), ubiquitin-conjugating
1953		13392 NM 017148	a	ESTs, Weakly similar to S53580 cysteine-rich protein - rat [R.norvegicus], RIKEN
			,	CDNA 0610025L06 gene, cysteine and glycine-rich protein 1, cysteine rich protein
				ES IS, Weakly similar to 112483 hypothetical protein DKFZp564B0769.1
545		3997 AA925771	:=	it marketish i totito sapietis, ciotte indec. 16721 liniAGE:4128659, mRNA, complete Icds. KIAA1604 protein SR rich matein
				ESTs, Weakly similar to T46332 hypothetical protein DKFZp434H0413.1
				[H.sapiens], Homo sapiens, clone MGC:9709 IMAGE:3850147, mRNA, complete
29	18226	18226 AA799641		ods, KIAA1253 protein, expressed sequence AW121759, expressed sequence
				C86123
				ESTS, Weakly similar to TGR3_HUMAN TGF-BETA RECEPTOR TYPE III
722	2757	2757 AA997851	[pp'	PRECURSOR [H.sapiens], Homo sapiens cDNA FLJ33157 fis, clone
				O LINGSONS STRUCKING
				ESTs, Weakly similar to TIE1 MOUSE TYROSINE-PROTEIN KINASE RECEPTOR
				TIE-1 PRECURSOR [M.musculus], Homo sapiens cDNA: FLJ23028 fis, clone
				LNG01852, highly similar to HSU08023 Human cellular proto-oncogene (c-mer)
				mRNA, RYK receptor-like tyrosine kinase, c-mer proto-oncogene tyrosine kinase,
905	3625 A	3625 A1028954	:=	receptor-like tyrosine kinase, tyrosine kinase receptor 1, tyrosine kinase with
000,				ESTs. Weakly similar to TMOD MOLISE TRODOMODILI IN TA minoculual Listers and the control of the
1,262	11696A	11696 AI171774	j; k	2 (cardiac), tropomodulin
				ESTS. Weakly similar to TRANSITIONAL ENDOBLASAND BETICING A STRAIGHT
				IM-musculus], Homo sapiens spermatonenesis associated factor (CDAE) = 100
				complete cds, RIKEN cDNA 4833413G10 gene, RIKEN cDNA 4933439R08 gene
	-	•		expressed sequence Al195026, katanin p60 (ATPase-containing) subunit A1,
1496	70.36 AI	70.36 A1231801	- pp 22	nuclear VCP-like, peroxisome biogenesis factor 1, spermatogenesis associated
		7	יים מהי מח	factor, valosin containing protein, valosin-containing protein

TAB' "	5.5			
Ĭ,		GenBank Acc.	L	Atty. Ref: 44921-5090-01-WO/210548B
لُت	GLGC ID No.	No.		Model Code Human Hr mologous Known Gene Name
24.70		17. 31 NM_054006	cc, dd	
				IMIGC: 13174 IMAGE:4224466, mRNA, complete cds, NRAS-related gene
	ر بيت			ESTs, Weakly similar to VAM5_HUMAN VESICULE-ASSOCIATED MEMBRANE
2394		11843 NM_053555	s 'o 'u	PROTEIN 5 (VAMP-5) (MYOBREVIN) (HSPC191) [H.sapiens], vesicle-associated
				Internibrarie protein 5, vesicle-associated membrane protein 5 (myobrevin)
				Manuscripted Mind (Power) Mind (Power)
				Hillings dene aj-felated expressed kinase 4,
2061	1	52 NM 019335	P:	inducible double stranded RNA denendent
5		241 16 NIM 013003	=	expressed sequence A/255394 nhosnhafidulathandaming NI math difference
928		19257 41030775		expressed sequence Al323765, histocompatibility 2, class II antigen E alpha maior
		27000		histocompatibility complex, class II, DR alpha
1709	192551	19255 M15562		expressed sequence Al323765, histocompatibility 2, class II antigen E alpha, major
		7000	,	histocompatibility complex, class II, DR alpha
1709	19256	W15562		expressed sequence Al323765, histocompatibility 2, class II antigen E alpha, major
1028	4967	4967 AI070179	× 3	nistocompatibility complex, class II, DR alpha
2451	15706N	-	× ===	expressed sequence Al324845, glia maturation factor, gamma
				expressed sequence AI451906, peroxisomal biogenesis factor 12
	· •			expressed sequence AI845868, histocompatibility 2, class II antigen A, beta 1.
1717	9223 N	9223 M36151		major histocompatibility complex, class II, DO beta, major histocompatibility
				complex, class II, DQ beta 1
298	16419A	16419 AA875102		expressed sequence AL022645, expressed sequence C76690, small nuclear
				monucieoprotein E, small nuclear ribonucleoprotein polypeptide E
179	320A	320 AA819905	PP.	expressed sequence AU022220, stearoyl-CoA desaturase (delta-9-desaturase),
128	11166A	11166 AA801346	n. o	stearoyi-Coenzyme A desaturase 1, stearoyi-coenzyme A desaturase 3
2507	1809N	-	-	expressed sequence AU042020, plexin B1, plexin B3
	-			expressed sequence AW212229, lipocalin 2 (oncogene 24p3)
2254	1816N	4		expressed sequence AW259572, thyroid hormone receptor, alpha (erythroblastic
360	16023 A	Γ	W. X	leukemia viral (v-erb-a) oncogene homolog, avian)
				expressed sequence BB168308, nicotinamide nucleotide transhydrogenase
1306	19004 AI175875		aa, bb	fatty acid binding protein 5 (psonasis-associated), fatty acid binding protein 5,
				epidermai

TABLE 3	E3	ConBonk Age		· 通常 · · · · · · · · · · · · · · · · · ·	
Ω	GLGC ID No.	No.	_	Himan Homologories Kromis Cons M	Afty. Ref. 44921-5090-01-WO/2105485
				Tarriar i idiliogoda Allowii Gene Name	nce Cluster Title
			<del>-</del>	GA binding protein transcripti	GA binding protein transcription factor, beta subunit 1 (53kD). GA hinding protein
				transcription factor, beta subu	transcription factor, beta subunit 2 (47kD), Homo sapiens cDNA F1 132440 fts.
				SKMUS2001662, moderately	SKMUS2001662, moderately similar to Oryctolagus cuniculus CARP mRNA pircent
			,	cDNA 1700012M14 gene, RIF	cDNA 1700012M14 gene, RIKEN cDNA 4933432B13 gene, ankwrin reneal domain
1900		18313 NM_013220	e K	2 (stretch responsive muscle)	2 (stretch responsive muscle), ankyrin repeat domain 5. cardiac ankyrin reneat
				protein, cardiac responsive adriamycin protein	driamycin protein
2081		25445 NM 021654		gap junction membrane chanr	gap junction membrane channel protein alpha 4, gap junction profein alpha 4, 3750
912		7451 AI029450	V. 7	(connexin 37)	OVIC 's abuse 's constant of the constant of t
2669	-	16 80 X62660	C f G	glutamyl-prolyl-tRNA synthetase	336
	ı		20,5	glutathione S-transferase A4	glutathione S-transferase A4, clutathione S-transferase
				Glycogen synthase 2 (liver), M	Glycogen synthase 2 (liver), Mus musculus, clone MGC:29379 IMAGE:5051695
1232	11! 85	4/170502		mRNA, complete cds, glycoge.	mRNA, complete cds, glycogen synthase 1 (muscle), glycogen synthase 1
2063	22/75/	221.75 NM 019358	77	glycogen synthase 3, brain	י וווחסמפין או היישים לי וווחסמפין
1161	2.96A	1112979	W V III C	glycoprotein 38, lung type-1 cel	glycoprotein 38, lung type-I cell membrane-associated olygoprotein
			۳,۸	GM2 ganglioside activator protein	fein
2539	(-06N	6.06 NW 134352	2	GPI-anchored metastasis-asso	GPI-anchored metastasis-associated nortein homolog plannings and the contract of the contract
	1	10102	a, y, 2	urokinase receptor, urokin	Urokinase receptor, urokinase plasminoden activator rossessioner activator,
				GRB2-related adaptor protein,	GRB2-related adaptor protein, GRB2-related adaptor protein 2 SH2 domain
121	16E52A	16E52 AA801130		3, Sh3 domain YSC-like 1, grow	3, Sh3 domain YSC-like 1, growth factor recentor hound protein 2, arough factor recentor hound protein 2
	-			receptor-bound protein 2, monocytic adaptor	ocytic adaptor
				GRB2-related adaptor protein, (	GRB2-related adaptor protein, GRB2-related adaptor protein 2, SH3 domain protein
2204	18023 NJ	18023 NM_030846	Q	3, Sh3 domain YSC-like 1, grow	3, Sh3 domain YSC-like 1, growth factor receptor bound protein 2, growth factor
	14184NI	14184 NM 031776	¥	receptor-bound protein 2, monocytic adaptor	ocytic adaptor
2325	14185N	M 031776	3	guanine deaminase	
-				guanine deaminase	
				guanine nucleotide binding prote	guanine nucleotide binding protein (G protein), alpha inhihiting activity polygonida
307	15887 AA875225	1875225		2, guanine nucleotide binding pr	2, guanine nucleotide binding protein, alpha inhibiting 2. guanine nucleotide binding
	<del> </del>			protein, alpha inhibiting 3	Billing opposition of the control of
				guanine nucleotide binding prote	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide
307	15888 AA875225		e, 99	2, guanine nucleotide binding pr	<ol> <li>guanine nucleotide binding protein, alpha inhibiting 2, guanine nucleotide binding</li> </ol>
				protein, alpha inhibiting 3	

TABLE	,	: -:	1	State Comment of the	
SEO		GenBank Acc			30-01-WO/2105485
<u>.</u>	GC 10	No.		Gene Name	
				guanine nucleotide binding protein (G protein), alpha inhibitin	livity polypeptide
2221		15886 NM_031035	r, bb, ll	2, guanine nucleotide binding protein, alpha inhibiting 2, guanine nucleotide binding lorotein, alpha inhibiting 3	ucleotide binding
				H2A histone family, member C. H2A histone family member D. H9A histone family.	74 histone family
				member I, H2A histone family, member I. H2A histone family, member I. H2A histone family, member N. H2A	mber N H2A
				histone family, member O, Homo sapiens. clone MGC:21597 IMAGE-4511035	GF-4511035
				mRNA, complete ods, Mus musculus, similar to H2A histone family member O	w member O
1170		10700		clone MGC:36202 IMAGE:5055276, mRNA, complete cds, expressed sequence	sed segmence
<u>e</u>		18343/AI13/495	D	R75370	anionhos pos
				H4 histone family, member D, H4 histone family, member H. H4 histone family	Stone family
				member I, H4 histone family, member J. H4 histone family, member K Mils	r K Mis
9	0000			musculus, H4 histone family. member A. clone MGC:30488 IMAGE:4205480	2.4205460
ş	CONNY	ZUUDO   AA89264/	c, d, r	mRNA, complete cds. histone 4 protein	,12001001
				H4 histone family, member D. H4 histone family member H H4 histone family.	tono fomily
<del></del> .				member I, H4 histone family, member J. H4 histone family member J. H4 histone family member K Mirs	r K Mis
21.40	20206	OCCUPATA COSCO		musculus, H4 histone family, member A, clone MGC:30488 IMAGE:4205460	:4205460
2	20000	NIVI_UZZ000	0	mRNA, complete cds, histone 4 protein	
				H4 histone family, member D, H4 histone family, member H, H4 histone family,	stone family,
				member I, H4 histone family, member J, H4 histone family, member K, Mus	r K, Mus
2149	6121	6121 NM 022686	٠ ت	musculus, H4 histone family, member A, clone MGC:30488 IMAGE:4205460,	:4205460,
1285	2208	1479479	(, ) (, )	mRNA, complete cds, histone 4 protein	
1270	0538	9538 41172097	00 to 1	HCCA2 protein	
1	2000	11,2031	1, III	heat shock factor 1, heat shock transcription factor 1	
2403	RROOM	RROUMING ORDER	), ∧, de, II, JJ,	HIF-1 responsive RTP801, Homo sapiens, Similar to RIKEN cDNA 1700037B15	1700037B15
25.2	72000	WINI JUDUSES	NX.	gene, clone MGC:9960 IMAGE:3877854, mRNA, complete cds	
2284	23202 USU 252	5252 U30725		high density lipoprotein binding protein (vigilin)	
1/1/	N 17 10	100000 M	85 83	histone deacetylase 1, histone deacetylase 2, histone deacetylase 3	
<u> </u>	A DOWN	ouso Alzsu884		HMBA-inducible	
2531	24609N	24609 NM 133585	p co	Homo sapiens cDNA FLJ12045 fis, clone HEMBB1001957, RIKEN cDNA	SDNA
-			V D G H	1200011N24 gene, optic atrophy 1 (autosomal dominant)	
1321	12999 AI176276		Z, QQ		
				Indino sapiens cuiva FLJ125/0 hs, clone NT2RM4000895	

TABLE 3	E3			
SEO D	GLGC ID No.	GenBank Acc. D No.		Ologonis Known Gene Name
835		3941 Al011598	* * * * * * * * * * * * * * * * * * *	Homo sapiens cDNA FLJ14042 fis, clone HEMBA1006038, weakly similar to LAMININ ALPHA-5 CHAIN, expressed sequence AA408762, expressed sequence AA408762, expressed sequence
2556	_	17530 NM_138877	n, o, ii	Homo sapiens cDNA FLJ14413 fis, clone HEMBA1004670, RIKEN cDNA 1500005G05 gene, cytochrome b5 reductase 1 (B5R.1), cytochrome b5 reductase b5 reductase 1 (NADH) (cytochrome b-5 reductase), diaphorase 1 (NADH)
2556		17532 NM_138877	<u>:-:</u>	Homo sapiens cDNA FLJ14413 fis, clone HEMBA1004670, RIKEN cDNA 1500005G05 gene, cytochrome b5 reductase 1 (B5R.1), cytochrome b5 reductase b5 reductase), cytochrome b6R.2, diaphorase (NADH) (cytochrome b-5 reductase), diaphorase 1 (NADH)
2556		25039 NM_138877	# 'ee'	Homo sapiens cDNA FLJ14413 fis, clone HEMBA1004670, RIKEN cDNA 1500005G05 gene, cytochrome b5 reductase 1 (B5R.1), cytochrome b5 reductase b5 reductase 1 (NADH) (cytochrome b-5 reductase), diaphorase 1 (NADH)
727		3353 AA998053	i=	Homo sapiens cDNA FLJ14455 fis, clone HEMBB1001908, highly similar to Human monocytic feutrasmis and a series finances and a series finances.
2404		20896 NM_053592 19159 AAR51953	- 'è	Homo sapiens cDNA FLJ25344 fis, clone TST01087, RIKEN cDNA 5031412 06
	8	200	> 5	Homo sapiens cDNA FLJ30862 fis, clone FEBRA2003675
2163		15697 NM_022939		Homo sapiens cDNA FLJ31164 fis, clone KIDNE1000104, weakly similar to SYNTAXIN 7, expressed sequence Al 1041521 syntaxin 12 contaxin 12 contaxin 12 contaxin 12
309	154107	15410 AA875268	jj, kk	Homo sapiens cDNA FLJ31499 fis, clone NT2NE2005441, weakly similar to
887	22592	22592 AI013740	n, o, w, x	Homo sapiens cDNA FLJ31762 fis, clone NT2RI2007754, weakly similar to INTESTINAL MEMBRANE A4 PROTEIN, hypothetical protein BC010116, hypothetical protein BC010116,
2673	602×	602 X68101	ee ff	Homo sapiens cDNA FLJ32122 fis, clone PEBLM1000144, moderately similar to Trg. KIAA1058 protein, enythroid differentiation regulator, expressed sequence
				AASSBOUT, expressed sequence R75174

A		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		7.7.65	
Ψ.,		GenBank Acc.			05485
2	GLGC ID No.	No.	Model Code Human H	mologous Known Gene Mame	7
22.7.		22 igilam 139253	70		
		1007001	3	element mRNA	—– ¥e
				Homo sapiens cDNA FLJ32449 fis, clone SKMUS2001662. moderately similar to	
1240		21284 AI170842	tq.	Oryctolagus cuniculus CARP mRNA, ankyrin repeat domain 2 (stretch resnonsive	 2
				muscle), ankyrin repeat domain 5, cardiac ankyrin repeat protein	
1600	J	16:40 AI638955	£	Homo sapiens cDNA FLJ32493 fis, clone SKNSH2000051, RNA binding motif	T
241		4A859519	d, h, l	protein 9, fox-1 homolog (C. elegans)	
				Tromo sapiens cDNA FLJ32971 fis, clone TESTI2008847	Γ
				Homo sapiens cDNA: FLJ21251 fis, clone COL01259, Homo sapiens, Similar to	T
1670	20456 H31144	131144	 	activated p21cdc42Hs kinase, clone MGC:15139 IMAGE:4302390, mRNA,	
				complete cds	
				Homo sapiens cDNA: FLJ22783 fis, clone KAIA1993, Homo sapiens mRNA frill	T
868		15247 AI014169	4	length insert cDNA done EUROIMAGE 703547. Homo saniens mRNAs chan	
			ממי מים	DKFZp434B102 (from clone DKFZp434B102). KIAA1376 protein	
				Homo sapiens mRNA for FLJ00083 protein, partial cds. RIKEN china 284703432547	1
	_			gene, RIKEN cDNA 2810047L02 gene, WD repeat domain 5 WD repeat domain 5 WD repeat domain	
492	14712A	14712 AA900860	#	58, glutamate rich WD repeat protein GRWD, hypothetical protein F1.11448	
			-	peroxisome biogenesis factor 7, recombination protein REC14	
				Homo sapiens mRNA; cDNA DKFZp434M2227 (from clone DKFZp434M2277)	$\top$
				Homo sapiens prostate-specific membrane antiden PSM mRNA. exon 6 alternative	
1594	3615 AI237645	237645 t		Splice variant, partial cds, RIKEN cDNA 2610028K12 gene, transferrin recentor	
				transferrin receptor (p90, CD71), transferrin receptor 2	
	-			Homo sapiens mRNA; cDNA DKFZp434M2227 (from clone DKFZp434M2227)	T
	-		_	Homo Sapiens prostate-specific membrane antigen PSM mRNA, exon 6 alternative	
1721	24844 M58040		n, v	Splice variant, partial cds, RIKEN cDNA 2610028K12 gene, transferrin receptor.	
				transferrin receptor (p90, CD71), transferrin receptor 2	
				Homo sapiens mRNA; cDNA DKFZp566P2324 (from clone DKFZp566P2324),	Т
			_	Indino sapiens, clone MGC:21553 IMAGE:4155396, mRNA, complete cds,	
513	4917 AA924140		m'	NIAAU193 gene product, hypothetical protein BC002980, hypothetical protein	
543	4285 AA925708		r, y, z, jj, kk	1-LAZO 14Z	
				Indino sapiens PINAS-29 mRNA, complete cds, WD repeat domain 1	Γ-

del Code Human Homologous Known Gene Name  1, o, II  ee, ff  aa, bb  RIII  RII	IABL	in S			The second secon
GLGC ID   No.   Model Code   Furman Homologous Known Gene Name   State   Sta	SEO		GenBank Acc.		このでは、 これのでは、 これのできない。 これのできないできない。 これのできない。 これのできない。 これのできない。 これのできない。 これのできない。 これのできない。 これのできない。 これのできない。 これのできない。 これの
18108   NM_139105   a, n, o, ii	₽	SLGC IC	O No.		Ologous Known Gene Name
18108 INM_139105 a, n, o, II		·			
99 9286 INM_023027 I, m 99 6882 A170783 Kk 14722 A1235284 gg 6 35 3A4963260 s, t 6 35 3A4963260 s, t 7 14023 INM_139256 c, s 98 664 Z75029 y, z, ee, ff 11375 A1231532 r 11375 A1231534 r 11375 A1231532 r 11375 A123153 r 11375 A123	256		8 NM 139105	.n.	IMAGE:2654341, mRNA, complete cds, expressed sequence AW546468,
9 9286 NNM_022598					expressed sequence C80305, ribonuclease/angiogenin inhibitor
14722 Al235284   99   99   99   99   99   99   99	216		5 NM_023027	m'j	Homo sapiens, clone IMAGE:4096427, mRNA, partial cds, heterogeneous nuclear
6 38 53 AA963260 S, t  2 233-47 AA860015 aa, bb  192 71 AU231565 S, t  193 865 AN71965 ee, ff  8004 AU231532	1236		41170702	11	
6 38 53/AA963260 s, t 2 233-47/AA860015 aa, bb 8 192 71/AI231566 s, t 1803 NM_ 139256 c 8 8653 AW71965 ee, ff 8 8004 AI231532 r 11375 AI237594 u, v 2 2006 NM_ 022936 aa 2 2009 9 NM_ 022598 d, r, aa, bb 8 2099 9 NM_ 022598 d, r			200	W.	deleted in colorectal carcinoma, myopalladin
8 192 71 AL231566 s, t 8 192 71 AL231566 s, t 1 1803 NM_139256 c 1 1803 NM_139256 c 8 192 77 AL231566 c, t 1 1803 NM_139256 c 8 192 77 AL231532 r, c.e., ff 1 1375 AL231532 r, c.e., ff 2 2006 NM_022936 aa 2 2008 NM_022936 w, x, aa, bb	1556		AI235284	99	Homo sapiens, clone IMAGE:5001663, mRNA, partial cds, antigen identified by
233.47 AA860015 aa, bb 192.71 AI231566 c 18004 AI231532 r 113.75 AI237594 u, v 2006 NM_022598 w, x, aa, bb 20959 NM_022598 d, r					Homo sapiens, clone MGC:11072 IMAGE:3688606 mRNA complete ade
2 23:47 AA860015 aa, bb 19 <u>6</u> 71 A1231566 s, t  1803 NM_139256 c 8665 A071965 ee, ff 8665 A071965 ee, ff 8004 A1231532 r 11375 A1237594 u, v 2006 NM_022936 aa 2006 NM_022936 aa 2009 NM_022936 u, x, aa, bb	9/9		AA963260	ý	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked), erythrocyte
2 23:47 AA860015 aa, bb 195 71 Al231566 s, t 2 1803 NM_ 139256 c 8 8655 A071965 ee, ff 8 8664 Z75029 y, z, ee, ff 113 75 A1237594 u, v 2 2006 NM_ 022936 aa 2 2006 NM_ 022936 w, x, aa, bb P 2 209:9 NM_ 022598 d, r					protein band 4.1-like 2
8 19; 71 Al231566 5, t  2 1803 NM_139256 c  8 8655 Al071965 6e, ff  8 8004 Al231532 r  113 75 Al237594 u, v  2 2006 NM_022936 aa  2 2008 NM_022936 w, x, aa, bb  P P P P P P P P P P P P P P P P P P	262		AA860015	aa, bb	Homo sapiens, clone MGC:12617 IMAGE:2964706, mRNA, complete cds, cyclin
2005 NM_022598 d, r  11803 NM_022598 d, r  11803 NM_022598 d, r  11803 NM_022598 d, r	1488	- 1	AI231566	s, t	IMD, CYCIIII WH
2005 NM_022598					Home spring Jone MGC:18164 IMAGE:4155088, mRNA, complete cds
209:59 NM_022598 d, r	2572		NM_139256	ပ	CDNA 111005H2A rene managidas class complete eds, RIKEN
8664 275029 y, z, ee, ff 8004 Al231532 r 11375 Al237594 u, v 2006 NM_022936 aa 2008 NM_022936 w, x, aa, bb 20959 NM_022598 d, r	2 2		AI071965	ee, ff	Homo capiene plans MCC-05020 MASS 2C, member 1
8004 AI231532	566		275029	y, z, ee, ff	Home carions alone MO 05500 III. OT MRNA, complete cds
8004 Al231532					Homo capiens, clone McCr.25500 MAGE: 4480702, mRNA, complete cds
2006 NM_022936 aa 2008 NM_022936 w, x, aa, bb 209'39 NM_022598 d, r	1486		AI231532	-	finder profess, dolle McC.20099 IMAGE:4828042, mRNA, complete cds, zinc
2006 NM_022936 aa 2008 NM_022936 w, x, aa, bb 20959 NM_022598 d, r	1592	11375/	AI237594	u, v	Homo capions Appendix Office (MAC) 144 (Vpe)
2006 NM_022936 aa 2008 NM_022936 w, x, aa, bb 209'39 NM_022598 d, r					Homo sapiens, clone MGC:9645 IMAGE:3690933, mKNA, complete cds
2008 NM_022936  w, x, aa, bb 20959 NM_022598  d, r	2162	2000			cDNA 2310063B19 gene, epoxide hydrolase 2. cytonlasmic, hynothetical protein
2008 NM_022936 w, x, aa, bb 20959 NM_022598 d, r	1	7		99	FLJ11743, hypothetical protein FLJ22408
2008 NM_022936 w, x, aa, bb 20959 NM_022598 d, r					Homo sapiens, clone MGC:9645 IMAGE:3922910, mRNA, complete cds, RIKEN
209'59 NM_022598 d, r	2162	2008 N		w, x, aa, bb	CDNA 2310063B19 gene, epoxide hydrolase 2, cytoplasmic, hypothetical protein
209÷9 NM_022598 d, r					Homo saniens Similar to BIKEN ADMA 40305332000
209:50 NM_022598 d, r					IMAGE:5269882 mRNA complete and Miss missardus State Andre Missard
209-50 NM_022598 d, r					protein DKFZp761J139, clone MGC:11924 IMAGE:3599595 mRNA commission of a
	2144	20959N			RIKEN cDNA 4930513009 gene, cellular nucleic acid binding protein, zinc finger
			7	-	protein 9 (a cellular retroviral nucleic acid binding protein)

1 7 7 1	1		,	MAN
ישני		GenBank Arr		
و	CI GC ID	) No.		000
				IMAN DE FONDO DAMA CONTROL CONTROL CONTROL CONTROL GOND MGC:33185
				my version of the control of the con
	_	· · ·		Protein DNF4P/013139, clone MGC:11924 IMAGE:3599595, mRNA, complete cds,
2144		20960 NM_022598	C, e, r	NINEN GLINA 4930513009 gene, cellular nucleic acid binding protein, zinc finger
				protein 9 (a cellular retroviral nucleic acid binding protein)
356		11966 AA891800	hh, ji, kk	hypothetical protein BC008246, inorganic pyrophosphatase, pyrophosphatase
				(morganic)
356		18128 AA891800	n, o	iiiybouteucai protein BCUU8246, inorganic pyrophosphatase, pyrophosphatase
23		21427 AA801181	ο, dd	(Introgation)
				hypothetical protein FLJ23151
700	-			righten from the control of the cont
20	6/31	6/31 NM 145096	hh	finger DUDC domois and finder 1, 2010 IIII get, DUTC domain containing 7, zinc
487		4732 AA900343	pp 's	milyer, United Wolfiam Containing 9
378		22903 AA892250	0	Inypouneucal protein DKFZp761C169, hypothetical protein SP192
1176		11238 AI137410	ee ff	hypothetical protein FLJ10514
716	21*19	21°19 AA997655	٩	hypothetical protein FLJ12888
783	22801	22801 AI009197	0	hypothetical protein FLJ14566
430	3879	3879 AA893237	0	hypothetical protein IMAGE3455200
427	17,31	17731 AA893194	1	hypothetical protein MBC3205
28	20980	20980 AA799633	. E	hypothetical protein MGC10974
555	9942	9942 AA942697	-	hypothetical protein MGC13016
535	23452		, 5	hypothetical protein MGC3133
			SS.	hypothetical protein MGC8974
2200	17917	17917 NM_024488	þ, v	hypothetical protein, MGC:8303, likely ortholog of rat CDK5 activator-binding protein
129	11995	11995 AA801352	n, o	C33
392	11994	11994 AA892507	두	Immature colon carcinoma transcript 1
$\vdash$				immature colon carcinoma transcript 1
178	18427 A	18427 AA819891	00	inositol 1,4,5-triphosphate receptor, type 1, ryanodine receptor 1 (skeletal),
1720	1586 M57728		200	ryanodine receptor 1, skeletal muscle
1730	15174N	756	) E	Inositol polyphosphate-5-phosphatase, 72 kDa
-	-			insulin-like growth factor 2 receptor
969	2492 A	2492 AA964866	 n'	interferon gamma receptor 2, interferon gamma receptor 2 (interferon gamma
				(narsqueer 1)

TAR! F 3	F 2	,,,,	\$ 3	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
C U	ا	- Incombant Age	T.	(2) Altv. Ref. 44921-5090-01-3Mic/0310548
<u> </u>	GIGCID	No Control Act	Model Code	
			300	numan Homologous Known Gene Name Human Homologous Sequence Cluster Title
2430		9059 NM_053783	ا, <del>ر</del> چ	Interferon gamma receptor, interferon gamma receptor 1
1893		20754 NM_013195	٩	interleukin 2 receptor, beta, interleukin 2 receptor, beta chain, interleukin 21
1279		4278 A1172304	q	interleukin 2 receptor, gamma (severe combined immunodeficiency), interleukin 2
		100	, v c x i	receptor, gamma chain
325		5384 AA891041		Consequent of the American Range and American Range.
2090	- !	20161 NM_021836	j, k, p, q, r	In B Ancorage in D prote access
2224		1731 NM_031047	英道	inction plakoglichin
1446	ı	7 AI229785	cc, dd	Kerafin 19 kerafin complex 1 avidio cono 40
				KIAA0438 gene product, Mus musculus, clone IMAGE:3499845, mRNA, nartial cds
			<u> </u>	goliath protein, hypothetical protein FLJ20552, hypothetical protein LOC51255
533		AA925150	_=	praja 1, praja 1, RING-H2 motif containing, rotein carrying the RING-H2 sequence
2543		NM 134406	3	motif, similar to RIKEN cDNA 1300002C13, zinc finger protein 364
474		22/201 A ABOOSO	J, KK	KIAA0602 protein, hypothetical protein FLJ20748
070	_l_	A4039209	В	KIAA1049 protein
8/0	- [	Ar013466	පි පි	KIAA1049 protein
000		3445 A7013/24	9	KlAA1052 protein. hypothetical protein FI.113942
જ		AA799494	ө	KIAA1075 protein hypothetical protein El 14050 times and otherina
2579		15761 NM 145001	33 E	KIAA1348 protein, protein phosphatase 1G (formerly 2C), magnesium-dependent,
		1000±1_mm	UC, UU, JJ, NA	gamma isoform
_				KIAA1453 protein, Mus musculus, Similar to ubiquitin specific protease 3, clone
				MGC:28886 IMAGE:4911201, mRNA, complete cds, RIKEN cDNA 4930511011
857		5595 AI012467	^	gene, Vhlh-interacting deubiquitinating enzyme 1, ubiquitin specific protease 2,
				ubiquitin specific protease 20
1872		38 NM 013114	da hh	KIAA1894 protein, pregnancy-associated plasma protein A, selectin P (granule
			20 (2)	membrane protein 140kD, antigen CD62), selectin, platelet
2421	13622	13622 NM_053713	aa, bb, II	Kruppel-like factor 1 (erythroid), Kruppel-like factor 2 (lung), Kruppel-like factor 4 (qut)
2421	22411	22411 NM_053713	d, t	Kruppel-like factor 1 (erythroid), Kruppel-like factor 2 (lung), Kruppel-like factor 4
	i			Kruppel-like factor 1 (erythroid) Kruppel-like factor 2 (lung) Krumol III.a factor 3
2421	25579In	25379 NM_053713		(gut)

TABLE 3	Е3	1	となるので、別となる。	Skoje
SEQ ID	GLGC ID No.	GenBank Acc. D No.		uman Homologõüs Known Gene Name
				Mitogen activated protein kinase 12 (Zipper (leucine) protein kinase), integrin linked kinase, mitogen activated protein kinase, kinase kinase, kinase kinas
2518		16713 NM_133409	Q	mitogen activated protein kinase kinase tinase 12, mitogen-activated protein kinase kinase kinase kinase kinase
				mitogen activated protein kinase kinase 6, mitogen activated protein kinase kinase Kinase 7, mitogen activated protein kinase kinase
2420		6684 NM_053703	爻	Kinase 4, mitogen-activated protein kinase 6, mitogen-activated protein kinase 8, mitogen-activated protein
332	2	21928 AA891302	b, I, m	kinase kinase 7
1182		12654 AI137864	cc, dd	mitogen-activated protein kinase kinase kinase 2
1316		17223 AI176140		MORF-related gene 15 MORF-related gene 15, RIKEN cDNA 1700060H10 nene testis evirasesed zono
355	П	21672 AA891789	f, g	189
				MORF-related gene X
				Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library,
				full insert sequence. Muse muserulus, cimilar to columnia in the columnia of the columnia in the columnia of t
				acetylqlucosamine (UDP-GicNAc) transporter) momber 3 glassians 2000-in
2588	5095	5095 NM_147140	>	IMAGE:5150304, mRNA, complete cds, solute carrier family 35 (CMP-sialing and
	-			transporter), member 1
2535	1463IN	1463 NM 134334	50	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810054L16:kidney-derived aspartic professe-like profess full income.
			SS 's	sequence, cathepsin D, cathepsin D (lysosomal aspartyl protein, run illser)
				Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110005M20; serine farting and contractions and contractions and contractions and contractions and contractions and contractions and contractions are contracted and contractions and contractions are contracted and contractions and contractions are contracted and contractions and contractions are contracted and con
				Sequence, Mus musculus adult male luno cDNA. RIKEN full-lands are in-
359	7050 A	7050 AA891824	0.0	clone:1200011B22:signal sequence receptor, delta, full insert sequence
	-			serine/threonine kinase 23
2008	2000			Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930547K11:rhlning channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. III in the channel 4.2 f. II in the channel
2007	2022UN	20223(MINI_022198	D, I, m	chloride channel 4-2
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TABL			7.		
JE JE	ľ	TisenBank Acc.		where the second of the second	All Dof Adod English and Manager and Manag
aİ.	GLG( ID)116.	0110			
<b>~</b>					Figure nomologous Sequence Cluster Title Mus musculus adult mala taxtis anno augman.
				clone:4932434L04;	clone:4932434L04:adaptor protein complex AP-2 alnha 2 subunit 6ul inco-
				sequence, adaptor p	sequence, adaptor protein complex AP-1, gamma 1 subunit. adaptor protein
_				complex AP-1, gam	complex AP-1, gamma 2 subunit, adaptor protein complex AP-2, alpha 1 subunit
1000				adaptor protein com	adaptor protein complex AP-2, alpha 2 subunit, adaptor-related protein complex 1,
0		10198 AIU/2063	0,0	gamma i subumit, a	gannina i subuniti, adaptor-related protein complex 2, alpha 2 subunit, alpha-c large
284		22 <b>7</b> 81 AA874926		Mus musculus dual	Mus musculus dual specificity phosphares T-DSD40 mBNA
	L			cDNA 5930436K22 c	cDNA 5930436K22 gene, protein phosphatase
465		22#83 AA894207		Mus musculus dual s	Mus musculus dual specificity phosphatase T-DSP10 mRNA, complete cds RIKFN
				CDNA 5930436K22 c	cDNA 5930436K22 gene, protein phosphatase
1090		22786 AI101659	99	IMus musculus dual s	Mus musculus dual specificity phosphatase T-DSP10 mRNA, complete cds, RIKEN
-				CDIVA 3930436KZZ g	CDNNA 3930436K22 gene, protein phosphatase
730/		ZUZ35 NM 053302	S, dd	cDNA 5930436K22	mus musculus dual specificity phosphatase T-DSP10 mRNA, complete cds, RIKEN cDNA 5930436K22 gene profile phosphatase T-DSP10 mRNA, complete cds, RIKEN
				Mus musculus endott	Mus musculus endothelin converting enzyme-2 mRNA complete contracting in the converting enzyme-2 mRNA complete contracting enzyme-2 mRNA contracting enzy
2406	- 1	21709 NM_053596	j, k, y, ll	converting enzyme 1,	converting enzyme 1, expressed sequence AW322500, mel transforming oncodened
				IIKG 1	
				ivius musculus testis e	winds musculus testis expressed homeobox mRNA, complete cds, RIKEN cDNA
,				3430405H0Z gene, R	5430405H02 gene, RIKEN cDNA 5730599009 gene, TG interacting factor,
200	19184	19184 AI178025	p, q, kk	lor(beta)-induced free transfer to the transfer	Tor (beta)-Induced transcription factor 2-like, TGFB-induced factor (TALE family
				Mis misculus Arract	Mis misculus Arrectin Lot 2 - (TALE family homeobox)
888	16584A	16584 AI013765	×	complete cds, RIKEN	complete cds, RIKEN cDNA 1200006117 nene arrestin 3 noting and 1200006117 nene
	-			expressed sequence A	expressed sequence Al326910, retinal Santionan
				Mus musculus, Arresti	Mus musculus, Arrestin, beta 2, clone MGC:6525 IMAGE:2651372 mRNA
1820	16581 N	16581 NM_012911	66	complete cds, RIKEN o	complete cds, RIKEN cDNA 1200006117 gene, arrestin 3. retinal. arrestin heta 2
				expressed sequence A	expressed sequence Al326910, retinal S-antigen
1965	2676NI	5676 NM_017188	ee, ff	Mus musculus, clone II	Mus musculus, clone IMAGE:3588380, mRNA, partial cds, unc-119 homolog (C.
2404	22400			Mis miscellis done	olog (C. elegans)
1617	100+C7	23460 NINI_U243/5	n, o	factor 10	factor 10
				71 MAN.	

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אל הלי	•	GenBank Acc.		TO SELECTION OF THE PARTY OF TH	** Atty. Ref. 44921-5090-01-WO/2105485
٩	GLGC ID No.	No.	Model Code Human Hom	ologous Known Gene Name Human Homologous Sequence Cluster	
				Mus musculus, glutathione S-transferase, mu type 3 (Yb3), clone MGC:30483 IMAGE:4166881, mRNA, complete cds, RIKEN cDNA 0610005A07 gene.	clone MGC:30483 005A07 gene.
658		23927 AA957007	8	glutathione S-transferase MZ (muscle), glutathione S-transferase M5, glutathione S- transferase mir 5 glutathione S-transferase M5, glutathione S-	erase M5, glutathione S
				Mus musculus, glutathione S-transferase, mu type 3 (Yb3), clone MGC:30483	3) clone MGC:30483
				IMAGE:4166881, mRNA, complete cds, RIKEN cDNA 0610005A07 gene, RIKEN	005A07 gene, RIKEN
2265	20862	20862 NM_031154	w, x	CDNA 1110004G14 gene, glutathione S-transferase M2 (muscle), glutathione S-	scle), glutathione S-
				Mus musculus, Similar to Acetyl-Co A acetyliransterase 1, mitochondral, clone	-transterase, mu 5
				MGC:39067 IMAGE:5365469, mRNA, complete cds, Mus musculus, Similar to	usculus, Similar to
				hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-	yme A thiolase/enoyl-
				Coenzyme A hydratase (trifunctional protein), beta subunit, clone MGC:7126	lone MGC:7126
				IMAGE:3158015, mRNA, complete cds, acetyl-Coenzyme A acyltransferase	acyltransferase
				(peroxisomal 3-oxoacyl-Coenzyme A thiolase), hydroxyacyl-Coenzyme A	Soenzyme A
2533	1728N	1728 NM 133618	*	dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase	zyme A hydratase
<del> -</del>			\	(trifunctional protein), beta subunit	
				Mus musculus, Similar to aspartyl-tRNA synthetase, clone MGC:6719	3C:6719
2432	25°94 N	25F94 NM 053799	ii. kk. ii	IMAGE:3586278, mRNA, complete cds, asparaginyl-tRNA synthetase, aspartyl-	nthetase, aspartyl-
-	<del> </del>			IKNA synthetase, lysyl-tRNA synthetase	
				Mus musculus, Similar to complement component 1, s subcomponent, clone	nponent, clone
_				MGC:19094 IMAGE:4196654, mRNA, complete cds, Mus musculus, Similar to	sculus, Similar to
74	2098 A	20998 AA799803	b. l. m	complement component 1, s subcomponent, clone MGC:28492 IMAGE:4166254,	92 IMAGE:4166254,
$\vdash$	<del> </del>			ImKNA, complete cds, complement component 1, s subcomponent, protein C	nent, protein C
				Mus musculus, Similar to coronin, actin binding protein, 2A, clone IMAGE:4984475,	one IMAGE:4984475,
2504	21695 NI	21695 NM_130411		mKNA, partial cds, coronin, actin binding protein 1A, coronin, actin binding protein,	actin binding protein,
				Mus musculus. Similar to cortactin isoform B. close McD: 18474 MACE: 2004 FED	74 IMACE: 2004FF0
		-		mRNA, complete cds, contactin, ems1 sequence (mammary tumor and squampins	mor and squamous
750	19058 AF054618		± 0	cell carcinoma-associated (p80/85 src substrate), hematopoietic cell specific I vn	lic cell specific I vn
-	3	T	E (20)	substrate 1, hematopoietic cell-specific Lyn substrate 1	
		-		Mus musculus, Similar to cyclin K, clone MGC:28173 IMAGE:3986609, mRNA,	3986609, mRNA,
2417	3454NN	3454 NM 053662	0.0	Complete cds, Paneth cell enhanced expression, RIKEN cDNA 1810009O10 gene,	. 1810009O10 gene,
	   	1		cyclin 1, cyclin 12	

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ا الا الا	בי ו ט	GenBank Acc.		
			ikionei code	would Code Human Hamologous Known Gene Name Human Homologous Sequence Cluster Title
				Mus musculus, Similar to cyclin K, clone MGC:28173 IMAGE:3986609, mRNA.
2417		3455 NM_053662	p, q, gg	complete cds, Paneth cell enhanced expression, RIKEN cDNA 1810009010 gene,
				Mis miscribis Similar to foth: aid his di
7377		19512 NM_053365	:=	IMAGE:3670866, mRNA. complete cds. fatty acid binding protein 4, adipocyte, clone MGC:18548
				Mus musculus, Similar to glutathione peroxidase 3 (plasma), clone MGC:19204
2131	_	NM_022525	S. dd	IMAGE:4237630, mRNA, complete cds, glutathione peroxidase 3, glutathione
17		22646 AA799301	0	peroxidase 3 (plasma)
				Mus musculus, Similar to ligatin, clone IMAGE:4982955, mRNA, partial cds. ligatin
				Mus musculus, Similar to N-arginine dibasic convertase 1, clone MGC,25477
1883		1310 NM_013159		IIIMAGE:4486176, mRNA, complete cds, insulin degrading enzyme, insulin-
				uegrading enzyme
	_			Mus musculus, Similar to phospholipase C, gamma 2 (phosphatidylinositol-specific).
				clone IMAGE:3983937, mRNA, partial cds, cell differentiation and embryonic
1891	1714	1714 NM_013187	a, 疾	development, expressed sequence Al894140, phospholipase C, gamma 1 (formerly
				subtype 148)
				Invited introduction of the independent of the inde
1175	9166	9166 AI137406	<u>*</u>	IMAGE:1054063, mRNA, complete cds, protein C receptor, endothelial, protein C
				receptor, endothelial (EPCR)
				Mus musculus, Similar to solute carrier family 22 (organic anion transporter),
				member 7, clone MGC:18877 IMAGE:4236556, mRNA, complete cds, expressed
2391	31 N	31 NM_053537	q	sequence Al648912, solute carrier family 22 (organic anion transporter), member 6,
-				Solute carrier family 22 (organic anion transporter), member 7
				Mus musculus, similar to src homology three (SH3) and cysteine rich domain, clone MGC:38869 IMAGE:5361431, mRNA, complete cds. RIKEN china 2610027402
	-	-		gene, RIKEN cDNA 2610301F02 gene, alpha-spectrin 1, erythroid. nesprin-1
753	20741 A	20741 AF084186		spectrin, alpha, erythrocytic 1 (elliptocytosis 2), spectrin, alpha, non-erythrocytic 1
			1 6	(alpha-fodrin), src homology three (SH3) and cysteine rich domain
2099	762N	762 NM 022245		Mus musculus, Similar to sulfite oxidase, clone MGC:28458 IMAGE:4160277,
				MRNA, complete cds, RIKEN cDNA 0610009N12 gene, cytochrome b-5
				mins missuins, similar to sumte oxidase, clone MGC:28458 IMAGE:4160277,
7221	14970JN	14970 NM_031127 a	a, h, l, n, o	In the substance was range to 1010044022 gene, RIKEN cDNA 2810034J18
				ביייני לייני ליייני ליייני לייני לייי

IABLE 3				一
SEO	GenBank Acc.	Acc		
<u>ල</u>	GLGC ID No.		Model Code Human Homo	logous Known Gene Name.
1617	18482 AI639151	66		
674	11500 AA963171	<u>8</u>		Musashi homolog 1(Drosophila), Musashi homolog 2 (Drosophila), RIKEN cDNA 4933434411 gene, expressed sequence AA959857, heterogeneous nuclear
116 1	10320 AA800855		E	nbonucleoprotein A/B, hypothetical protein DC50, musashi homolog 1 (Drosophila)
2537	817 NM 134350			myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse).
2443 1	6761 NM 05385	T		myxovirus (influenza virus) resistance 2
	18 109 AI104528	->		N-acetyltransterase 1 (arylamine N-acetyltransferase)
91 2	11,65 AA800179	s, t		(17kD, B17)
2011 17	75,02 NM 017357	7 00		Neural visinin-like protein 1, RIKEN cDNA 4921521K07 gene, expressed sequence
	3931 AI008697			Al8465/0, hippocalcin like 4, visinin-like 1
	2 16 A1176500			neuroligin 1, neuroligin 2, neuroligin 3
1564 22	22 17 Ai235948			Nidogen (enactin), nidogen (Nidogen (Nidogen (enactin), nidogen (N
			-	micdear localization cinnal deleted in values in the contraction in th
80 18	18:78 AA799888	돌		Signal protein absent in velo-cardio-facial patients
2	10030Z AI009019			nuclear receptor subfamily 2, group F, member 6
	22 NM 024388	× ×	-	nuclear receptor subfamily 4, group A, member 1
4	4622 NM 053463		-	nuclear receptor subfamily 4, group A, member 1
		$\top$	-	nucleobindin, nucleobindin 1
2319 202	20210 NM_031710	n' ^		odorant receptor S1 gene, olfactory receptor 41, olfactory receptor, family 6,
				Paired basic amino acid cleaving enzyme (furin), paired basic amino acid cleaving
2529 253	25369 NM_133559	E,		enzyme (furin, membrane associated receptor protein), proprotein convertase
				Subuistinkexin type 3, proprotein convertase subtilisin/kexin type 4 paired basic amino acid cleaving enzyme (furing membrane accounts)
	16330 NM_019331	# 'i' ∏		protein), proprotein convertase subtilisin/kexin type 3, proprotein convertase
2364 158	15867 NM_053289	a, h, l, w, x	×.×	Subulisitir/Rexitir type 4
				parcreatus-associated protein

TABLE 3			Programme of the second	CHARLE V.	
א ה	9	GenBank Acc.		Alty Ref 44991-5000 A Micharder	OPACEADE
Ω	GLGC ID No.	<u>o</u>	Model Code Human Hom	Ologotis Known Gene Memo	CO#CO 7/O
1006		8539 AI059175	<sub>O</sub>		
2478		15391 NM_057114	P	pericentriolar material 1	
2137		9240 NM_022540	i, k, w. x	peroxiredoxin 1	
1879		46 NM_013151	D. a	peroxiredoxin 3	
1865		20878 NM 013085	P	plasminogen activator, tissue	
				plasminogen activator, urokinase	
	_		a, p, q, y, z,	poliovirus receptor, poliovirus receptor-related 1, poliovirus receptor-related 1	7.0
1931		923 NM_017076	ee, ff	(nerpesvirus entry mediator C; nectin), poliovirus receptor-related 2 (herpesvirus	svirus
0200			a, d, r, y, z,	entry mediator b), poliovirus sensitivity, tumor-associated antigen 1	
5/77		18654 NM_031358	ee, ff, kk	rectifiing change of annel, subfamily J, member 11, potassium inwardly-	inwardly-
2273	40CCC NIA	02000		Dotassium invigrally coefficient 11	
4700	10000 ININ 031358	A_031358	d, I, m, jj, kk	rectifying channel subtamily J, member 11, potassium inwardly-	inwardly-
3 6	43010L23803	3803	n, o	DOLL Acceptage Granter, Subdilling J, Member 11	
18/3	7854 NM	7854 NM_013115	h, -	LOU domain, class 2, transcription factor 3, POU transcription factor	
				prostaglandin F receptor, prostaglandin F receptor (FP)	
2326	4325 NM_031784		0	protein inhibitor of activated STAT 1, protein inhibitor of activated STAT 3 profein	Infain
				inhibitor of activated STAT gamma, protein inhibitor of activated STAT	
2429	1016 NM_053772		r, 9g	protein kinase (cAMP-dependent, catalytic) inhibitor alpha, protein kinase inhibitor	hibitor
_				alpha	
-				PRP31 pre-mRNA processing factor 31 homolog (yeast), RIKEN cDNA	T
2087	20035 NM_021754		a, y, z	1500019016 gene, nucleolar protein 5, nucleolar protein 5A (56kD with KKF)	
				repeatl, nucleolar protein NOP5/NOP58	)
2460	18798 NM_053978		h, l, n, o	RAB11a, member RAS oncogene family, RAB28, member RAS oncogene family	, imily
2016	20778 NM_019124			expressed sequence AW496496	
2490	11632 NM_057212		٩	rabaptin 5, rabaptin-5	
				Ras-induced senescence 1	
2008	15037 NM_017347		e. r	Rattus norvegicus extracellular signal-regulated kinase 7 mRNA, complete ede	ę
				mitogen activated protein kinase 3, mitogen-activated protein kinase 7	 ŝ
			-	Rattus norvegicus kallistatin mRNA, complete da, serine (or cysteine) proteinase	0360
1407	6455 AI179984	_	aa. bb	Inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor) member	mhor .
236	15160 AA859346		u, v	1, serine protease inhibitor 2	
2154	17808 NM_022699		Sc. dd	nbonuclease P (38kD)	T
2122	1867 NM_022510		S K	Iribosomal protein L30	
		1		ribosomal protein L4	1
					_

TABLE 3	3		Sec. Sec.	
SEO		IGenBank-Acc		· · · · · · · · · · · · · · · · · · ·
으	GLGC ID No.	No.	Model Code	
1897		20864 NM_013215	b, I, m	RIKEN cDNA 0610025K21 gene, aldo-keto reductase family 7, me
2252		6525 NM_031129		RIKEN cDNA 0610040H15 gene, RIKEN cDNA 2210409E12 gene, transcription
591	4-2	14763 4404481	5	RIKEN cDNA 1110007F23 gene, angiopoietin-like 3, angiopoietin-like 3, angiopoietin-like 4, ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin), ficolin
510		4907 AA924091	ž	(collagen/fibrinogen domain containing) 1, ficolin B RIKEN cDNA 1110031102 gene, gene rich cluster, B gene, hypothetical protein
2397	21940	21940 NM_053568		RIKEN CHARAZERA AND ARCARIA MARAMATA MA
				RIKEN CDNA 1300003A17 gene, RIKEN CDNA 3222402004 gene, expressed
420	07070	07070		sequence C76800, hypothetical protein DKF2p761B2423, myeloid/lymphoid or mixed-lineage leukemia, nucleolar and coiled-body phosphoprotein 1, nucleolar and
2	21747	FA0032313	0	coiled-body phosphprotein 1
				RIKEN cDNA 1300003A17 gene, RIKEN cDNA 3222402O04 gene, expressed sequence C76800, hypothetical protein DKF2n764R2423, myslyiddhymahold or
2160	24283	24283 NM 022869	+	mixed-lineage leukemia, nucleolar and coiled-body phosphoprotein 1, nucleolar and
				Colled-body phosphprotein 1
				KIKEN cDNA 1300010C19 gene, RIKEN cDNA 5730543C08 gene, Ras-related GTP-binding protein, expressed sequence Al255374 small GTP-sea hamala (S
2459	15343	15343 NM_053973	33	cerevisiae)
C#7	) (2011	11635/AA859645	J, K, II	RIKEN cDNA 1300011D16 gene, attractin, testis infracellular mediator protein
2128	10404	4242 MM 022521	£	RIKEN cDNA 1300019H02 gene, RIKEN cDNA 2900006B13 gene, ornithine
200	11368/	11368 AI007948	E   E	aminotransferase, ornithine aminotransferase (gyrate atrophy)
1342	103107	10310 AI176961		IRIKEN cDNA 1500006009 gene, hypothetical protein FLJ23445
1			2	RIKEN cDNA 1500031N16 gene, mitochondrial ribosomal protein L12
2555	8468	8468 NM_138861	p	prolactin-like protein M, proliferin, proliferin 2
				RIKEN cDNA 1700024D23 gene, RIKEN cDNA 4731413G05 gene, potassium
				channel TREK-2, potassium channel, subfamily K, member 2, potassium channel,
134	1754 A	1754 AA817837	_ <del>*</del>	Subramily K, member 2 (TREK-1), potassium channel, subfamily K, member 5,
				potassium channel, subramily N, member 5 (1ASK-2)

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رين ا	8	GenBank Acc.			Color Delicate Trace Trace Colored Col
		No.	Model Code	Model Code Human He nologous Known Gene Name Human Homologous Sequence Cluster Title	quence Cluster Title
9	. }	21:20 AA799526	p, q, gg	RIKEN cDNA 1700043E (18kD)	RIKEN cDNA 1700043E15 gene, small nuclear ribonucleoprotein D3 polypeptide (18kD)
1255		17529 A1171460	- 'u	RIKEN cDNA 1810026B04 gene, (17-beta) dehydrogenase 8, hypot FL 114431, oxidoreductase 1 ICPA	RIKEN cDNA 1810026B04 gene, dicarbonyl/L-xylulose reductase, hydroxysteroid (17-beta) dehydrogenase 8, hypothetical protein BC014057, hypothetical protein FLJ14431, oxidoradictase ILCPA
1699		24520 L20869	a)	RIKEN cDNA 2010002L1 derived 3 gamma	RIKEN cDNA 2010002L15 gene, pancreatitis-associated protein, regenerating islet- derived 3 gamma
628		884 AA946362		RIKEN CDNA 201006G	RIKEN cDNA 2010006G21 gene. RIKEN cDNA 2810425K19 gene. sorting gevin 5
423		19124 AA893022	:=	RIKEN cDNA 2310016C	RIKEN cDNA 2310016C16 gene, RIKEN cDNA 3110050F08 gene, glutathione peroxidase 4, glutathione peroxidase 4 (phospholipid hydroperoxidase)
434		16168 AA893280	a, y, z	RIKEN cDNA 2310076L09 ge differentiation-related protein	RIKEN cDNA 2310076L09 gene, adipose differentiation related protein, adipose differentiation-related protein
				RIKEN cDNA 2410002J2 AV278559, expressed se	RIKEN cDNA 2410002J21 gene, activator of CREM in testis, expressed sequence AV278559, expressed sequence AW123232, four and a half LIM domains 2,
665	]	12529 AA957362	P	paxillin, transforming grov GAP/TBC-containing	paxillin, transforming growth factor beta 1 induced transcript 1, vascular Rab-GAP/TBC-containing
576		AA943766	×-	RIKEN cDNA 2410004D1	RIKEN cDNA 2410004D18 gene, RIKEN cDNA 4930485D02 gene,
2109	1 1	13480 NM 022390		RIKEN CDNA 2610008L0	RIKEN cDNA 2610008L04 gene, guinoid dihydropteridine reductase
2345		17556 NM 031975	*	RIKEN cDNA 2610009E1	RIKEN cDNA 2610009E16 gene, parathymosin, prothymosin alpha
2517	90,4	NM_133386	ee, ff	RIKEN cDNA 2610037M1	RIKEN cDNA 2610037M15 gene, sphingosine kinase 1, sphingosine kinase 2
				RIKEN CDNA 2610103M1	RIKEN cDNA 2610103M17 gene, excision repair cross-complementing rodent
•				repair deficiency, complei rodent repair deficiency, c	repair deliciency, complementation group 1, excision repair cross-complementing fodent repair deficiency, complementation group 1 (includes overlapping antisense
411	21972,	21972 AA892791	:=	(ecuenbes	
263	42227	4222 AA860024	h, l, w, x	RIKEN cDNA 2610301D0	RIKEN cDNA 2610301D06 gene, eukaryotic translation elongation factor 1 gamma
871	16984 /	ļ	aa, bb	RIKEN cDNA 2610301D0	RIKEN cDNA 2610301D06 gene, eukaryotic translation elongation factor 1 gamma
2006	163821	16382 NM_017343	ල දි	RIKEN cDNA 2900073G1.	RIKEN cDNA 2900073G15 gene, myosin regulatory light chain
2607	21583 877900		bb, kk	RIKEN cDNA 2900073G1 (RLC), myosin, light polypu	RIKEN cDNA 2900073G15 gene, Rat mRNA for myosin regulatory light chain (RLC), myosin, light polypeptide, regulatory, non-sarcomeric (20kD)

TABLE 3	en en		" (	The state of the s	Att. Ref Adopt. Fright Michiganisass
SEO		GenBank Acc.			
<u>.</u>	ਲ	No.	Model Code Human Horn	Human Homologous known Gene Name	Human Homologous Sequence Cluster Title
827		18438 AI010930	e, r		RIKEN cDNA 3100001N19 gene, ribosomal protein L14
1154		18439 AI111877	Į.		RIKEN cDNA 3100001N19 gene, ribosomal protein L14
2166		18107 NM_022949	f, g		RIKEN cDNA 3100001N19 gene, ribosomal protein L14
		000000			RIKEN cDNA 3200002106 gene, dynein, cytoplasmic, intermediate chain 2, dynein,
744/		135ZININ_U5388U	aa		cytoplasmic, intermediate polypeptide 2, hypothetical protein MGC20486
700		4 4 0 4 70 6 7	:		RIKEN cDNA 4930425N13 gene, hexosaminidase A, hexosaminidase A (alpha
138		14101 AA81/86/	=		(polypeptide)
1272		16293 AI172183	ပ		RIKEN cDNA 4930441F12 gene, reticulon 1, reticulon 2, reticulon 2 (Z-band associated protein)
3					RIKEN CDNA 4930544G11 gene, expressed sequence Al324259, ras homolog 9
1394		7; 13/AI179356	w, x		(RhoC), ras homolog A2, ras homolog gene family, member C
			y, z, ee, ff,		
2553	- [	23, 66 NM_138839	촟		RIKEN cDNA 4930579A11 gene, likely ortholog of rat vacuole membrane protein 1
2200		COSCSO PAIN			RIKEN cDNA 5031400M07 gene, homocysteine-inducible, endoplasmic reticulum
2007	- [	100.20 MINI UD3DZ3	00		stress-inducible, ubiquitin-like domaiń member 1, hypothetical protein FLJ22313
					RIKEN cDNA 5730414C17 gene, hippocampus abundant gene transcript 1,
336		21851 AA891535	jo G		hypothetical protein DKFZp564L0864 similar to HIAT1, hypothetical protein
	l	T	35 (2)		1 LJ 14/JJ
	-	-			RIKEN cDNA 5730454C12 gene, expressed sequence C79945, glutamine fructose-
	·				6-phosphate transaminase 1, glutamine fructose-6-phosphate transaminase 2,
	7007	1040001			glutamine-fructose-6-phosphate transaminase 2, phosphoribosyl pyrophosphate
220	(30/2)	reor A1043695	_		amidotransferase
2622	1/2000	NEUTALI ACCOC	: : 2.		RIKEN cDNA 5/30592LZ1 gene, hypothetical protein FLJ14927, proprotein
7707	- (	T	o, u, v		convertase subtilisin/kexin type 5, thrombospondin, thrombospondin type 1 domain
8 5	- (	1/303/AA8/4990	u, v, w, x		RIKEN cDNA 6330407G11 gene, hypothetical protein FLJ10342
743/	-	T	cc, dd		RIKEN cDNA 6720463E02 gene, dynein light chain 2
					RIKEN cDNA C030018L16 gene, SMC (segregation of mitotic chromosomes 1)-like
					1 (yeast), SMC (structural maintenace of chromosomes 1)-like 2 (S. cerevisiae),
					SMC (structural maintenance of chromosomes 1)-like 1 (S. cerevisiae), SMC1
6	400004				structural maintenance of chromosomes 1-like 1 (yeast), SMC4 structural
797	1011827	16/382 AA8/488/	=		maintenance of chromosomes 4-like 1 (yeast)

TABLE	TABI E 3		> <b>^</b>	,
i iii	   	GenBank Acc.		
<u>ء</u>	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name Human Homologous Sequence Cluster Iffle
2454		161-52 NM_053961	h, I, n, o	RIKEN cDNA C030022K24 gene, chromosome 12 open reading frame 8, endonlasmic retirulum protein 20.
2454		16553 NM 053961	h. I	RIKEN CDNA C030022K24 gene, chromosome 12 open reading frame 8,
1007		70007		RNA polymerase II transcriptional coactivator, activated RNA polymerase II
7601		23480 KU2816	8 8	transcription cofactor 4
1518		13645 A 232694	£	SEC24 related gene family, member C (S. cerevisiae)
/84		9150 AI009198	=	serine/fhreonine kinase receptor associated protein. unr-interaction protein
504	16976	16976  A A 901341	۵	sialyltransferase, sialyltransferase 7 ((apha-N-acetylneuraminyl 2,3-beta-galactosyl-
2165		18104 NIM 022948	1. N	1,3)-N-acetyl galactosaminde alpha-2,6-sialyltransferase) B
3 8		10107 NINI 022340		sideroflexin 1, sideroflexin 2, sideroflexin 3
26.5	77207	1440000	66 :	signal recognition particle 68kD
193	87,877	23428 AIT 13320	=	similar to arginyl-tRNA synthetase
8	3600	3600 NM 012751	а	Solute carrier family 2 (facilitated alucase transmorter) member 4
1788	3601	3601 NM_012751	-	solute carrier family 2 (facilitated olucose transporter) member 4
25	1/468/	1/468 AA892545	-	solute carrier family 22 (organic cation transporter), member 1-like
2200		MA OFFICE	1 1 1	solute carrier family 27 (fatty acid transporter), member 1, solute carrier family 27
5023	83	USCECU_WINITECO	aa, oo	(fatty acid transporter), member 4
1921	24695	24695 NM 017049		solute carrier family 4 (anion exchanger), member 3, solute carrier family 4, anion
288	15116 A	15116 AA874928	2 4	exchanger, member 3
1585	1404	4404 A1937009	- 1	Sorting nextr 4
300	1000	900 NIM 004400	E -	spermidine synthase, spermine synthase
2000	N 700	IM UST 123	D	stanniocalcin, stanniocalcin 1
6030	200761	COCCCO MINI OD JCI	p, q, y, z	STAT induced STAT inhibitor 3, cytokine inducible SH2-containing protein 3
1437	15078 A	15078 AI228830	j, k	Stearovt-CoA desaturase (delta-9-desaturase) stearovt-CoA
2339	15077 N	15077 NM 031841		Acadulase A desalutase (John acadulase A desalutase), steatofic A desalutase A
604	4207 A	4207   AA945591	×××	steatuyr-volv desaturase (delta-s-desaturase), stearoyr-voenzyme A desaturase 2
2150	20509 N	g	h r 11 V	suomai celi denved factor 2, stromai celi-denved factor 2-like 1
		T	2	Synaprosomal-associated protein, 23kD
744	15772 AB015645	•	55 G	thyrotropin releasing hormone receptor, thyrotropin releasing hormone receptor 2,
			33.62	iniyodopin-feleasing normone feceptor

TABLE 3	62			· · · · · · · · · · · · · · · · · · ·
SEO		GenBank Acc		1986年 1987年
٥	GLGC ID No.	No.	Model Code	Model Code Human Homologous Known Gene Name Human Homologous Sequence Cluster Title
i i			a, l, n, o, x,	
1553		15004 AI235224	z, Kk	(erythroid potentiating activity, collagenase inhibitor)
			a, I, k, n, o,	tissue inhibitor of metalloproteinase, tissue inhibitor of metalloproteinase 1
2435	15002	15002 NM_053819	x, z, hh, kk	(erythroid potentiating activity, collagenase inhibitor)
2425	4000	070070	a, I, K, n, o,	tissue inhibitor of metalloproteinase, tissue inhibitor of metalloproteinase 1
242	SUUCI	ST85CU MINI COUCT	X, Z, NN, KK	(erythroid potentiating activity, collagenase inhibitor)
32	18706	18706 AA799471	D	titin-cap (telethonin)
477	17243	17243 AA899894	ſ	TRAM-like protein, translocating chain-associating membrane protein
쬺	8089	A1045600	w, x	TRAM-like protein, translocating chain-associating membrane protein
2134	120	7: 05 NM_022534	:=	transcobalamin 2. transcobalamin II: macrocytic anemia
2253	13, 29	VM_031131	n, o, hh	transforming growth factor, beta 2
1887	21. 22	UM 013174	j, &	transforming growth factor heta 3
1887	21:23	UM_013174	D'd	Itansforming growth factor, bata 2
126	12,399/	VA801307	00. II	franctuming ground and a collection of the colle
774	12:498/	1008689	5.4	tomoforming, adultic colleging protein 1
439	26897	A893515		uarsionning, addic colled-coll containing protein 1
	31	010000	=	translocation protein 1
700	40777	1000		Treacher Collins Franceschetti syndrome 1, homolog, Treacher Collins-
B	143421	14:4Z/AA904090	n, l, S, t	Franceschetti syndrome 1, expressed sequence AA408847
				tumor necrosis factor receptor superfamily, member 12, tumor necrosis factor
				receptor superfamily, member 12 (translocating chain-association membrane
			1	protein), tumor necrosis factor receptor superfamily, member 1A, tumor necrosis
1000	4504	4504 Nills 040004	a, s, t, ee, π,	factor receptor superfamily, member 1a, tumor necrosis factor receptor superfamily,
1227	1701	W_013031	J, KK	member 22, tumor necrosis factor receptor superfamily, member 23
3	S 100	3019/A11/6388	l, K	tumor protein p53-binding protein
	A 02.2		n, 0, W, X	TYRO protein tyrosine kinase binding protein
200	IO400 A			ubiquinol-cytochrome c reductase (6.4kD) subunit
07.1	22/08 A	ZZ/U8 AA946U63	u, v	ubiquitin-like 3
7267	18596 N	18596 NM 031325	u, v	UDP-glucose dehydrogenase
			a, j, k, p, q,	
2267	18597 N		y, z, ee, ff	UDP-glucose dehydrogenase
/027	4584 N		0	vipirin, viral hemorrhagic septicemia virus(VHSV) induced gene 1
0/77	N 2500		t, g	voltage-dependent anion channel 1
7777	10//N	16/7/JNM_031354	E I	voltage-dependent anion channel 2

TABLE 4		Atty. Ref. 44921-5090-01-WO/2105485
Model	code	
Adrenergic Agonist		(1113)
Alkylating Agents	a b	various
Adriamycin		various
Adriamycin	d d	120, 168
Amphotericin B		6, 24
BI: Alternate	e f	6
BI: Core Tox Markers		168, 336
Clenbuterol: Alternate	<u>g</u>	168, 336
Clenbuterol: Core Tox Markers	h	24
Clenbuterol: Alternate		24
Clenbuterol: Core Tox Markers		6
Cyclophosphamide: Alternate	k	6
Cyclophosphamide: Core Tox Markers		6, 48, 192
Epinephrine: Alternate	m	6, 48, 192
Epinephrine: Core Tox Markers	n	24
Epinephrine: Alternate	0	24
pinephrine: Core Tox Markers	р	3, 6
Epirubicin	q	3, 6
Hydralazine: Alternate	r	6, 192
Hydralazine: Core Tox Markers	s	6 .
fosphamide: Alternate	t	6
fosphamide: Core Tox Markers	u	48, 144
soproterenol: Alternate	V	48, 144
soproterenol: Core Tox Markers	w	24
soproterenol: Alternate	х	24
soproterenol: Core Tox Markers	у	3, 6
Inoxidil: Alternate	Z	3, 6
finoxidil: Core Tox Markers	aa	24, 360
orepinephrine: Alternate	bb	24, 360
orepinephrine: Alternate orepinephrine: Core Tox Markers	cc	24
orepinephrine: Core Tox Markers orepinephrine: Alternate	dd	24
oreninenhrine: Cara Tarakt	ee	3, 6
orepinephrine: Core Tox Markers henylpropanolamine	ff	3, 6
henvintopariolamine	gg	3
henylpropanolamine osiglitazone	hh	6, 24
eneral	ii	24
	jj	various
eneral Core Tox Markers	kk	various
asculature Agents	11	various

LGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	en N
15002	93.1848			188.7073	
17736			762.4182	584.9220	133.91
15003	90.1662		472.1444	74.9787	266.08
11531	88.3378		707.5785		129.47
17735	88.1250		1147.6615		216.88
19040	87.5598		97.4225		435.22
17734	86.8816		1099.6429	248.9995	69.86
1892	86.7420		578.1713	996.2423	363.52
17401	86.6157	1311.1640	474.9087	1178.1967	332.29
22321	85.6582	404.6838	160.3726	584.6204	187.58
10071	85.6582	555.2923	198.1929	166.4941	84.17
15510	85.5585	193.2422		256.3717	89.84
14213	85.3723	58.2154	44.9524	283.7898	52.47
17161	85.0532	587.4333	43.1912	4.8459	16.23
11530	85.0000	721.6317	355.2130	193.6993	89.147
22499	84.9867		412.9801	194.6598	129.93
20743	84.6011	43.9754	12.0409	20.1660	11.362
16168	84.3085	110.1523	18.0460	156.2806	27.23
1271	83.7500	322.1775	121.4265	171.7767	45.17
574	83.1383	57.0368	11.4631	80.9952	15.333
15540	83.0984	997.6258	268.7816	592.6405	136.063
17217		222.6751	196.0708	49.6568	39.20
19710	83.0785	299.9600	61.9276	408.5918	79.050
18654	82.8723	95.2966	31.4037	47.0879	21.051
7196	82.8258	115.9148	55.4920	221.2713	63.026
923	82.8059	241.5608	48.6689	167.6215	40.834
18389	82.5665	80.3798	60.4940	15.2547	11.665
14206	82.0745	1698.2519	653.3550	804.3228	432.996
	82.0545	32.6432	13.0018	78.1153	56.068
10185	81.9082	19.2150	5.2091	31.5730	10.404
20448	81.5359	510.4135	424.2980	65.6248	72.186
23781	81.3098	74.7232	26.9707	38.5429	15.272
606	81.2566	22.0283	48.8072	-43.9928	28.744
17601	81.1968	148.6699	25.4993	203.0924	39.345
357	81.1636	75.3102	54.7364	23.9249	12.680
18888	81.1303	18.1279	6.8135	30.9872	11.170
20983	81.0904	336.6510	76.3729	482.8464	107.781
20449	81.0040	704.6277	547.1217	85.9070	122.791
4327	80.9375	138.6356	37.5198	90.1494	26.295
5496	80.9309	50.8946	12.7471	68.9254	13.465
19481	80.9309	75.3548	23.3920	131.9767	42.027
1977	80.8910	384.3716	104.5183	557.5178	106.121
21663	80.7912	1000.0403	524.6985	361.5352	120.143
13940	80.6316	46.2156	17.8341	85.3171	35.690
14970	80.5386	52.0507	17.0768	81.4804	20.098
23058	80.3258	181.5442	53.5652	285.5204	70.946
355	80.0266	80.9323	65.3081	7.7442	
1530	80.0066	140.4712	33.2319	194.9259	23.549
18597	79.8670	286.4668	206.7383	88.5584	41.210
24431	79.8670	278.2754	246.5034		38.858
12118	79.8338	1249.9245	697.4559	69.8804	50.493
22675	79.8005	75.4184	38.8554	522.6811	245.1043
18313	79.7872	4005.3077	732.8548	29.4800	18.4798

GLGC ID	LDA Score	Mean Tox		Ref. 44921-5090-(	
1521	79.7141		SD Tox	Mean Nontox	SD Nontox
11422	79.7074	120.070	<u>3</u> 53.5310	66.7321	32.2
21654	79.4415	. 0.00		114.0781	31.3
2629	79.2819			198 1299	56.8
17908	79.2819			19.6594	9.49
15349		148.8453		40.8903	23.32
18396	79.1622 79.1622	20.5876		5.2367	7.47
5297		99.0622		40.7672	29.00
23868	79.1223	438.7151		198.4258	74.33
18190	79.0691	696.3200	1	201.9544	193.61
4832	78.9960	93.7200		143.9221	
20919	78.9761	590.5971	146.1748	886.5180	34.99
17590	78.9561	416.6138		297.7708	205.81
	78.9162	74.0367	21,4162	47.6340	87.82
244	78.9096	177.7682	130.8882	59.6868	15.38
2628	78.8564	44.9283			32.34
12580	78.7566	32.9518	9.7960	9.0629	12.43
15867	78.7035	81.2703	45.4669	19.1548	9.15
3337	78.6104	39.5081	9.7943	38.1658	53.49
19252	78.5572	466.7698	45.7445	56.9440	15.70
3244	78.4774	129.7236	33.9837	567.3424	97.14
16081	78.3777	202.8438	112.5844	177.7022	32.598
15281	78.2779	170.8618		84.0263	61.559
1715	78.2114	150.0634	35.8977	121.2837	28.791
20856	78.1582	823.1658	26.4880	111.5965	27.472
10016	78.0984	310.8434	173.6071	1104.4375	180.641
12978	78.0918	240.0713	90.6794	198.7584	58.386
2846	78.0585	41.5447	187.0521	72.7926	27.100
622	77.9189	27.005	12.8468	63.7379	19.455
23869	77.7726	27.3665	7.5757	45.8306	19.121
20855	77.7527	161.8403	143.4543	38.7388	52.518
223	77.6662	539.5765	102.8442	705.3220	119.792
21445	77.5798	84.7102	79.8305	11.2148	19.494
1377	77.5798	58.4069	47.4152	9.3169	20.305
1714	77.5598	37.4036	11.7847	58.0973	19.441
11423	77.5266	128.4936	26.6958	176.9989	41.124
18108		126.9625	37.6497	205.5892	65.968
2150	77.4934	201.3502	36.4083	156.6728	22.5172
2555	77.4601	120.5581	20.2371	153.8331	33.2591
356	77.4202	78.3837	37.8776	45.1706	
23368	77.4003	153.3145	116.5924	37.9370	21.4351
19279	77.3803	286.7193	78.0081	410.2601	35.8682
21653	77.3604	145.1303	22.8084	175.9706	90.1102
21950	77.3138	193.7593	75.5197	114.0782	22.2452
1475	77.2074	635.8636	108.3591	771.6337	37.2720
3292	77.1676	987.8538 1	118.1009	79.7411	137.9339
	77.1343	46.3794	53.4058	-2.2895	129.4689
21662	77.1210	25.1074	18.0661		28.6104
15379	77.1011	69.7288	26.6900	3.2638	10.9879
3600	77.0811	351.9825	98.1033	110.1162	36.4938
6606	91.6955	4.4.	137.7211	482.5987	117.8029
15004	88.8697	4400 = 4==	600.2896	1800.9361	632.4547
21796	88.5705		147.4609	309.0121	203.5315
3014	88.4508	112.1745	49.0365	261.0573 253.1593	79.3455

SLGC ID	LDA Score	Mean Tox	SD Tox	INGO TO A TO THE OWNER OF THE OWNER O	
23038			<u> </u>	Mean Nontox	
7665					121.6
23123	87.0080				63.90
7414	86.6356				81.16
11684	86.5160				52.29
22197	86.3497			193.3221	50.52
24246	86.2832	246.4543		114.9586	42.99
22378		406.3073		269.3370	65.81
24209	86.1237	156.7941	51.2980	274.8932	59.25
	85.1263	84.9209	55.8163	0.6268	38.94
5461	85.0731	227.7101	79.5985	115.4327	36.27
21632	84.7340	486.9037	172.5911	193.9329	83.91
18206	84.4415	298.2611	43.6493	219.0292	
3669	84.3152	54.9250	16.7575	26.5427	50.44
24022	84.0691	60.1513	17.4583	103.0718	16.76
17540	83.8830	614.5749	238.0756	340.9067	26.31
12664	83.5705	53.1247	29.4909	114.3550	100.11
15042	83.5638	125.6087	59.0746		32.54
10072	83.4574	256.6850	119.5995	41.6963	32.66
16154	83.4043	161.8671	82.4309	103.8417	62.88
2742	83.1782	-100.5665	101.5237	73.5311	71.26
6632	82.8191	210.1464		59.4249	79.42
22432	82.7992	212.3237	58.6494	121.7572	39.14
18598	82.5864	101.0807	57.3487	121.2644	31.81
2459	82.5665	107.0807	72.7916	-0.8437	35.260
12086	82.4934	1207.7704	889.6888	93.8630	160.082
23725	82.4867	37.5563	11.7940	58.1680	16.298
8494	82.4535	326.7101	61.7201	218.5422	62.44
2301		619.4279	83.5414	459.5236	98.65
23964	82.4402	75.4272	15.8549	116.2465	30.861
	82.3072	142.6538	32.3372	84.4648	29.807
4420	82.2407	310.0578	85.6928	450.6251	91.369
8495	82.2207	177.6911	31.6153	130.5767	
14494	82.1875	172.9672	31.0657	227.6112	28.812
15283	82.0213	405.2720	78.5347	303.0143	36.864
9317	82.0146	500.5706	75.1872	682.2943	67.454
11426	81.9947	337.2493	90.1085	553.0815	145.596
13634	81.8750	1369.2711	485.0771	906,0004	151.489
19387	81.8617	536.2792	140.6484	806.0391	179.852
24051	81.8152	94.5799	22.7796	364.3634	84.454
13460	81.7753	218.7623	66.2870	145.6245	33.816
6412	81.7686	13.4985	5.4822	337.3528	64.686
9611	81.6223	12.2893		27.2459	12.381
4074	81.5891	7.4619	25.4226	57.7584	32.712
6548	81.5226	375.7787	29.5408	64.5731	43.948
12946	81.5093		105.0735	210.2905	78.220
20035	81.5027	148.1603	34.5002	220.6648	40.706
3905	81.4960	346.7378	149.5983	164.0392	57.348
12979		170.3486	48.0159	90.3576	60.541
22545	81.4827	966.0172	724.9628	294.8817	100.157
21660	81.4827	128.2348	54.8824	203.6431	60.824
	81.4561	2382.4932	487.4179	1592.8149	514.867
18529	81.4362	447.6552	91.3266	285.9677	71.7319
22666	81.3963	182.6728	89.9086	75.6578	
21166	81.3963	531.8921	175.0606	305.9588	31.7036 75.1422

<u>.</u>	ADRENERGIC	AGONIST	Atty. R	ef. 44921-5090-	01-WO/2105485
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
15277	-	1029.9606	170.9360		
18830		5708.1764	1748.0224		1 10.00
16053	01.2000		280.9336		, 000.000
8938		21.3583	23.4652		
22591	81.0904	50.7375	12.5625		<u> </u>
21185	81.0904	441.0886	76.5297		148.1893
21785	81.0439	163.0715	48.9946	93.7917	30.5701

GLGC ID LDA Score   Mean Tox   SD Tox   Mean Nontox   SD North						
25468	84.1196			Mean Nontox	SD Nontox	
20225	84.0526				2425.39	
25600		30.0414		97.4470	57.32	
25469	83.8852	47.2206			19.532	
17160	83.6459	1791.5476		4544.7412	1788.242	
	83.2440	2068.9455		1697.7590	423.38	
1684 4565	83.1196	2947.0329	3556.7192	6788.5893	2953.799	
	82.6651	24.4325	9.4147	43.6687	14.196	
10320 4474	82.3493	47.9014		80.4636	26.63	
20440	82.3397	73.5205	23.9619	38.7337	27.316	
	81.9522	23.8482	22.9362	51.6998	18.95	
20313	81.6890	11.6843	11.8859	29.5962	10.719	
455	81.6029	3635.2910	906.2374	5012.3749	1060.904	
20450	81.5694	48.8815	13.0695	73.0041	22.315	
309	81.4976	588.1575	79.2127	476.1954	81.200	
8269	81.4211	15.6709	4.3619	21.9461	9.516	
15573	81.3493	84.8163	10.9516	105.8035		
16947	81.2010	53.0476	11.7092	76.8846	18.100	
15083	81.1914	34.2199	13.4606	68.3728	21.955	
25496	81.1292	204.2343	26.9706	157.0878	27.255	
25495	81.1292	178.3991	19.0513	140.0664	37.210	
6654	81.0574	57.3908	16.9442	32.3728	33.963	
22355	81.0431	18.9000	5.0085	32.1376	13.527	
25705	80.8900	543.7402	141.5809		12.816	
24228	80.8804	279.7133	119.0250	357.5528	114.822	
381	80.7368	19.6870	6.7439	157.8901	45.990	
24643	80.6029	169.1690	56.3307	29.2547	10.702	
22583	80.5598	18.3818	5.5890	68.4159	74.127	
2413	80.5072	745.6790	62.8685	24.0195	5.751	
4684	80.4880	87.7172	15.7335	623.5517	103.764	
2832	80.2967	123.6875	17.2399	55.6888	21.884	
15846	80.2440	33.1607	19.0091	151.2548	23.911	
26039	80.1818	57.8518	11.0042	68.4972	33.942	
298	80.0431	37.0221	12.7922	75.8213	15.246	
1108	80.0239	18.0748		59.1687	23.462	
20073	80.0144	7.9412	7.6995	33.1729	11.881	
10248	79.9282	376.3496	16.4752	40.4131	19.179	
767	79.8565	4.3235	53.6001	306.4258	85.425°	
1894	79.7847	295.3987	13.7955	23.0547	15.9343	
18864	79.7799	132.5974	119.1209	147.5070	73.9222	
13595	79.7703	76.1675	18.7576	166.8307	35.1741	
15056	79.7273	6.2067	12.9824	97.0513	18.1780	
385	79.6986	19.5439	6.1665	22.2468	15.6667	
17427	79.5837	318.0867	15.0876	46.3407	22.6844	
20536	79.5837		65.6813	220.1336	64.8948	
200	79.5598	37.0290	24.7335	11.5981	22.3424	
24473	79.4450	55.6074	13.1527	79.4381	22.5161	
18895	79.4450	147.2555	34.7970	207.7485	46.3524	
16448	79.4450	120.9271	21.8233	163.6937	34.7664	
17154	79.3636	96.2256	119.9279	285.0267	130.8231	
20732		1193.0218	321.9846	854.9913	204.4564	
9073	79.2440	13.7055	5.1709	23.4555	9.0599	
17923	79.0670	39.3991	11.2447	21.7348	14.0843	
11923	79.0335	75.8414	12.2287	104.9544	26.5959	

	LDA Score	Mean Tox	Atty. Ref. 44921-5090-01-WO/21054 SD Tox   Mean Nontox   SD Nontox			
25572	78.9809					
18867	78.9234		219.8318			
20998	78.7751		161.5664		00.01	
18032	78.7703		22.1110	278.2811		
16934	78.7512	59.1653		89.4354		
22150	78.7416	217.3971		34.9678		
20864	78.7177	9.1197	42.1239	150.5825	44.28	
20224	78.6555	25.7235	8.3097	24.8080	14.96	
14543	78.6459	41.7789	11.4037	54.8352	23.46	
21928	78.6029	26.2219	18.8904	4.6710	27.26	
8587	78.6029		9.3320	40.2590	12.37	
25752	78.5837	21.3555	10.7080	42.0994	16.82	
167	78.5598	25.6894	42.8635	-49.0965	50.27	
20554	78.5598	385.7359	146.7072	589.7799	173.84	
23215		37.0486	18.4306	76.2388	36.77	
16018	78.5072	76.8105	11.1928	100.4547	26.889	
15990	78.4354	258.9146	45.4960	201.5170	58.227	
15990	78.3493	87.3962	18.5131	117.5183	26.566	
	78.3397	70.4733	26.2187	18.9494	42.629	
25525	78.1722	124.7945	36.3359	78.6745	47.638	
25770	78.0144	91.4328	51.3572	161.4990	59.929	
23294	77.9378	125.3066	16.9407	158.0675	35.676	
25659	77.8852	37.2458	13.2464	90.6507		
25262	77.8756	29.1337	6.8117	42.6468	61.255	
21013	77.8038	232.9595	46.2884	183.4911	14.524	
25765	77.8038	39.7965	17.4557	66.0129	49.019	
8844	77.7799	27.1377	10.8488	55.1368	19.306	
20754	77.6986	52.0605	10.6921	71.2943	26.706	
24597	77.6794	622.3761	105.4979		15.035	
25790	77.6459	39.4384	14.4912	480.5779	107.311	
20779	77.6459	160.1499	17.6749	59.6624	16.237	
2881	77.6029	297.0551	79.9493	123.7358	27.798	
17214	77.5646	144.7695	33.6226	399.1987	92.477	
20509	77.5072	23.2482	6.0971	105.3812	24.344	
4242	77.4163	323.5089	80.1901	36.1861	15.108	
13882	77.4019	757.9745	193.5464	238.1027	64.1769	
11218	77.3828	66.3258		1049.9153	293.967	
20549	77.3589	33.1582	39.0734	128.6068	49.132	
18023	77.3493	45.3195	11.8610	50.5349	19.7998	
31	77.2344		12.0265	64.6300	17.5364	
25232	77.1388	59.3374	11.7844	78.8431	21.613	
1948	77.1100	19.7318	7.8509	34.4586	15.7297	
15777	77.0861	136.4836	36.7570	81.9549	42.8659	
13283	77.0335	20.3161	7.1718	35.9811	18.4974	
17226	76.9952	13.0325	4.6449	21.3358	9.3227	
20878	76.9904	252.0797	52.3846	189.5066	46.2914	
22205		28.4037	7.4850	39.7258	15.8441	
25235	76.9713	889.7006	90.5304	762.5673	130.2308	
4235	76.9282	21.8555	3.4653	28.8335	9.5388	
461	76.8995	407.8426	55.6413	323.2472	67.5158	
10453	88.3684	58.8866	10.7413	100.2864	30.1009	
	86.5072	54.6916	28.6474	133.6145	48.4319	
23096	86.4976	305.3999	77.1263	103.2969	113.9204	
5969	86.0335	582.3748	81.2828	425.0370	122.6622	

GLGC ID   LDA Score   Mean Tox   SD Tox   Mean Nontox   SD Nontox							
15084				wean Nontox	SD Nontox		
22771	85.6651		.0.0007				
3094	85.4641			384.5877	92.29		
3352	85.1818			87.5210	51.02		
19358	85.0670	749.4440		444.0767	130.17		
6458	84.5694			2499.7431	927.542		
9171	84.4641	10.2135		34.5288	21.55		
17832	84.3828	83.4184 1873.7747		125.7671	37.29		
1687	84.3301	1518.0092		5678.4901	2278.95		
4151	84.0957			4500.8610	1744.474		
1689	83.7512	398.7729	74.0807	605.7236	162.811		
6092	83.5694	3534.9897	4805.9317	9151.5643	3989.726		
8712		14.9530	7.8629	27.7916	11.211		
13802	83.2871	76.7061	30.7397	9.5956	49.148		
2813	83.1914	86.8262	20.4133	140.1087	38.480		
8291	83.0335	345.9580	80.9262	230.5143	104.416		
17089	82.6124	29.9570	8.6052	52.6233	17.745		
	82.5502	1436.7260	238.9832	1082.6013	400.261		
3781	82.4976	-3.7295	24.1581	30.8117	26.021		
12805	82.4641	64.5057	23.9316	11.2774	53.472		
19944	82.3589	124.7257	31.3315	230.2468			
16652	82.3493	80.1161	33.8281	126.1162	82.979		
11563	82.3301	207.7992	49.7971	115.4617	39.891		
14530	82.1196	98.2636	21.6303	68.0352	54.559		
21364	82.0861	95.9159	78.2647	264.3087	19.195		
16335	82.0574	72.0214	170.4047	269.4336	122.682		
5913	81.9713	41.5357	16.7042	77.0752	133.295		
6917	81.9522	207.1085	70.5504	107.6603	24.014		
14594	81.8469	23.9145	32.6840	-21.2989	60.965		
9788	81.8230	122.9006	46.7684		26.1810		
23043	81.7799	122.6782	21.5207	207.8074	64.552		
2880	81.6746	37.0159	14.8125	172.4627	44.1924		
14337	81.6651	239.9225	32.1748	61.6067	21.7007		
5726	81.4545	59.7409	16.5892	308.3251	50.5088		
9521	81.3493	65.8090	13.5422	92.9327	28.6776		
8440	81.3301	156.6240	30.9800	92.0760	22.2797		
17495	81.3206	544.9712	92.4873	104.9144	36.1090		
7060	81.3206	383.8079	117.4177	375.0940	90.9501		
21119	81.2967	191.4324	26.9123	296.2564	75.5050		
1182	81.2871	70.2302	18.8770	239.7644	45.3520		
15786	81.2775	149.8647	38.0848	107.7135	26.2306		
6789	81.2584	636.6515		88.9610	41.4774		
6658	81.1818	90.9486	175.1664	462.0210	85.3071		
8515	81.1722	284.2977	22.1946	135.2010	31.2399		
11561	81.1100	101.8620	162.9443	519.0955	137.7033		
9801	81.0957	127.8069	27.5891	64.7334	22.7099		
8356	81.0335	126.3052	29.6080	206.6474	71.1527		
17614	81.0239		28.1786	178.4201	42.6519		
1685	81.0144	114.4329	43.6818	184.2400	51.7067		
9186	80.9809	8546.8465	11550.1541	16297.7927	9670.1461		
24012	80.9426	20.6067	24.7195	53.3468	31.2583		
24129	80.8660	1380.0285	367.9359	922.5454	231.8686		
17917	80.8565	97.4502	24.3140	148.3880	38.5966		
	00.0000	49.7315	112.7341	-210.2743	164.0051		

TABLE 5B	: ALKYLATIN	Atty. F	Ref. 44921-5090-	01-WO/2105485	
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
17892	80.8230	133.1790	82.8102	500.4147	308.6848
23385		34.8506	19.6899		
2214		23.1353	15.6220	48.1076	
11632	80.7703	245.8868	52.8498	339.3667	77.4808
13887	80.7608	42.0020	14.9669	76.6187	25.7957
16713		245.9244	52.1236	336.8610	
6276	80.7512	36.0211	47.9516	103.7553	
9409	80.7273	32.7671	11.1490	55.0538	23,5680
11628	80.7081	203.6646	44.9926	304.7981	79.1293
8468	80.6124	152.0274	44.8297	257.8287	84.3043
18691	80.6124	2396.4705	628.0103	3968.4435	
6334	80.4880	366.9402	55.6784	300.3871	52.9436
21990	80.4450	97.6227	50.6873	16.0942	66.0429
3319	80.3923	16.8291	13.8402	35.5651	15.6556

<u>i ime</u> point	(s): 120, 16	3 hrs	-	ef. 44921-5090-0	1-440120154		
GLGC ID	LDA Score	Mean Tox	SD Tox Mean Nontox SD Nontox				
20065	99.2723						
17829	99.0125		131.6683				
25468	98.9085		64.2024				
25469	98.9085		50.1188	6119.8636			
1684	98.7526			4528.3633	1796.102		
21938	98.7006			6770.3787	2960.191		
19255	98.4927			72.0647	24.088		
19256	98.2328		24.3850	228.8471	100.514		
20482	98.0769		52.0641	416.7285	142.505		
18883	97.6611	5168.1262	986.3126	1597.9097	904.774		
1174	97.5052	158.0252	29.5322	67.9355	25.701		
18907	97.4532	29.3875	14.7446	-49.4517	23.390		
16448		17.1561	12.0112	446.2084	255.578		
16924	97.4532	49.2018	12.3050	283.1604	132.089		
	97.4532	14.3123	39.7356	227.5564	105.714		
4594	97.1933	20.8843	8.3975	87.7948			
956	96.8295	56.2043	24.1425	221.5609	53.180		
18881	96.5696	42.5293	9.7059	18.4425	95.711		
16610	96.5177	441.4807	35.9444	757.8194	7.791		
17227	96.4657	617.3444	94.1237	374.3329	180.8820		
17760	96.1538	497.1910	48.6205		70.7076		
15056	94.9584	0.6888	2.5754	303.5142	78.380		
25765	94.2308	30.6901	6.3798	22.1041	15.6263		
24775	94.1268	4.3639	8.9454	65.7805	19.4180		
1586	93.9709	153.0619	16.0525	40.0668	20.4915		
9223	93.9709	-2.5494		102.3870	23.5273		
24506	93.4511	20.7437	13.2241	59.7208	46.1898		
4418	93.2952	31.9637	16.1857	93.1557	47.7833		
2079	93.1393	1233.9396	4.3417	34.4959	29.6694		
20888	92.8794	745.0763	75.7770	1579.3870	253.4903		
21623	92.8794		70.1047	490.9188	132.2520		
17599	92.8170	1333.2177	151.5873	1989.0003	390.5994		
23225	92.7235	301.5754	145.1718	67.4111	46.5538		
25517		12.3479	5.7285	90.0362	220.5098		
17226	92.7235	38.8209	17.6003	164.9523	104.4392		
14966	92.6611	359.4217	64.3602	189.1713	43.8908		
	92.4636	-29.1245	18.8958	40.2943	45.7010		
1522	92.2557	308.6408	59.6964	163.1935	73.1540		
22773	92.0998	255.7841	74.9933	460.0795			
11152	92.0894	557.2671	220.7868	211.5257	111.7997 80.2627		
16925	91.9335	512.6284	202.3815	979.1897			
23778	91.4761	23.6922	6.0522	57.9147	171.7185		
17541	91.2578	198.5566	46.9188	81.2000	31.2877		
16018	91.0499	323.8912	34.7586		50.4977		
20073	90.6861	0.9459	5.7273	201.5575	57.4594		
4405	90.4366	15.8925	3.3639	40.0808	19.4090		
24695	90.3742	453.4644	75.2141	25.0584	13.1488		
25676	90.2287	59.5410		299.0488	61.7532		
17727	89.9064	577.4152	41.7671	167.6913	66.3227		
18065	89.8545	116.8633	53.1830	411.9085	74.7992		
14968	89.8025		24.0688	63.5006	21.4720		
6108	89.6985	96.0389	40.7561	255.4619	81.4502		
21695	89.4491	752.4260	142.3411	469.9789	105.7585		
22435		-9.1950	9.6046	35.1283	73.3789		
00	09.300/	1158.4434	173.1666	735.9354	180.0352		

Timepoint(s): 120, 168 hrs  GLGC ID LDA Score   Mean Tox   SD Tox   Mean Nontox   SD Nontox								
17759	89.282			Mean Nontox	SD Nontox			
21746	89.230		7 110 100	0 7.0200				
10498	89.1892				123.990			
16426	89.0229			1378.3258	276.581			
16217	88.9293			1682.6068	491.685			
1291	88.8669			2337.2435	632.616			
17731	88.8150		52.9019	255.6265	54.964			
436	88.7734		34.1005	85.8118	43.380			
25770	88.7630	1 0.000	6.2549	58.2561	17.368			
9388	88.5551			161.0254	59.871			
1867	88.4615		19.5702	-58.0892	46.851			
19646	88.3576		39.6208	651.7755	124.566			
16780			16.9079	149.3923	60.396			
16926	88.3472		19.0973	70.4368	20.044;			
3203	88.1913		183.1247	1064.0928	211.896			
16228	88.0873		67.5512	351.1566	73.423			
	88.0873		13.9522	45.7859	27.5614			
3244	88.0353		39.9570	175.4901				
1845	87.9418		18.1201	50.3417	33.1031			
12299	87.8690	789.9328	138.4112	431.7056	75.5274			
767	87.8274	-4.0207	11.9887	22.9078	111.2095			
4450	87.8274	653.2107	95.7838	463.9743	15.9351			
15570	87.8274	250.1856	112.2506	625.2026	94.0993			
20971	87.6819	114.4825	5.4332	92.3298	205.6496			
17057	87.5780	76.2930	6.5559	58.1030	20.5939			
9501	87.5676	161.4916	20.5486	118.3188	16.5216			
17285	87.4636	337.5447	23.6994		23.2574			
15569	87.3597	138.4769	81.8986	238.4030	68.7203			
20816	87.3077	405.3420	105.9939	454.1432	185.9486			
3430	87.2973	214.2634	88.1351	780.2926	230.1953			
20960	87.2661	664.9480	46.3234	106.9822	26.1705			
15517	87.2141	44.6913	7.7999	520.9765	116.5653			
·19040	87.1622	172.6411	24.4019	69.8491	20.3743			
5159	87.0998	318.5259	70.6302	255.7760	77.7245			
17742	86.9854	30.4573	23.9803	172.3592	76.4086			
3431	86.9335	1176.3691	361.7949	-4.7075	9.8579			
16649	86.8919	357.9935		617.0483	144.4116			
18867	86.8295	384.3156	33.4191	258.8069	55.7162			
4130	86.7360	105.3641	106.1680	180.4287	69.4099			
16716	86.6944	158.3732	54.5557	243.3050	74.1218			
24354	86.6944	29.2853	16.1545	219.5175	55.3518			
1803	86.5800	197.6202	4.1889	14.8199	15.0056			
15957	86.5281	176.1742	27.0128	148.6496	26.7689			
16520	86.5177		109.7266	367.4182	101.7904			
11384	86.4865	86.0059	29.0386	42.2329	18.0939			
15052	86.4345	46.1577	5.5310	33.2389	10.9879			
17301	86.3721	2047.1863	228.9277	2747.7425	646.9050			
25716	86.3306	207.3871	108.1265	504.5765	154.1255			
1323	86.3202	423.6299	94.7456	813.2816	361.4851			
1687	98.8565	326.3527	54.9693	182.5352	77.4476			
1689		82.8701	42 5093	4478.5712	1762.4439			
6073	98.8565	83.5162	88.7163	9117.3811	4011.1269			
17832	98.8046	-23.4120	6.7898	63.8808	46.0409			
11032	98.7526	35.6451	35.6118	5650.1374	2300.8816			

<u> Timepoint</u>	: ADRIAMY( (s): 120, 168	hrs		ef. 44921-5090-0	1-WO/201548
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
26150	98.7526		46.3755		1982.7759
19358	98.4407		60.4569	2484.3599	939.6377
1685	98.3888		165.9362	16287.4406	
3780	98.3888		696.9890	308.2735	265.9432
1688	97.9730	143.6612	153.4284	9096.8112	5251.4573
2142	97.8690	114.9472	27.2867	-4.6144	40.7838
6276	97.5572	-1.8410	8.4152	103.3040	45.7359
21206	97.5052	111.3423	20.6905	-8.2238	44.4836
23115	97.5052	275.7943	51.5085	131.3923	55.0440
6059	97.0894	56.1530	14.9334	129.2172	34.035
1686	96.7775	-356.6447	90.3239	51.4239	168.8423
4930	96.6736	606.4752	64.1424	358.1455	95.2190
5507	96.2058	480.9383	116.1597	1109.3895	300.9933
17761	96.1538	748.3425	80.4399	452.8424	114.6100
11372	96.0499	90.7225	34.9830	263.2703	80.0173
14604	95.5821	298.7850	52.7556	584.8230	153.8914
12450	95.4782	471.8425	103.1775	924.4552	227.0174
11017	95.2183	16.6967	16.2266	104.8072	46.8270
10780	95.1663	345.7198	67.6483	191.4259	56.3170
17830	94.9064	-7.6949	5.1508	49.0813	42.5974
11724	94.7505	26.0631	12.0626	109.3173	47.9814
6997	94.5426	79.2642	30.2114	188.0745	56.7248
11227	94.3347	832.7849	40.8394	1173.5756	267.1579
17762	94.2308	730.4753	71.4551	508.3838	106.3994
17220	94.0748	224.2669	20.5587	372.5064	93.4378
16293	94.0229	108.0721	31.6073	217.9964	58.4308
8445	93.9189	35.5784	7.9567	9.0655	16.5974
3368	93.8669	48.2527	7.5780	24.8418	19.4550
12011	93.8150	489.1382	31.7598	655.5020	104.9197
18513	93.7110	124.8409	46.0884	285.5847	99.4405
13116	93.5031	291.3307	20.1486	223.3274	37.7300
14257	93.4511	101.8823	52.7822	279.1938	98.7108
12582	93.3992	-3.6689	8.4496	44.9685	27.3215
13082	93.2432	24.9612	6.3814	-9.3904	26.1971
18528	93.1913	173.4085	49.5727	439.3200	173.2623
2852	92.7755	166.4303	85.8937	432.7807	134.9900
2782	92.7235	99.1453	22.4863	55.6580	44.3586
14337	92.6195	227.2382	17.8487	307.6037	50.7651
4049	92.5676	96.1146	31.5224	43.6756	131.4153
19474	92.5676	186.0493	45.7526	453.9572	169.6835
10930	92.5156	93.0461	14.7709	39.4755	35.8064
23957	92.4012	332.6110	76.8212	115.7446	64.8693
20738	92.0998	232.8163	27.7875	315.7514	54.1323
9775	91.9854	328.5683	66.0503	179.1884	43.0925
16003	91.9439	302.8644	33.7938	207.5909	56.7946
3085	91.8919	219.8210	26.6963	161.9272	32.8118
7292	91.8919	67.0870	15.6586	120.4053	31.0428
4716	91.7775	218.7680	47.3553	124.6232	29.1857
19451	91.7360	22 7486	6.1882	61.4203	32.6047
3269	91.7360	36.0455	11.6086	93.1567	41.7681
4 100 00					
17644 23012	91.5281	323.3049 241.8912	35.6007	455.3627	88.8272

Timepoint(s): 120, 168 hrs				ef. 44921-5090-0	1-WO/2015485
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
14861		52.0096	7.7895	33.9505	11.2329
6658		82.5245	17.0202	134.7365	31.4251
5322	91.3098	30.7770	13.0747	-10.0923	19.8566

Timepoin	t(s): 6, 24 h	rs	Atty. Ref. 44921-5090-01-WO/210			
GLGC ID	LDA Score	Mean Tox	SD Tox			
643	99.324:	216.9566		Mean Nontox		
20082	98.908	165.2679	36.6385			
910	98.5967	81.2270		64.8118	22.92	
17541	98.4927		77.7199	25.0230	9.47	
1169	98.3368		6.0570	79.7447		
20506	98.3368			48.6961	12.14	
912	98.2328		10.3246	19.9840	6.15	
25705	98.1809		57.5386	379.7166	61.77	
1170	98.1289	129.9053	177.3847	355.4504	100.282	
18403	96.3098	1700.8952	7.4611	74.3075	19.96	
15956	96.2578		143.8684	2752.9468	558.388	
1503	96.1019		10.4705	51.1452	16.361	
19238	95.8420		15.6676	54.6586	18.676	
18654			13.8001	196.2968	48.198	
24219	95.0104	0, 00	35.6079	219.3176	64.054	
1841	94.0748		49.1940	295.3830		
634	93.5551	106.7482	12.8901	60.8845	84.811	
21975	93.0249	361.5323	117.1735	93.8808	27.621	
	92.9834	259.5442	22.8223	180.7023	48.161	
911	92.6611	37.9401	28.6107	-19.3470	79.823	
18647	92.6195	249.5819	17.4494	173.6777	24.291	
16714	92.4532	30.4504	6.9013	12.1320	54.120	
18706	91.9439	415.0758	123.4227	1162 5400	5.354	
4325	91.9335	63.3989	14.4718	1163.5138	504.923	
1497	91.6840	1644.8464	189.9219	28.7876	11.2487	
15150	91.5800	95.3715	15.0073	2685.9776	946.5933	
11865	91.1123	35.8316	6.2345	154.5278	39.0994	
20740	90.8940	804.7740	146.0843	64.6226	19.4464	
15402	90.8524	242.9727	21.7656	447.8767	140.3697	
20801	90.6861	126.2442	20.7386	331.3109	61.9613	
6653	90.6445	185.4673	19.4279	78.0618	18.0951	
4504	90.3222	304.6935		131.5378	35.2556	
52	90.2703	121.3335	83.1008	164.7594	52.9684	
20724	90.1767	30.8177	27.1611	73.6168	21.2811	
20982	89.8545	117.2682	4.7813	17.2729	11.3466	
11857	89.3971	43.7652	31.4452	222.4598	50.1804	
15884	89.3451	500.6086	10.1433	97.7911	43.8492	
22646	89.3347	112.1522	60.3145	724.0523	187.8326	
15391	88.8669	575.7964	19.2104	68.7152	17.3910	
20177	88.5135		61.0521	383.9391	91.6424	
1638	88.3576	13.6744	10.3461	42.3135	19.1616	
21657	88.2432	110.5316	10.5506	153.0325	50.0039	
322	88.1809	1364.8628	180.0082	951.9256	227.3234	
4477	88.1393	59.4921	26.4817	18.7707	10.4430	
635	87.8170	27.0503	7.0810	14.4620	5.9998	
7927	87.7859	278.4199	126.0403	92.7541	36.8862	
15269	87.6715	88.2266	7.6636	64.7494	21.2123	
5733		296.3984	14.3654	233.6963	46.3899	
18655	87.6611	30.5929	18.7185	-0.0338		
17661	87.6195	58.6545	32.8191	156.4812	6.7457	
20483	87.5156	277.5417	36.7459	189.1638	62.5568	
1396	87.4636	2157.1056	652.1908		49.1745	
	87.1414	37.6173	12.6511	20.5672	1012.8776	
17936	87.0998	45.0405	7.1106	20.0072	6.2547	

ELGC ID	t(s): 6, 24 hrs		, ·		
22903		Mean Tox	SD Tox	Mean Nontox.	SD Nontox
25550	86.8919 86.8295	249.5228			29.6702
25104		218.7412			28.0744
15707		173.3228			91.0804
9084	86.7464	19.1016	5.2982	45.7955	24.2428
20959	86.6944	24.0231	5.9793	42.6019	15.6389
20448	86.6944	293.4018	28.9076	219.0742	62.2940
15460	86.6320	149.8320	70.9074	79.5449	131.0411
20619	86.5904 86.5904	105.8124	11.3399	103.1174	74.2204
24279	86.5800	8.7819	3.4581	22.1526	13.3341
4235	86.4761	24.9137	15.3730	-8.8212	19.5805
15642	86.4657	440.9827	50.9818	323.9580	67.5564
6499		471.4492	90.6235	261.8865	66.5316
1498	86.0603	26.4101	18.4710	67.7942	25.1315
25907	85.9667	1828.3416	477.9028	3037.1137	1026.7384
16221	85.8940	34.7316	14.8217	7.2962	10.2408
2881	85.8628 85.8524	389.3234	99.4201	749.3613	303.1582
18389		248.3743	36.6335	398.4306	92.5954
16518	85.8004 85.7484	214.1060	148.3985	840.1938	467.3910
1298		1047.5740	127.2169	770.9344	277.9102
8899	85.6549	45.8414	7.7269	25.8116	21.4468
14995	85.6445	1148.2060	114.5846	885.3715	149.8441
23340	85.6029	21.5158	5.3712	11.3393	16.3173
18731	85.5925	180.8155	58.3779	246.6393	47.2515
20916	85.4886	224.1048	21.9383	168.9408	32.7527
1760	85.4782	71.4310	19.9888	39.3071	14.0772
25290	85.2807	119.4358	30.8964	183.4883	42.1376
25589	85.2703	689.4077	164.7814	387.2016	107.0111
16419	85.1871	331.9741	32.5161	255.7043	60.6365
20461	85.1767	371.6173	29.5948	297.6059	53.4572
11353	85.1351	55.1955	13.7311	86.3242	45.4222
16123	85.1247	63.3792	10.8105	45.6297	14.4738
15281	85.0104	202.3612	59.3562	104.8820	47.3069
25650	84.9688	166.7673	28.0582	122.4601	30.0519
22196	84.8233	21.1735	8.8572	46.3942	26.6247
	84.7609	70.2694	7.7501	49.8076	17.7310
13358 17658	84.7089	39.8028	10.2977	24.4382	10.4002
	84.5530	71.5205	14.8852	41.0076	20.4000
1834	84.5530	8.8770	2.9883	21.1344	12.8485
19864	84.4387	38.7348	8.4642	19.6016	10.4356
363	84.3451	21.1611	19.4238	45.2277	20.3060
882 17264	84.3347	58.0744	19.1515	21.1244	14.8712
13420	84.2931	40.0066	5.1747	27.0710	8.2749
11454	84.2516	539.8793	61.9590	449.4794	101.2766
	84.1788	346.1348	92.1226	208.8677	61.9861
21007	84.1788	241.3877	56.8287	110.2139	87.7943
1037	84.1268	43.2151	15.4363	13.8391	18.6849
22411	84.0748	165.2394	47.3941	91.9562	36.9579
20065 14718	84.0644	190.9918	130.8571	27.0036	20.4934
	99.5842	230.6674	92.5533	24.3979	17.5884
10345	99.4802	785.7281	263.4749	109.0319	43.9117
21353 5689	99.3763	619.7295	135.9931	249.8067	54.2198
2009	98.8565	92.1895	15.8960	15.2510	19.4734

TABLE 5D: ADRIAMYCIN  Timepoint(s): 6, 24 hrs  GLGC ID   LDA Score   Mean Tox   ISD Tox   IMage   ISD Tox   IMage   ISD Tox								
		Mean Tox	SD Tox					
18525					SD Nonto			
21361		147,2292	11.1460	83.6691				
18744	98.3368	233,1903	38.2309	77.8154				
21254	98.3368	328.6679	54.1566	108.4112				
4107	98.2848	287.3556	71.3956	620.6906	122.07			
4730	97.8170	550.6699	113335	108.7256	67.62			
12802	97.6091	282.1259	113.3865	1080.5117	209.69			
3932	97.3493	225.9943	49.2121	144.4730	34.58			
2856	97.2973	711.0095	24.7725	399.0604	84.69			
12662	96.7775	23.0931	112.6609	1241.6349	244.24			
12346	95.3222	110.3221	8.1247	86.0459	31.00			
15959	95.2183		20.4632	683.4106	437.61			
22261	94.7505	130.9661	43.3624	284.5307	67.58			
15197	94.5426	78.6864	10.2432	41.9082	16.70			
8786	94.2308	183.6678	36.5280	312.3558	63.26			
5430	93.7526	364.1967	47.0109	261.2237	46.300			
21275		95.4299	30.6522	23.1385	11.623			
6550	93.7526	588.1090	149.1494	280.4007				
9649	93.6071	282.7144	36.3233	453.0715	62.045			
19729	93.2952	22.8734	10.8883	73.5961	99.932			
22490	93.0769	294.7338	58.5447	104.6943	32.909			
	93.0353	562.3828	33.0440	440.7810	58.817			
14594	93.0249	62.1960	25.5700	-21.1329	76.624			
11761	92.9314	90.0729	18.6131		25.852			
13966	92.8794	153.8149	18.0076	158.6863	40.732			
3740	92.5156	255.3806	20.7166	104.6423	27.472			
2341	92.4636	360.3613	21.4285	183,4331	40.913			
23831	92.4116	333.1632	29.7634	257.4395	68.503			
2661	92.4116	45.7200	21.1768	244.7664	55.862			
2655	92.2973	399.7943	115.7514	-68.4445	135.4444			
6357	92.2037	380.5703	17.8610	177.9087	66.9156			
14524	92.1933	160.2642	37.6385	308.6225	44.8102			
6039	92.1414	880.5708	128.2510	74.1406	22.8551			
4866	92.0894	353.6625		563.6415	89.7156			
7524	91.9854	867.7427	66.7457	186.8359	112.6854			
3242	91.8919	149.1652	119.4344	559.3273	92.3745			
8980	91.7775	93.2571	21.1623	252.5094	83.0593			
6121	91.7256	32.3956	24.9282	44.7612	14.5846			
14028	91.6216	274.8718	10.0648	11.1461	8.1731			
16752	91.5281	26.0467	46.6289	122.5672	55.7250			
15645	91.4137	897.7752	17.7967	108.3065	52.2097			
24012	91.3098	1729.6850	238.9347	459.8227	155.6830			
21757	91.1642		410.6969	924.6174	229.0811			
16493	91.1123	75.1816	6.6705	54.0852	17.9561			
18885	91.0603	149.5420	28.0005	224.4010	49.8893			
14525	90.9459	147.5520	8.9873	117.6945	23.2465			
11901	90.8004	35.2680	6.0949	13.2939	9.0161			
23444		321.5218	26.4281	200.4564	94.9507			
2529	90.8004	380.3160	32.3748	290.4801				
9380	90.8004	178.6648	13.5051	263.5560	51.9021			
9828	90.7900	28.9561	34.5402	181 8779	77.6532			
	90.7380	146.9447	22.3959	81.0911	73 5947			
7489	90.6445	1017.3793	54.3100		27.0328			
4770	90.5925	190.6164	6.5190	1200.2119	224.7209			

Timepoin	TABLE 5D: ADRIAMYCIN Atty. Ref. 44921-5090-01-WO/21054 Timepoint(s): 6, 24 hrs									
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox					
15416	90.5821	100.5402	25.4513	50.1430	23.0422					
9942	90.5821	520.4679	58.6501	329.0809						
6758	90.4262	40.7626	12.4545	15.5272	11,1309					
9579	90.2703	73.0852	12,2775	30.0760	21.5387					
6789	90.2183	690.1254	114.6606	463.6435						
6686	90.1663	202.7423	35.4602	335.5334	59.0684					
18943	90.1143	248.4443	46.8046	150.0480	42,4641					
8110	89.9584	73.2159	13.8912	39.5861	15.8997					
6974	89.8649	439.9621	60.1488	672.7254	169.4559					
15173	89.8129	154.5984	25.7401	248.0312	62.7376					

	LDA Score	Mean Tox	SD Tox	Mean Nontox	len N
363	98.5522	95.3786			SD Nontox
13683	98.3971	113.7606			
21975	98.3454				38.08
17765	98.2937				
6581	98.1386				
15829	97.7766	364.9374		87.0805	18.95
17255	97.4147			49.3079	69.68
17764	97.2596			50.9973	17.69
2005	97.2596	101.5426		1942.2845	392.72
25098	97.0010	59.0112	20.2833	40.1465	17.54
21445	96.7942	83.5574	12.7713	15.8721	17.71
1466	96.5357	801.7236	22.0419	10.5575	22.81
16173	96.4840	71.5274	189.5122	447.2700	108.99
24520	96.4840	146.3410	24.0334	13.4328	26.38
20795	96.3289		37.4706	51.0250	39.24
4541	96.0703	240.0478	37.8245	112.2033	63.61
1168	96.0186	256.8396	28.7640	444.4358	105.520
1063	95.9152	24.4684	6.3814	6.1080	6.53
15888	95.8118	61.3382	11.7391	22.6010	13.933
16725		545.6914	33.0164	791.2888	146.013
1530	95.5016	26.3318	3.1236	14.6195	8.624
1808	95.2947	134.4930	4.7830	193.4364	41.991
23307	95.0879	260.5106	50.7959	95.4451	156.350
18269	94.9845	105.8904	5.7454	68.7553	19.946
15037	94.8811	186.7768	10.2046	265.5162	47.385
	94.8811	88.3486	75.2186	250.9847	68.116
18135	94.7260	205.3204	27.7518	138.8598	28.359
12638	94.7260	52.7372	4.9146	31.4438	13.462
14927	94.7260	86.6624	5.9265	58.9483	26.417
4832	94.6743	622.8410	30.7624	878.0888	210.541
18647	94.6225	299.1670	48.9037	173.8138	53.711
12364	94.3123	88.0436	10.9307	150.4199	39.852
20982	94.2606	128.8742	22.8767	221.8559	
6963	94.2089	284.6574	21.5556	177.3548	50.802
14997	94.0538	532.5096	26.2041	745.6824	55.045
17782	94.0021	212.7698	5.1155	262.7259	155.893
4133	93.9504	69.4434	7.0420	103.9600	45.998
18316	93.8469	1812.8340	67.9489	1337.5132	20.969
21076	93.8469	126.1870	2.2627	122.7885	363.588
4003	93.7435	156.9270	23.7070	105.5632	28.687
10888	93.7435	72.2890	4.9749		36.616
16712	93.6401	270.7052	24.4385	52.5194	31.162
11949	93.6401	47.0104	2.6055	378.4982	64.295
20889	93.5884	446.4512	48.3340	32.8307	10.414
25470	93.4850	145.7756	6.8738	289.2922	81.517
11840	93.4333	99.4078	18.4037	113.0224	50.442
18160	93.2782	1544.5864	208.8434	67.5322	17.1482
18315	93.1748	1659.1842		2365.1941	472.0023
23568	93.1231	56.3398	92.4979	1137.8314	341.4328
8289	93.0714	54.4228	3.6719	39.6928	10.9466
9254	93.0714		6.8826	100.8121	37.8497
22972	93.0196	192.8216	8.2676	252.4518	48.2105
16319	92.9679	73.0742	1.3045	61.4735	15.6494
	52.3013	51.1142	16.3777	22.3746	14.1136

LGC ID	: 6 hrs LDA Score	Mean Tox	SD Tox	INA COMPANY	
23362					SD Nontox
12365	92.9162				
24248	92.8645				75.00
10660	92.8128				130.06
3474	92.8128	412.6048		68.1244	17.64
3879	92.7611			562.5296	105.32
21683	92.7611	62.0656		143.3410	47.35
23310	92.7611	71.7498	9.5771	49.1710	36.42
16942	92.7611	111.5548		79.1597	28.49
8661	92.7094	1147.5794	59.7372	1474.2555	240.63
6782	92.7094	46.7326	22.0667	12.0085	69.69
15438	92.7094	532.9708	37.1082	386.4038	89.61
20888	92.6577	243.1736	4.7951	237.9922	63.33
15887	92.3992	761.7078	90.3406	492.1469	133.04
25997		445.4306	32.0721	735.9139	265.17
6892	92.3475	35.7280	2.7572	21.6537	9.86
16524	92.2958	109.7348	24.9276	68.1920	36.06
162	92.1406	26.0014	0.6163	24.0262	6.603
14621	91.9338	72.0436	6.2772	42.2120	23.71
3473	91.9338	133.9782	5.3673	169.1670	37.009
21523	91.9338	110.2048	7.6062	151.5009	31.249
11950	91.8821	84.9384	49.7825	190.7646	64.755
	91.7270	76.9350	19.8714	36.5774	18.931
4447	91.7270	41.4458	5.2281	22.4024	11.659
17083	91.7270	64.1218	2.3053	68.1787	24.996
22845	91.7270	656.6956	10.3788	665.3096	137.039
1571	91.6753	220.1688	11.2160	172.4479	54.227
24113	91.5719	31.8484	9.3282	10.0764	12.679
1011	91.5719	24.4862	1.0211	20.7041	10.907
13682	91.5202	151.1948	22.7722	289.9873	111.560
23705	91.5202	195.9970	10.0343	265.2100	
167	91.4685	926.7020	100.1165	583.3957	68.816
14981	91.4685	6611.0257	235.5070	6602.9446	174.463
20960	91.4168	695.7130	40.8447	521.5618	2802.373
239	91.4168	196.8380	5.6170	165.2513	116.560
17257	91.3650	237.8380	26.6343	365.0675	98.862
1638	91.3650	97.1086	11.0557	152.8822	115.543
6980	91.3133	86.7840	16.2914	148.3850	49.904
1097	91.3133	189.8588	26.8178	303.5643	43.178
1311	91.3133	50.1778	2.7926	34.6061	100.057
20484	91.2616	6292.0150	199.9022	6403.6069	14.663
25104	91.2099	346.4496	54.9456	173.4618	2308.210
21654	91.2099	244.6286	15.9412	204.8756	89.954
25371	91.2099	100.7812	3.4622	93.1960	76.073
22763	91.1582	65.3412	9.0858		36.5943
18068	91.1582	104.6786	6.5163	40.9351	12.9578
13392	91.0548	152.4578	10.2255	83.3030	14.9982
9541	91.0548	488.1294	15.4711	201.4157	39.0008
18333	90.9514	173.1502	14.7010	403.9521	109.5222
4636	99.3795	467.8500	242.2832	228.8726	46.5199
22042	98.9659	339.3684		131.1787	56.8828
21740	98.0352	456.0868	75.1597	100.0167	61.0272
4278	98.0352	88.0498	33.4311	276.7652	87.8126

Timepoint(s) GLGC ID	I DA Coore			Atty. Ref. 44921-509	
	LDA Score	Mean Tox	SD Tox	Mean Nontox	ISD Nontox
11702			106.4546	133.7083	
5615			21 8574		
24089			199.6779		
2729		217.5804	28.4467	480.5092	
18271	97.4664	1192.3508	147.8088	425.4314	
18272	97.3113	311.4518	36.7572	111.1531	237.790
14117	97.3113	797.5784	46.3252	1161.1975	64.349
2539	97.1562	117.4486	21.7002	20.8249	224.409
24081	97.0527	-62.7924	31.5162		28.970
14380	96.9493	504.6868	7.6012	90.4001	56.90
5030	96.8976	82.5804	8.5740	390.4853	119.358
2795	96.6391	298.0746	45.1563	42.2192	16.399
6640	96.4323	305.9566	6.6347	168.7500	44.643
1802	96.3806	236.6206	22.6923	226.6775	61.706
3003	96.2771	246.2542	50.4901	153.6587	39.996
1332	96.1220	228.1560	31.2654	71.2325	64.271
23005	96.0703	175.9890	33.8935	429.7260	110.622
13080	95.7084	85.6216		95.2413	68.926
4027	95.7084	48.1146	26.0184	15.9478	28.174
23390	95.6050	470.7924	7.9320	93.0816	38.497
1998	95.6050	76.4118	49.6561	330.5827	66.628
22487	95.5533	44.6356	10.4035	39.4215	33.825
9976	95.4498	382.7352	7.2312	20.8012	10.678
23409	95.2430	313.2406	36.1940	643.5721	171.4413
11563	95.0879	265.1508	29.4152	662.0116	240.1169
19545	95.0879	299.6418	85.7612	116.7885	54.9933
3445	95.0362	60.3296	25.9007	186.3541	56.9413
19136	94.9845	206.3296	5.0442	105.8003	33.8827
13633	94.9328	296.3566	7.5037	198.4383	69.3125
21713	94.8811	481.7274	37.8149	343.6374	114.7507
22239	94.7777	557.4628	59.8614	871.3903	177.2559
14031	94.7777	519.4526	7.8441	468.5614	146.5563
12187	94.7777	32.1638	4.9841	17.2851	14.4646
2662	94.7260	107.6768	8.7988	43.0391	42.0097
22651	94.6743	35.5306	2.4043	58.1739	31.4068
4350	94.6743	1021.8184	82.2183	718.8303	160.0003
2063	94.5708	189.4486	40.1721	454.7927	165.5004
22283	94.5708	259.2196	24.3214	180.7968	39.3014
23857	94.4157	232.8566	51.7414	116.3481	45.1469
22801	94.4157	85.9380	1.3338	86.3077	26.8114
12928	94.3640	412.0660	27.0817	581.3531	107.7824
16388		639.0730	34.3105	870.5713	154.9074
8539	94.2606 94.1572	78.9200	3.6489	54.1389	35.0319
18890		33.9334	5.6627	71.6343	28.8032
5482	94.1055	511.3890	58.1729	834.1214	206.9359
18891	94.0538	152.1414	16.7076	261.6230	74.9412
12387	94.0538	190.5174	36.4661	330.1107	82.2822
168	94.0021	137.1570	27.5767	72.2882	
13029	94.0021	3581.2472	233.5294	2629.7285	27.0901
10658	93.8987	349.4770	49.3092	202.0514	522.3154
18916	93.8987	550.8180	120.3156	1363.6323	85.9922
	93.7435	450.5048	105.1152	245.5299	875.3128
18796	93.7435	32.7492	3.3795	9.1513	86.3405 22.1154

Timepoint(s)	TABLE 5E: AMPHOTERICIN B			Atty. Ref. 44921-509	0-01-WO/2105485
GLGC ID		Mean Tox		Mean Nontox	SD Nontox
21942				1379.6582	346,2585
18438	3311 100	. 00:1010		471.0373	
22218	93.6401	59.8046	9.9566	114.3250	

imepoint(s	BI ): 168, 336 h	rs	Atty: R	ef. 44921-5090-0	1-WO/2105
LGC ID	LDA Score	Mean Tox	SD Tox	Truy.	
15269	99.1192	143.8120	5.7662		SD Nonto
16427	98.9119	293.9709	76.0378		
15570	98.7047	177.3863	33.8858		347.5
15572	98.6528	258.6041	46.1393		205.60
18018	98.3938	570.0360	50.5394		421.18
4467	98.2383	316.5336	74.2216	915.5382	131.19
17063	97.9793	190.2210	73.2469	868.8061	273.10
15409	97.8756	1357.7633	248.1126	62.1965	24.27
14989	97.8756	425.8114	34.0340	526.2359	158.93
16420	97.8238	217.8023	16.7923	731.4218	156.31
6451	97.8238	71.3897		328.5433	49.30
17064	97.7202	130.5931	11.3390	161.7444	46.78
11115	97.4093	72.2707	54.8801	44.3384	18.64
19244	97.3057	2814.2426	15.0501	0.3074	22.25
15884	97.2539	422.5439	322.2026	1805.7654	295.13
15408	97.2021	525.5060	22.9208	723.9240	187.24
4259	96.9430	1589.8659	96.4312	264.8164	76.42
16780	96.8912	132.2681	190.8676	1025.3792	173.31
20807	96.8912	2241.1979	14.2080	70.4168	19.81
20844	96.8912	2864.5389	298.0859	1305.3610	278.84
4843	96.7876		435.1075	1576.0314	350.96
23250	96.6839	291.0541	19.8623	433.1671	72.730
17688	96.5285	183.6347	12.5762	249.1065	35.03
25563	96.4767	104.5840	4.9652	153.8945	29.235
22731	96.4249	290.8960	20.1097	451.4426	96.703
25679	96.4249	346.8796	16.1784	509.2853	93.213
17712	96.4249	2129.1789	260.7942	1410.0568	268.293
18107	96.1658	1109.7723	136.2022	1728.1144	289.994
7148	96.1658	702.3460	107.3752	412.5137	101.443
9501	96.1140	200.7584	19.5780	307.2611	61.569
18573	96.1140	184.4760	22.5023	118.2863	22.968
17507	96.1140	240.8931	12.9388	340.8501	59.926
1324	96.0622	231.2563	37.7161	440.2135	233.053
4235	96.0622	330.9949	70.2060	605.9855	116.167
17729	95.9585	201.4274	20.5710	326.0595	67.822
15622	95.9585	1997.6343	242.8843	1321.3071	222.114
20745	95.8031	70.8847	27.2907	222.8664	74.569
23709	95.8031	238.6544	25.7200	358.9398	58.082
11116	95.5959	800.6951	103.7246	1254.5985	283.866
16204	95.5959	183.2179	22.4486	36.4703	57.4160
2697		1805.7873	167.8985	1271.9758	199.9240
15462	95.5440	3434.9464	560.8371	2244.3433	399.1160
18054	95.4922	35.9110	6.6465	75.7932	21.5556
14504	95.4922	65.8467	8.7215	126.5834	31.3531
20630		281.8043	46.7470	529.6716	116.9672
19222	95.4922	726.8354	195.8009	344.2470	142.6618
17301	95.3886	743.1596	63.3540	1114.0604	186.0991
19768	95.2850	210.4029	40.2492	503.6307	155.1346
21672	95.2850	565.7791	47.6790	797.6082	121.6587
20810	95.2332	216.0100	29.2689	375.5837	81.6117
5050	95.2332	3040.8551	331.0841	2016.2404	403.9704
18539	95.2332	272.5644	48.9227	517.4997	119.5573
10008	95.2332	282.9924	41.5679	560.5237	195.9350

SLGC ID		Mean Tox	SD Tox	Mean Nontox	SD Nonto
15492	95.0777				
24564	95.0777	128.0414	14.8501		
23142	94.9741	38.8103		33.0010	
18305	94.9223	3321.3837	543.0109		8.7
10744	94.8187	76.7056	11.9271	179.7331	
4243	94.8187	51.3371	7.6677		57.0
20421	94.7668	55.9446	5.1641	93.8936	27.3
17306	94.7150	7304.2837	1238.4613	86.7888	18.29
25399	94.7150	506.0113	135.7842	4648.0647	1089.58
16610	94.7150	427.9930	57.2292	216.0530	114.93
450	94.6114	5628.8407	997.6780	756.9338	181.26
17731	94.5596	167.9773	24.2283	3736.9132	767.68
4517	94.5078	33.0951	3.7148	86.0909	43.68
21957	94.4560	172.8843	14.1950	65.2515	21.23
20917	94.4041	69.7076	13.0813	243.8138	43.13
15116	94.3523	50.5716	5.5540	127.3824	31.02
6425	94.3005	102.3871	19.7933	82.9210	19.44
11997	94.0415	414.8107	87.2466	171.8848	36.82
19319	94.0415	65.5060	4.3582	678.7777	122.39
17136	93.9896	98.7824	42.6359	93.1397	20.90
11992	93.8860	141.6666	19.0249	523.0232	369.98
11405	93.8860	28.9459	2.4888	254.9445	70.69
7602	93.7306	367.7629	42.0093	44.7777	10.64
24263	93.6269	0.6497	12.9179	527.9297	87.06
11352	93.5233	195.3599	21.5531	46.8636 302.1285	23.78
16178	93.4715	208.3697	21.0391	295.5385	63.22
15202	93.4197	1737.1439	249.5668		48.81
14957	93.4197	61.9469	12.0382	1014.0869	354.98
17517	93.3679	177.5686	26.8054	110.9589	25.22
8899	93.3161	607.7543	71.7051	285.1725	56.44
18569	93.3161	639.0183	226.0855	890.1090	150.36
21063	93.2642	80.9499	13.0064	1610.4958	609.723
18031	93.1606	211.9716	31.3364	139.6931	42.665
25120	93.1088	39.7119	10.6457	388.4117	96.775
1314	93.1088	444.5903	54.8862	78.4173 660.5187	20.947
21940	93.0570	63.2817	8.9608		118.377
23854	93.0052	1073.0710	186.4309	115.0101	32.711
17158	93.0052	434.7516	56.7880	708.7255	172.271
22891	92.9534	93.1706	5.2413	746.7869 112.8740	209.755
21108	92.9534	4.3739	4.9960		28.620
11296	92.9016	22.9944	8.0878	26.9621	13.467
16099	92.9016	324.4046	32.7306	47.6528	13.300
3910	92.9016	94.1221	12.6656	430.8522	62.082
25184	92.8497	6.6997	8.9605	145.7204	35.261
1762	92.8497	48.8919	10.4947	37.3945	16.692
17176	92.7979	4333.4994	629.4033	61.6225	74.342
1942	92.7979	4.4739	4.1363	2685.8048	801.152
25041	92.7461	79.9310	17.4453	45.8718	33.368
6158	99.0155	148.6926	39.9027	154.7853	45.167
22716	98.9119	36.5181	8.5602	709.5511	245.485
2046	97.9275	47.7550	10.7271	173.9637	67.4242
4585		2159.8191	200.3457	138.1307 1318.4097	44.9137

TABLE 5F:			Atty R	ef '44921 5000'0	4 1410/04054					
Timepoint(s	TABLE 5F: BI Atty. Ref. 44921-5090-01-WO/210548 Timepoint(s): 168, 336 hrs									
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox					
15260		656.9087	60.8892							
18915	97.8238		70.5634							
6984	97.7202	500.2131	65.2292							
9412	97.4611	169.6379		46.2183	79.0802					
18151	97.3057	559.5641	76.8065	329.0736						
26213	96.9948	1580.0974	522.2003							
6154	96.9948	319.6549	207.7988	577.7325 1576.8974	256.1040					
5111	96.9948	136.3579	16.9041		653.0310					
18125	96.9948	189.1237	21,4034	365.5307	127.5558					
19783	96.8912	989.0276	159.3433	301.4020	62.3747					
6157	96.8912	842.2940	210.1032	599.8644	106.5752					
22387	96.7358	1315.2459	88.4913	2306.7073	831.1001					
18854	96.5803	71.1124		912.7375	160.7472					
	2310000	11.1124	18.6730	192.2503	50.5585					

Timepoint(s): 168, 336 hrs  GLGC ID   LDA Score   Mean Tox   SD Tox   Mean Nontox   ISD Nontox							
	LDA Score		SD Tox	Mean Nontox	SD Nontox		
25632	99.3264			1452.4351	453.88		
15571	99.3264			1439.4661			
22385	99.2746	26.5514	7.3273	150.1247	471.63		
15269	99.1192		5.7662	234.9980	70.476		
16427	98.9119	293.9709	76.0378	1283.4863	46.124		
6153	98.9119	150.6609	30.1435	624.8155	347.514		
16426	98.8601	445.4373	127.9431	1680.7222	220.253		
15569	98.8601	79.5913	23.8286	453.5891	492.377		
15570	98.7047	177.3863	33.8858	624.5648	185.857		
15438	98.7047	78.9779	17.4427	239.1726	205.603		
15572	98.6528	258.6041	46.1393	1039.6946	61.915		
17739	98.6528	15.4303	9.4566		421.183		
4130	98.4974	61.2480	21.2773	103.6351	45.201		
18018	98.3938	570.0360	50.5394	243.1962	73.882		
20482	98.2383	6403.8013	1409.8117	915.5382	131.193		
4467	98.2383	316.5336	74.2216	1600.0454	881.638		
2413	98.0829	393.6166		868.8061	273.109		
17063	97.9793	190.2210	25.8964	628.0039	103.043		
18541	97.9275	2922.2450	73.2469	62.1965	24.274		
25702	97.9275	1261.0071	346.1391	1704.9167	296.481		
15409	97.8756	1357.7633	209.6912	715.4030	124.591		
14989	97.8756	425.8114	248.1126	526.2359	158.937		
16420	97.8238	217.8023	34.0340	731.4218	156.318		
8137	97.8238	168.5100	16.7923	328.5433	49.307		
6451	97.8238		14.2689	307.4580	67.1326		
4468	97.8238	71.3897	11.3390	161.7444	46.7828		
17064	97.7202	87.6101	25.7620	262.8633	84.0179		
25354	97.7202	130.5931	54.8801	44.3384	18.6413		
5049	97.6166	20.4040	4.4352	-11.0156	14.5137		
26030	97.5648	363.0054	70.0509	739.1010	168.4697		
16938	97.4611	2307.6020	329.0437	1120.6411	311.6302		
17687	97.4011	3439.4409	525.2792	2017.9291	347.7134		
12639		47.6730	4.3707	86.8021	19.2858		
11115	97.4093	2790.0180	354.1100	1711.9500	272.3493		
25691	97.4093	72.2707	15.0501	0.3074	22.2583		
	97.3057	1740.7939	305.2158	1038.8671	189.4342		
19244 15884	97.3057	2814.2426	322.2026	1805.7654	295.1347		
16918	97.2539	422.5439	22.9208	723.9240	187.2425		
16953	97.2539	3050.6176	559.0742	1652.1325	378.1626		
	97.2539	2207.6737	341.0509	1297.4032	254.3387		
15408	97.2021	525.5060	96.4312	264.8164	76.4260		
10498	97.2021	2408.9659	311.0810	1372.0887	260.9108		
20812	97.2021	2893.6953	338.0681	1737.4178	310.0129		
15876	97.0984	2416.0907	321.7240	1512.9364	235.4590		
18606	97.0466	1476.4840	266.8140	819.8315			
25671	96.9430	324.9419	104.2810	107.2333	169.2263		
18611	96.9430	3369.4430	364.8138	2174.7458	60.3073		
4259	96.9430	1589.8659	190.8676	1025.3792	408.7371		
16780	96.8912	132.2681	14.2080	70.4168	173.3154		
20807	96.8912	2241.1979	298.0859	1305.3610	19.8154		
17066	96.8912	215.0906	53.7980		278.8448		
20844	96.8912	2864.5389	435.1075	99.7993 1576.0314	31.2393		
25716	96.8394	2028.4791	100.10/0	(5/6 0314)	350.9617		

LGC ID	I DA Scoro				
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
600	96.8394				
4843	96.7876		19.8623		
10109	96.7876		324.8451	1261.4348	
22386	96.7358		28.6494	347.3349	
23250	96.6839	183.6347	12.5762	249.1065	170.16
17204	96.6321	6358.7441	945.0776	3624.5860	35.03
18542	96.6321	3140.0374	530.3402	1708.6288	854.35
17688	96.5285	104.5840	4.9652	153.8945	425.39
25647	96.5285	650.2900	186.4918	245.2281	29.23
20617	96.5285	637.2713	207.0703	247.7263	126.68
20925	96.4767	2342.9944	432.2362	1295.9411	121.29
24264	96.4767	104.7866	21.8573		323.28
25563	96.4767	290.8960	20.1097	225.9280	54.90
22731	96.4249	346.8796	16.1784	451.4426	96.70
25679	96.4249	2129.1789	260.7942	509.2853	93.21
17712	96.4249	1109.7723	136.2022	1410.0568	268.29
815	96.3731	2569.5176	392.7349	1728.1144	289.99
17203	96.2176	4186.3824		1481.5505	341.74
18107	96.1658	702.3460	491.1366	2494.9794	708.94
7148	96.1658	200.7584	107.3752	412.5137	101.44
9501	96.1140	184.4760	19.5780	307.2611	61.56
18573	96.1140		22.5023	118.2863	22.96
17507	96.1140	240.8931	12.9388	340.8501	59.92
1324	96.0622	231.2563	37.7161	440.2135	233.053
4235	96.0622	330.9949	70.2060	605.9855	116.16
17729	95.9585	201.4274	20.5710	326.0595	67.822
15622	95.9585	1997.6343	242.8843	1321.3071	222.114
17305	95.9585	70.8847	27.2907	222.8664	74.569
10878	95.9067	7999.9451	1186.2557	4595.7351	1347.784
961		2431.5641	292.1642	1628.2188	275.347
20745	95.9067	198.4494	29.5912	108.3837	57.271
23709	95.8031	238.6544	25.7200	358.9398	58.082
11116	95.8031	800.6951	103.7246	1254.5985	283.866
16204	95.5959	183.2179	22.4486	36.4703	57.416
2697	95.5959	1805.7873	167.8985	1271.9758	199.924
	95.5440	3434.9464	560.8371	2244.3433	399.116
15462 18054	95.5440	35.9110	6.6465	75.7932	21.555
	95.4922	65.8467	8.7215	126.5834	31.353
18686	95.4922	1443.8354	186.2988	905.4019	225.726
14504	95.4922	281.8043	46.7470	529.6716	116.967
20630	95.4922	726.8354	195.8009	344.2470	142.661
16613	95.4922	39.2830	12.2343	95.9704	27.539
19222	95.3886	743.1596	63.3540	1114.0604	186.099
17301	95.2850	210.4029	40.2492	503.6307	155.134
19768	95.2850	565.7791	47.6790	797.6082	121.658
21672	95.2332	216.0100	29.2689	375.5837	
20810	95.2332	3040.8551	331.0841	2016.2404	81.611
5050	95.2332	272.5644	48.9227	517.4997	403.970
18539	95.2332	282.9924	41.5679	560.5237	119.557
6158	99.0155	148.6926	39.9027	709.5511	195.9350
6155	98.9119	839.7963	183.1871		245.485
22716	98.9119	36.5181	8.5602	2774.3626	698.1220
16909	98.9119	497.3220	47.7755	173.9637	67.4242

Timepoint(s	BICore To 3): 168, 336 i	irs .	Atty. R	ef. 44921-5090-0	)1-WO/210548
		Mean Tox	SD Tox		SD Nontox
6156		178.0871	39.9577	654.5772	
5596		48.9820		146.3433	
2852	98.6010	135.1614	25.3872	432.1795	
17358	98.3938	3310.9373	322.5242	1747.5259	419.0780
24072	98.3420	58.5759	11.6797	18.3395	10.2706
3780	98.2902	1800.6897	455.8818	316.9184	306.7920
19094	98.0311	3011.3891	403.2544	1729.2848	310.2172
24310	98.0311	86.8350	30.7300	309.9478	93.2590
23927	97.9793	472.3723	134.9741	110.8209	89.1579
2046	97.9275	47.7550	10.7271	138.1307	44.9137
4585	97.8238	2159.8191	200.3457	1318.4097	247.8512
15260	97.8238	656.9087	60.8892	376.9953	93.6401
18915	97.8238	398.7401	70.5634	954.6520	267.1831
6984	97.7202	500.2131	65.2292	216.7627	79.0802
13161	97.5648	5.6410	12.7952	143.5556	64.4179
24521	97.5648	11366.8939	2042.0096	5437.9333	1388.7504
26133	97.5130	651.9266	291.6274	185.0980	106.2449
9412	97.4611	169.6379	42.7022	46.2183	51.4983
2103	97.4093	4941.1484	817.8208	2596.4749	595.6015
23687	97.3057	7377.1766	1444.2335	3148.1445	977.5333
18151	97.3057	559.5641	76.8065	329.0736	68.4657
6205	97.2021	277.4434	24.5348	437.3203	83.2028
10820	97.1503	3615.7761	669.0368	1860.5891	450.3442
26213	96.9948	1580.0974	522.2003	577.7325	256.1040
6154	96.9948	319.6549	207.7988	1576.8974	653.0310
5111	96.9948	136.3579	16.9041	365.5307	127.5558
18125	96.9948	189.1237	21.4034	301.4020	62.3747
22717	96.9430	213.9299	65.0869	656.9763	184.0001
3271	96.9430	281.7454	23.0722	472.8696	88.7627
19783	96.8912	989.0276	159.3433	599.8644	106.5752
6157	96.8912	842.2940	210.1032	2306.7073	831.1001
24268	96.7876	48.9863	15.7598	152.4360	
22930	96.7876	65.0423	24.9483	332.5378	46.6498
10971	96.7358	89.8383	19.1440	42.0165	143.1938 15.5461
22387	96.7358	1315.2459	88.4913	912.7375	160.7472
17155	96.5803	1013.4049	154.9830	552.1988	158.2252
18854	96.5803	71.1124	18.6730	192.2503	50.5585

Timepoint(s	CLENBUTER ): 24 hrs		Atty. Ref. 44921-5090-01-WO/2105			
GLGC ID	LDA Score	Mean Tox		<u></u>		
15867	99.1736				SD Nonto	
23651	98.8120	194.9143	58.0033	38.0902		
21000	98.3988			43.9816		
24859	97.9855			22.8672	19.99	
16696	97.7273	197.2963		22.8379	19.87	
17215	97.6756	86.5150		302.8795	59.39	
23868	97.6756	67.3360		168.1356	43.57	
15191	97.5723	517.4620	0.0101	218.8534	231.60	
12580	97.5207		1-0.,007	183.9005	563.83	
20589	97.4690	33.8560	1.6003	19.5502	9.47	
1523	97.2624	490.8580	164.2942	148.3860	88.28	
19549	97.2107	149.7348	3.2732	212.0033	52.060	
16918	97.1591	5.7080	2.5474	42.7500	22.303	
22321	97.1074	2852.3920	322.0410	1657.2857	390.323	
11997		391.6135	39.1905	173.4379	96.533	
574	97.1074	460.1595	17.7043	677.7722	123.636	
25802	96.8492	972.5473	57.9899	604.4586	158.030	
15640	96.7975	954.9178	117.8821	599.8418	153.605	
	96.7459	287.6770	20.3299	141.2940	60.359	
15641	96.6426	379.4980	27.4243	173.5264	86.478	
18122	96.4876	81.8923	21.0338	18.9802		
20983	96.4360	332.2185	11.0218	478.6360	40.607	
19040	96.3843	413.5660	26.6772	254.2652	109.830	
17383	96.3843	88.0838	27.3070	10.2342	77.286	
9124	96.3326	336.2755	42.6549	213.0618	30.905	
4222	96.1777	1250.4435	53.0154	980.8498	41.874	
24886	96.1260	2331.6990	152.3483	1651.3200	131.695	
14360	96.0744	36.1613	0.5510	44.3514	275.635	
18798	96.0744	95.4560	5.1882	138.5010	21.343	
8212	95.9194	614.5205	13.5571		28.225	
762	95.7645	152.8628	1.6805	494.4720	131.821	
21950	95.7645	561.8000	19.6699	139.5041	37.1730	
22739	95.6612	268.0643	10.2046	768.0125	138.7978	
3465	95.5579	58.9048	9.0152	360.3747	61.7718	
1991	95.5062	224.6573	17.4598	111.0300	28.1320	
90	95.4029	107.5228	3.0356	136.2908	59.3718	
4544	95.3512	107.7215	6.2954	86.4029	43.9802	
17448	95.3512	-9.6045		178.6031	50.1877	
18881	95.3512	31.2700	2.7934	21.3649	22.5631	
25458	95.2996	110.9095	2.8162	18.6383	8.1524	
19341	95.2479	43.4835	33.1610	41.1543	67.0274	
24885	95.1963	1835.8660	1.7363	66.3774	21.9607	
15201	95.1963	3447.9930	223.0581	1171.0566	257.6347	
16847	95.1446	1621.7053	458.2868	2274.6547	448.0018	
20462	95.1446	1536.0618	248.3307	1115.3956	189.9822	
20933	95.0930		362.5987	1030.1922	185.5571	
11849	95.0930	140.2160	5.3279	183.7717	499.2990	
7854	95.0413	1348.1815	101.5179	940.8007	195.9938	
243	94.9897	34.1235	1.8506	26.2060	24.5871	
16330		913.7335	133.1663	620.8041	113.0845	
19190	94.9897	208.1708	4.2219	172.8530	33.5156	
17105	94.9380	801.4863	75.5527	497.5050	140.9583	
14247	94.9380	2202.6573	193.9224	1532.7357	345.1211	
1444/1	94.9380	28.7498	0.7245		UTU. 12 1 11	

Fig. CLENBUTEROL  Atty. Ref. 44921-5090-01-WO/2105  Atty. Ref. 44921-5090-01-WO/2105  Atty. Ref. 44921-5090-01-WO/2105  Atty. Ref. 44921-5090-01-WO/2105								
16434			SD Tox	Mean Nontox	SD Nonto			
20896	94.8864			567.2230				
17214	94.8864	72.1373		118.7357	34.02			
16215	94.8864	63.4888	7.5354	106.4495	25.15			
15440	94.8347	316.8333	41.2945	212.9282	44.66			
23340	94.8347	24.4390	0.5360	30.9137	9.38			
	94.8347	317.6923	10.8281	245.6657	47.67			
202	94.7831	28.1825	1.2809	42.2180	14.85			
815	94.7314	2351.3360	351.2531	1485.8238	349.89			
16852	94.7314	202.9568	4.4363	255.8691	49.63			
15135	94.6798	1485.1895	200.7632	995.1288	219.00			
23869	94.6798	6.7505	3.2502	42.9405				
15840	94.6798	15.1773	4.6253	37.7956	61.78			
17807	94.6798	3050.4535	95.1550	2477.4667	12.35			
21917	94.6281	86.9305	4.6467	137.4482	409.946			
20417	94.6281	171.0010	5.7342	236.4262	40.174			
15106	94.5764	3986.4233	554.1719	2605.0488	62.647			
19393	94.5248	392.8538	28.4966	276.7454	527.257			
18305	94.5248	3108.5365	254.2765		55.008			
20614	94.4731	33.2960	0.8997	2115.2642	466.009			
19148	94.4731	162.5390	12.0865	17.2533	215.002			
20812	94.4215	2524.2418	310.7088	241.5954	48.051			
11387	94.4215	24.3165	8.4346	1742.5280	321.419			
21663	94.3698	535.2730	120.9507	60.1168	18.515			
4407	94.3182	44.3680		381.9249	189.068			
16553	94.2149	138.8333	4.4238	77.2069	21.930			
17563	94.1632	2528.9760	7.2284	89.3026	43.477			
17104	94.1116	888.3135	243.6174	1831.8476	310.851			
15136	94.1116	1550.7555	96.7579	619.6440	131.646			
5667	94.0599	1565.0848	126.5704	1071.5638	272.976			
12700	94.0599	15.2875	155.3555	1149.7767	190.533			
7163	94.0083	308.1465	1.2689	26.5546	20.724			
24536	94.0083	1336.5868	6.2251	370.5876	101.830			
8097	94.0083	725.6370	76.3393	998.3660	188.713			
16552	93.9566		40.6999	490.8906	133.812			
16220	93.8533	71.9468	10.6071	39.0058	18.9272			
23781	93.8533	3225.4738	485.8578	1864.4315	643.9048			
17100	93.8533	63.4873	5.8225	39.6359	17.0077			
13568	93.8533	1816.9928	108.1590	1309.9654	296.8518			
14970	93.8017	75.5443	6.1284	113.8145	27.0108			
583	93.8017	41.7940	4.8105	80.6715	20.5675			
19372	93.7500	87.3378	18.3387	171.2200	61.4637			
546	93.7500	182.6410	60.6879	72.6182	72.3788			
21027	93.7500	137.4413	19.6260	230.4553	50.8993			
20427	93.6983	97.0588	7.6188	154.9087	44.8005			
1488	93.5950	1679.2218	278.6166	1200.9108	217.2295			
3446	93.5950	102.2283	1.1813	98.9079	21.2632			
15875		19.6823	2.4857	35.2313	11.3942			
10185	93.5434	2132.7075	125.5746	1566.0871	298.0037			
22744	93.5434	10.2845	14.2827	31.2524	10.4128			
23173	99.2252	26.3855	0.9038	56.3983	16.8105			
	98.9669	3285.0910	237.6414	1561.3912	460.0075			
18909	98.7603	937.3875	51.1807	1658.6110	377.4156			
3250	98.7603	932.5275	75.0879	436.9967	155.0918			

TABLE 5H: Timepoint(s	CLENBUTER c): 24 hrs	ROL	Atty. Re	f. 44921-5090-01	-WO/2105485
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
10269	98.6054		73.6783	1983.5484	405.8705
16917	98.6054		92.3903	1493.2819	
16394	98.4504			777.8052	
5228	98.3988	264.5018		16.9613	
9150	98.3988	425.9990	11.6271	625.5024	
13826	98.3471	959.6915	29.5016	1391.9748	
4049	98.3471	232.0925	71.2955	43.4387	130.5291
19195	98.2955	2867.3528	237.4438	1646.6852	385.3403
23521	98.2438	15.8948	10.1974	85.5762	34.5074
4048	98.2438	112.3103	34.8237	18.8858	
14342	98.1921	169.8480	19.1182	82.8344	
19191	98.1921	1912.4983	226.5763	912.4426	
21465	98.1405	398.0138	5.2214	282.1062	96.4138
19424	98.0888	22852.8073	1223.8235	10347.0804	4848.3980
21195	97.9855	85.3645	2.0547	136.0304	39.9561
21509	97.9855	851.4765	90.0193	444.9262	134.9011
13070	97.8822	20.3425	6.5792	92.7588	
19456	97.7789	53.7898	13.3891	3.0805	36.1093
14431	97.6240	-11.4243	13.8465	45.8984	18.3298
18507	97.5723	890.7598	54.0094	510.0488	133.8710
894	97.5723	488.7110	71.4370	212.9295	78.5750
5132	97.5723	753.3963	27.3536	1123.9945	230.3786
15476	97.5723	534.1638	108.0037	302.1699	75.7980
6766	97.5207	442.2773	30.2284	190.8744	119.2936
14327	97.5207	92.8413	18.2257	-22.9178	40.5514
13267	97.3140	33.1610	4.2081	90.1076	35.5488
3132	97.3140	423.2630	66.3606	207.8763	67.9326
895	97.2107	190.0450	68.7690	60.1332	32.1107
15615	97.1591	3745.5935	141.6091	2517.3568	580.3879
13831	97.1074	66.2998	1.5392	65.2944	48.3849
3982	97.0558	99.4585	33.3773	267.5928	71.6883
20953	97.0558	541.4905	37.0747	839.0732	146.8665
16916	97.0041	436.7440	92.2636	892.1272	212.8023
19162	97.0041	4861.1903	641.2854	2851.0457	564.9066
13093	97.0041	753.5148	47.9504	1161.0444	236.7827
14642	96.9525	488.6555		189.7023	97.4228
24209	96.9008	100.0273	24.0329	3.0026	41.9427
20042	96.9008	983.4830	271.6577	438.3391	252.0171
7844	96.9008	50.6993	11.6162	147.1081	55.0968
15315	96.7459	4371.5658	256.4395	2784.8724	703.2430
10919	96.7459	2680.9605	730.9256	842.5857	660.8402
22183	96.7459	3676.6128	291.7861	2288.9363	582.5234
4834	96.7459	96.4443	2.4637	49.5111	45.2846
17529	96.6942	47.9468	3.0703	91.7341	28.0182
19359	96.6942	3751.8920	348.1457	1991.9891	550.4905
21761	96.6942	239.5320	14.7073	398.1517	99.5533
15942	96.6426	187.9785	17.0105	335.3510	75.9353
15107	96.5909	13902.3560	4964.6238	5563.0289	2417.1411
11598	96.5393	32 8070	32.3996	191.2678	68.0074
22318	96.4876	81.2843	29.3126	222.9738	79.4138
12999	96.4360	438.6615	39.1895	337.9044	309.5522
10820	96.4360	3053.7868	269.0123	1868.3510	470.1964
	<u></u> L			1000,0010	770.1304

Timepoint(s	CLENBUTER s): 24 hrs	ROL	Atty. Re	f. 44921-5090-01	-WO/2105485
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
24521	96.4360		1630.5121	5462.1901	
22030			2981.2204	11062.6238	
3755			17.71/7		39.8654
21189				734.5168	132.8529
8728 4893				132.7466	23.6850
893	96.2810	25.3940		18.0604	
14929	96.2810 96.2293	378.1673	73.8535	182.9926	66.3423
22914	96.2293	944.6818	123.9670	573.7854	134.7102
896	96.1777	1737.1080	63.7535	2437.6827	483.1667
000	. 30.1771	49.6703	13.3825	7.9432	16.0018

imepoint(s):		Tox Markers	- 11-9	f, 44921-5090-0	1-VVO/20154
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
1809	99.5868		90.6707	25.8207	
15867	99.1736		167.6115	38.0902	
11113	99.1219		7.5655	36.0548	
23651	98.8120	194.9143	58.0033	43.9816	.0.101
21000	98.3988	10.9638	0.2819	22.8672	160.607
24859	97.9855	102.9063	22.0298		19.992
15003	97.7273	833.1818	204.8023	22.8379	19.872
16696	97.7273	197.2963	8.1224	93.6247	186.902
17215	97.6756	86.5150	6.6657	302.8795	59.399
23868	97.6756	67.3360	8.0151	168.1356	43.573
15191	97.5723	517.4620	128.7504	218.8534	231.608
12580	97.5207	33.8560	1.6003	183.9005	563.839
20589	97.4690	490.8580	164.2942	19.5502	9.473
15002	97.4174	846.2003	185.8784	148.3860	88.287
1523	97.2624	149.7348	3.2732	207.2146	184.923
19549	97.2107	5.7080	2.5474	212.0033	52.060°
16918	97.1591	2852.3920	322.0410	42.7500	22.303
22321	97.1074	391.6135		1657.2857	390.3238
11997	97.1074	460.1595	39.1905	173.4379	96.5339
574	96.8492	972.5473	17.7043	677.7722	123.6360
25802	96.7975	954.9178	57.9899	604.4586	158.0302
15640	96.7459	287.6770	117.8821	599.8418	153.6054
15641	96.6426	379.4980	20.3299	141.2940	60.3599
17736	96.6426	1148.7220	27.4243	173.5264	86.4782
18122	96.4876	81.8923	124.6063	622.3568	364.0063
20983	96.4360	332.2185	21.0338	18.9802	40.6070
19040	96.3843	413.5660	11.0218	478.6360	109.8306
17383	96.3843		26.6772	254.2652	77.2862
9124	96.3326	88.0838	27.3070	10.2342	30.9053
4222	96.1777	336.2755	42.6549	213.0618	41.8746
24886	96.1260	1250.4435	53.0154	980.8498	131.6958
14360	96.0744	2331.6990	152.3483	1651.3200	275.6352
18798	96.0744	36.1613	0.5510	44.3514	21.3431
8212	95.9194	95.4560	5.1882	138.5010	28.2251
762	95.7645	614.5205	13.5571	494.4720	131.8211
21950	95.7645	152.8628	1.6805	139.5041	37.1730
22739	95.6612	561.8000	19.6699	768.0125	138.7978
3465	95.5579	268.0643	10.2046	360.3747	61.7718
1991	95.5062	58.9048	9.0152	111.0300	28.1320
23731		224.6573	17.4598	136.2908	59.3718
90	95.4545	257.6383	25.4512	159.8238	45.0087
4544	95.4029	107.5228	3.0356	86.4029	43.9802
17448	95.3512	107.7215	6.2954	178.6031	50.1877
18881	95.3512	-9.6045	2.7934	21.3649	22.5631
25458	95.3512	31.2700	2.8162	18.6383	8.1524
19341	95.2996	110.9095	33.1610	41.1543	67.0274
24885	95.2479	43.4835	1.7363	66.3774	21.9607
15201	95.1963	1835.8660	223.0581	1171.0566	257.6347
16847	95.1963	3447.9930	458.2868	2274.6547	
	95.1446	1621.7053	248.3307	1115.3956	448.0018
20462	95.1446	1536.0618	362.5987	1030.1922	189.9822
20933	95.0930	140.2160	5.3279	183.7717	185.5571
11849	95.0930	1348.1815	101.5179	940.8007	499.2990 195.9938

LGC ID	: 24 hrs		. 4.	f. 44921-5090-0	:=== 10 11
	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
13480	95.0413		6.5557	161.7956	
7854	95.0413		1.8506	26.2060	39.924
243	94.9897	913.7335	133.1663	620.8041	
16330	94.9897	208.1708	4.2219	172.8530	113.084
19190	94.9380	801.4863	75.5527	497.5050	33.515
17105	94.9380	2202.6573	193.9224	1532.7357	140.958
14247	94.9380	28.7498	0.7245	25.4779	345.121
16434	94.8864	379.5328	21.2458	567.2230	13.233
20896	94.8864	72.1373	6.2647	118.7357	119.839
17214	94.8864	63.4888	7.5354	106.4495	34.029
16215	94.8347	316.8333	41.2945	212,0200	25.157
15440	94.8347	24.4390	0.5360	212.9282	44.664
23340	94.8347	317.6923	10.8281	30.9137	9.385
202	94.7831	28.1825	1.2809	245.6657	47.677
815	94.7314	2351.3360	351.2531	42.2180	14.854
16852	94.7314	202.9568	4.4363	1485.8238	349.890
15135	94.6798	1485.1895	200.7632	255.8691	49.633
23869	94.6798	6.7505	3.2502	995.1288	219.005
15840	94.6798	15.1773	4.6253	42.9405	61.786
17807	94.6798	3050.4535		37.7956	12.3562
21917	94.6281	86.9305	95.1550	2477.4667	409.9463
20417	94.6281	171.0010	4.6467	137.4482	40.1744
15106	94.5764	3986.4233	5.7342	236.4262	62.6471
19393	94.5248	392.8538	554.1719	2605.0488	527.2574
18305	94.5248	3108.5365	28.4966	276.7454	55.0084
20614	94.4731	33.2960	254.2765	2115.2642	466.0092
19148	94.4731	162.5390	0.8997	17.2533	215.0029
20812	94.4215	2524.2418	12.0865	241.5954	48.0514
11387	94.4215	24.3165	310.7088	1742.5280	321.4198
21663	94.3698	535.2730	8.4346	60.1168	18.5151
4407	94.3182	44.3680	120.9507	381.9249	189.0689
16553	94.2149	138.8333	4.4238	77.2069	21.9306
17563	94.1632	2528.9760	7.2284	89.3026	43.4774
17104	94.1116	888.3135	243.6174	1831.8476	310.8510
20872	94.1116	1900.1203	96.7579	619.6440	131.6469
15136	94.1116		134.8184	1375.7230	300.8359
5667	94.0599	1550.7555	126.5704	1071.5638	272.9769
12700	94.0599	1565.0848	155.3555	1149.7767	190.5336
7163	94.0083	15.2875	1.2689	26.5546	20.7245
24536	94.0083	308.1465	6.2251	370.5876	101.8306
8097	94.0083	1336.5868	76.3393	998.3660	188.7130
16552	93.9566	725.6370	40.6999	490.8906	133.8125
16220	93.8533	71.9468	10.6071	39.0058	18.9272
23781	93.8533	3225.4738	485.8578	1864.4315	643.9048
17100		63.4873	5.8225	39.6359	17.0077
13568	93.8533	1816.9928	108.1590	1309.9654	296.8518
14970	93.8533	75.5443	6.1284	113.8145	27.0108
583	93.8017	41.7940	4.8105	80.6715	20.5675
22744	93.8017	87.3378	18.3387	171.2200	61.4637
23173	99.2252	26.3855	0 9038	56.3983	16.8105
23015	98.9669	3285.0910	237.6414	1561.3912	460.0075
18909	98.7603	133.8138	5.4560	77.9200	22.1910
2303	98.7603	937.3875	51.1807	1658.6110	377.4156

LGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
3250	98.7603	932.5275			
10269	98.6054	2964.3253			155.0918
16917	98.6054	796.6000			405.8705
15004	98.4504	1686.5413	198.8730	1493.2819	318.9380
16394	98.4504	1993.7018	204.4622	331.7738	260.3911
5228	98.3988	264.5018		777.8052	287.2109
9150	98.3988	425.9990		16.9613	42.9061
13826	98.3471	959.6915	11.6271	625.5024	106.3371
4049	98.3471	232.0925	29.5016	1391.9748	237.8672
19195	98.2955	2867.3528	71.2955	43.4387	130.5291
23521	98.2438	15.8948	237.4438	1646.6852	385.3403
4048	98.2438	112.3103	10.1974	85.5762	34.5074
14342	98.1921	169.8480	34.8237	18.8858	77.2543
19191	98.1921	1912.4983	19.1182	82.8344	27.6432
21465	98.1405	398.0138	226.5763	912.4426	269.2696
19424	98.0888	22852.8073	5.2214	282.1062	96.4138
5227	98.0888		1223.8235	10347.0804	4848.3980
4969	98.0372	386.4903	69.7187	152.5409	48.8669
21195	97.9855	178.1593	143.2056	-19.0442	46.4550
21509	97.9855	85.3645	2.0547	136.0304	39.9561
13070	97.8822	851.4765	90.0193	444.9262	134.9011
19456	97.7789	20.3425	6.5792	92.7588	36.1270
14431		53.7898	13.3891	3.0805	36.1093
18507	97.6240	-11.4243	13.8465	45.8984	18.3298
894	97.5723 97.5723	890.7598	54.0094	510.0488	133.8710
5132	97.5723	488.7110	71.4370	212.9295	78.5750
15476	97.5723	753.3963	27.3536	1123.9945	230.3786
6766	97.5207	534.1638	108.0037	302.1699	75.7980
14327	97.5207	442.2773	30.2284	190.8744	119.2936
13267	97.3140	92.8413	18.2257	-22.9178	40.5514
3132	97.3140	33.1610	4.2081	90.1076	35.5488
895	97.3140	423.2630	66.3606	207.8763	67.9326
15615	97.2107	190.0450	68.7690	60.1332	32.1107
13831	97.1591	3745.5935	141.6091	2517.3568	580.3879
3982	97.1074	66.2998	1.5392	65.2944	48.3849
20953	97.0558	99.4585	33.3773	267.5928	71.6883
16916	97.0558	541.4905	37.0747	839.0732	146.8665
19162	97.0041	436.7440	92.2636	892.1272	212.8023
13093	97.0041	4861.1903	641.2854	2851.0457	564.9066
14642	97.0041	753.5148	47.9504	1161.0444	236.7827
24209	96.9525	488.6555	82.0127	189.7023	97.4228
	96.9008	100.0273	24.0329	3.0026	41.9427
20042	96.9008	983.4830	271.6577	438.3391	252.0171
7844	96.9008	50.6993	11.6162	147.1081	55.0968
15315	96.7459	4371.5658	256.4395	2784.8724	703.2430
10919	96.7459	2680.9605	730.9256	842.5857	660.8402
22183	96.7459	3676.6128	291.7861	2288.9363	582.5234
4834	96.7459	96.4443	2.4637	49.5111	
17529	96.6942	47.9468	3.0703	91.7341	45.2846
19359	96.6942	3751 8020	348 1457	1991.9891	28.0182
21761	96.6942	239.5320	14.7073	398.1517	550.4905
15942	96.6426	187.9785	17.0105	335.3510	99.5533
15107	96.5909	13902.3560	4964.6238	5563.0289	75.9353 2417.1411

Timepoint(s)		Tox Markers	Atty. Re	ef. 44921-5090-0	1-WO/2015485
GLGC ID		Mean Tox	SD Tox	Mean Nontox	SD Nontox
11598			32.3996		
6015		56.6675			
22318	96.4876				
12999	96.4360				
10820	96.4360	3053.7868		1868.3510	
24521	. 96.4360	9943.4675		5462.1901	470.1964
22030	96.3326	22085.9835	2981,2204	11062.6238	1452.6442
3755	96.3326	46.9560	17.4174	122.4291	4208.6729
21189	96.2810	1111.8165	148.7927		39.8654
8728	96.2810	77.5193	13.7142	734.5168	132.8529
4893	96.2810	25.3940	44.0374	132.7466	23.6850
893	96.2810	378.1673	73.8535	18.0604	11.8525
14929	96.2293	944.6818	123.9670	182.9926	66.3423
22914	96.2293	1737.1080		573.7854	134.7102
896	96.1777		63.7535	2437.6827	483.1667
	30.1777	49.6703	13.3825	7.9432	16.0018

TABLE 5J: CLENBUTEROL  Atty. Ref. 44921-5090-01-WO/210548  GLGC ID   LDA Score   Mean Tox   SD Tox   Mean Nontox   SD Nontox							
	LDA Score		SD Tox	Mean Nontox	SD Nontox		
15191			52.4545	170.8348	500.477		
945		134.3437	6.0542	-12.6304			
20740		1340.9600	37.6412	448.7949	136.381		
21147	99.6388	41.2293	0.3146	18.0479			
23806	99.5356	13.5270	2.1598	60.1184			
10878	99.4840	1562.5993	0.6741	1634.2253	25.403		
15190	99.3808	3461.6643	487.6477	233.6376	283.988		
15189	99.3808	3694.3787	503.1788	329.6283	289.143		
24716	99.3808	72.2240	15.4827	-7.4551	310.620		
13930	99.3292	413.1923	21.7059	110.7163	11.115		
23368	99.3292	218.4663	5.4029	406.7741	65.701		
2629	99.2776	55.7473	2.8928		91.922		
20555	99.2776	11.0847	0.4816	21.3916	17.004		
23705	99.1744	97.8843	16.9478	27.9069	10.155		
25730	99.1228	399.7273	10.3185	265.3709	68.291		
15032	99.1228	31.6433		224.2822	72.945		
21709	99.0712	543.6700	0.0984	38.3319	10.077		
23715	99.0712	94.8683	42.4038	253.3641	57.356		
20734	99.0196	339.2357	16.8393	9.9387	25.114		
20735	98.9680	365.3143	52.4888	94.2550	46.160		
2453	98.9164	30.1920	51.6737	101.7314	46.498		
21654	98.8648		0.5191	53.0373	29.695		
8829	98.8648	572.4030	49.6785	203.9429	73.210		
20456	98.8132	505.2817	40.4494	267.9187	70.035		
3292	98.8132	3.9490	0.1578	22.3578	32.745		
20702	98.8132	223.3543	132.5781	-1.3809	27.726		
1228	98.7616	48.1140	6.8500	149.9956	64.965		
190	98.7616	134.1093	1.0635	192.5306	40.063		
1824	98.7100	64.3393	8.8634	-4.6305	25.246		
622		54.2170	5.5644	112.5691	25.784		
11635	98.6584	17.4750	0.5633	45.3087	19.105		
10248	98.6584	69.4783	5.2594	135.5475	28.8584		
	98.6584	421.4460	3.2657	307.6573	85.3529		
6598	98.6584	65.9897	8.8529	23.0423	10.4630		
19710	98.6584	89.4057	2.6970	48.5489	23.0344		
3910	98.6068	118.1183	0.3407	145.4331	35.4410		
17217	98.6068	257.0393	5.0020	405.4736	80.5839		
21682	98.5552	184.9510	96.4663	-9.7676	54.3813		
355	98.5036	94.2290	12.0303	9.8934	28.6974		
16312	98.4520	285.0370	77.1088	67.3643	35.2005		
17590	98.4520	90.5147	4.1203	48.3731			
18695	98.4520	217.4283	76.3852	35.0061	16.1590		
733	98.4004	61.5817	0.4070	84.3478	39.0491		
12580	98.4004	62.9820	11.9219	19.4747	27.7086		
20127	98.2972	93.0660	7.5880	30.6760	9.1851		
21115	98.2972	231.9090	10.3353		20.9299		
13005	98.2972	39.8907	4.6011	102.9476	53.5277		
16029	98.2972	81.3597	27.8106	18.4472	7.3766		
12978	98.2972	174.3473	30.0006	13.8859	19.1912		
356	98.2456	165.1347	24.9797	78.0023	51.9326		
25761	98.2456	27.2957	*** ··	41.3534	45.3902		
18597	98.1940	278.9343	0.9103	10.3706	13.3401		
14250	98.1940	352.4563	56.3348	94.5047	63.0400		
		302.7000	54.8318	145.1721	51.5631		

imepoint(s	): 6 hrs		•	ef. 44921-5090-0	1-440/21004
	LDA Score		SD Tox	Mean Nontox	SD Nontox
23044			72.5360		
17556	98.1424		4.5099	418.5919	
21653	98.0908		36,0854	116.2228	
4512	98.0908	136.4383	56.5763	23.1132	-
16030	98.0908	46.1457	31.5041	-6.3851	27.37
17532	97.9876	166.7917	5.1276	264.8779	16.65
20161	97.9360	231.1267	105.1007	36.2762	55.68
357	97.9360	85.4477	19.1172	25.4313	39.26
11203	97.9360	94.6200	7.3173	50.3291	18.01
24019	97.9360	104.0047	17.2367	27.0516	16.11
20614	97.8844	42.7467	1.2769	17.2406	25.40
. 244	97.8844	196.2470	29.2619	63.1635	214.88
16249	97.8844	42.3113	4.1646	-4.0842	44.19
21683	97.8328	271.7527	92.8744	48.5984	48.63
21657	97.7812	1448.9427	42.7862	954.6483	33.99
9423	97.7812	477.6037	161.5233	167.2220	229.32
25567	97.7812	138.8263	11.4355		78.060
1921	97.7812	181.9453	43.7093	67.6319 81.4987	35.717
19085	97.7296	103.0713	12.4950		23.231
5384	97.7296	329.6763	123.8702	52.2006	14.077
16197	97.7296	160.0660	0.8063	42.1950	55.746
18694	97.7296	85.3757	71.6381	161.5913	52.336
6153	97.6780	184.3700	32.7761	-7.2428 622.7538	25.718
25072	97.6780	25.2017	6.0933	-6.1292	222.115
17336	97.6780	38.8513	6.0298	15.6028	14.891
21975	97.6264	509.6623	141.1960	180.4975	7.699
24674	97.6264	39.2367	0.4022	33.2995	77.576
1097	97.6264	113.2633	13.0527	303.5668	26.824
17337	97.6264	274.9593	43.2507	141.9581	99.739
11483	97.5748	255.8617	50.3113	99.1670	42.969
15353	97.5748	54.9167	15.7750	19.2374	43.759
2736	97.5748	211.0247	16.5303	358.5069	16.865
15640	97.5232	143.6827	1.3775	141.8909	62.999
804	97.5232	135.3840	26.7548	52.3425	61.065
17301	97.5232	148.7857	39.6259	502.6110	29.2084
15570	97.5232	193.2387	49.8258	622.6698	155.5782
1295	97.5232	27.4813	7.8249	75.2102	207.2827
19086	97.4716	157.9933	20.0631	75.1020	19.217
17658	97.4716	4.3310	3.7428	41.4360	28.1408
15301	97.4200	275.7437	37.4354	100.2767	20.5048
25090	97.3684	441.3950	92.2155	140.5463	84.4844
9240	97.3684	933.6183	14.9587	1170.9649	81.4944 183.3070
1804	97.3684	8526.9873	141.8813	6460.4813	2181.5948
15468	97.3168	1408.7463	8.4715	1311.6313	222.0564
18349	97.2652	386.7867	121.1182	174.8812	
25883	97.2136	4776.3063	68.5880	3422.5719	62.5378 915.0306
1609	97.2136	1613.7737	301.0304	872.2018	288.7875
20746	97.2136	272.4527	22.3631	492.5344	
15192	99.9484	245.0187	6.7325	70.9741	121.2973
18472	99.8968	261.0007	4.7005	67.1399	40.1911
3049	99.8968	1215.6133	12.3725	248.1956	41.9499
15984	99.8452	492.0337	8.2519	247.8687	126.6890 57.6010

imepoint(s): 6 hrs  GLGC ID   LDA Score   Mean Tox   SD Tox   Mean Nontox   SD Nortox   SD							
15078	99.8452		SD Tox	Mean Nontox	SD Nonto		
6988	99.7420		1.8675	206.5969			
24200	99.7420		21.8467	12.9282	79.2		
6844	99.7420		51.0588	650.5468			
23424	99.6388	-15.2123	3.7916	158.4966	89.8		
13619	99.6388	495.8370	8.8821	309.6446	63.2		
13240		260.5140	8.2960	135.0774	46.7		
5943	99.5872	384.1850	26.2196	46.0984	41.10		
14209	99.5872	2.5757	7.2305	117.6422	43.8		
2348	99.5872	95.2830	0.6904	186.1088	61.09		
22765	99.5872	235.1720	0.4753	280.7291	97.6		
11467	99.5356	111.5053	3.6676	22.9075	22.69		
	99.5356	216.0630	2.1991	139.6584			
23025	99.4840	-14.1163	0.4311	27.1357	38.00		
23471	99.4840	283.3903	14.5924	77.3412	41.44		
22381	99.4840	175.8840	6.3195	103.3030	35.07		
22081	99.4840	94.4403	6.8233	229.1844	23.74		
4626	99.4324	91.5253	4.1731	27.8457	47.76		
15157	99.4324	39.1553	0.2282	65.6418	26.42		
13353	99.3808	116.6127	5.6815	200.6327	20.21		
9059	99.3808	636.5220	39.1324		32.27		
4018	99.3808	27.1503	4.5802	271.8312	79.82		
22152	99.3292	57.3433	2.7280	-11.2888	10.83		
7315	99.3292	214.7143	34.5163	-0.2891	20.20		
15051	99.2776	615.7103	141.6182	10.0917	25.31		
5675	99.2776	1314.5897	174.2619	119.3141	105.81		
2331	99.2260	1230.4933	59.9098	156.0669	123.35		
11873	99.2260	964.7597	160.1007	389.0874	358.26		
13266	99.2260	349.0043		147.0140	109.619		
11871	99.2260	3316.3687	67.6682	94.0862	43.15		
3050	99.1744	615.6347	720.1954	43.1452	326.888		
2605	99.1744	36.3433	84.2415	87.5598	59.609		
21740	99.1228	697.6160	10.6257	302.2771	139.091		
6532	99.1228	933.6980	38.4674	276.3875	85.520		
12435	99.1228	116.6823	54.8957	449.2898	126.955		
3619	99.1228	46.3957	3.7442	229.7496	48.251		
23038	99.1228		0.1635	57.9467	16.186		
2729	99.0712	155.3643 193.8313	13.0636	20.6635	122.979		
9796	99.0712	48.0417	10.9173	480.0400	152.568		
5210	99.0712	52.3533	4.7084	6.8524	13.411		
15892	99.0196		1.8222	96.2220	21.667		
6715	99.0196	334.6830	40.5811	58.3685	50.300		
15042	99.0196	96.9987	8.6659	42.9113	17.273		
9083	99.0196	147.0083	7.5527	44.1413	36.594		
16631	99.0196	118.1750	6.7094	251.4949	62.406		
16976	99.0196	599.9867	112.2449	64.6549	72.307		
4797		630.3390	110.0159	244.6155	67.755		
8477	98.9680	239.9153	2.9022	150.0514	44.975		
18473	98.9164	1373.4903	73.9002	595.5884	183.345		
24375	98.9164	502.5353	39.9997	204.2286	69.689		
3207	98.9164	168.6763	3.3642	109.8936	32.656		
	98.9164	-77.1093	28.2336	241.8528	97.3643		
13634	98.8648	1647.6060	76.4982	822.0337	216.6497		
15374	98.8648	179.9300	10.9265	101.8803	26.4536		

TABLE 5J: Timepoint(s	CLENBUTER ): 6 hrs	OL	Atty. R	ef. 44921-5090-0	1-WO/210548
GLGC ID		Mean Tox	SD Tox	Mean Nontox	SD Nontox
22697		76.7463			
21596	98.8648			312.3243	
23631	98.8132	475.8523			
657	98.8132	630.2727			
10659	98.7616		15.9078	156.3555	0111000
10971	98.7100	110.4397	11.4396		15.6427
4479		495.3427		160.3289	83.4252
2372	98.7100		0.4810	43.1912	19.0817
8820	98.7100		15.6944	399.3163	123.0551
22317	98.7100	75.9110	17.8196	190.4315	45.8238

niteholUf(2):	6 nrs	re Tox Markers	Atty. Re	f. 44921-5090-01	-WO/21054
ELGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	ICO No.
15191	100.0000		52.4545		SD Nontox
945	99.9484	134.3437	6.0542	1.0.00.70	
20740	99.8452	1340.9600	37.6412	-12.6304	30.069
21147	99.6388	41.2293	0.3146	448.7949	136.38
23806	99.5356	13.5270	2.1598	18.0479	11.210
10878	99.4840	1562.5993		60.1184	25.403
15190	99.3808	3461.6643	0.6741	1634.2253	283.988
15189	99.3808	3694.3787	487.6477	233.6376	289.143
24716	99.3808	72.2240	503.1788	329.6283	310.620
13930	99.3292	413.1923	15.4827	7.4551	11.115
23368	99.3292	218.4663	21.7059	110.7163	65.701
2629	99.2776	55.7473	5.4029	406.7741	91.922
20555	99.2776	11.0847	2.8928	21.3916	17.004
11113	99.1744	174.2973	0.4816	27.9069	10.155
23705	99.1744		52.1552	35.8404	17.958
25730	99.1228	97.8843	16.9478	265.3709	68.291
15032	99.1228	399.7273	10.3185	224.2822	72.945
1809	99.1228	31.6433	0.0984	38.3319	10.077
21709	99.0712	180.1930	66.3027	26.7980	76.575
23715	99.0712	543.6700	42.4038	253.3641	57.356
20734	99.0196	94.8683	16.8393	9.9387	25.114
11114	98.9680	339.2357	52.4888	94.2550	46.160
20735	98.9680	362.1807	141.4201	30.5894	32.3749
2453	98.9164	365.3143	51.6737	101.7314	46.4986
21654	98.8648	30.1920	0.5191	53.0373	29.6950
8829	98.8648	572.4030	49.6785	203.9429	73.2109
20456	98.8132	505.2817	40.4494	267.9187	70.0353
3292	98.8132	3.9490	0.1578	22.3578	32.7458
20702	98.8132	223.3543	132.5781	-1.3809	27.7261
1228	98.7616	48.1140	6.8500	149.9956	64.9653
190	98.7616	134.1093	1.0635	192.5306	40.0635
1824	98.7100	64.3393	8.8634	-4.6305	25.2465
622	98.6584	54.2170	5.5644	112.5691	25.7844
11635		17.4750	0.5633	45.3087	19.1055
10248	98.6584	69.4783	5.2594	135.5475	28.8584
6598	98.6584	421.4460	3.2657	307.6573	85.3529
19710	98.6584	65.9897	8.8529	23.0423	10.4630
3910	98.6584	89.4057	2.6970	48.5489	23.0344
17217	98.6068	118.1183	0.3407	145.4331	35.4410
21682	98.6068	257.0393	5.0020	405.4736	80.5839
355	98.5552	184.9510	96.4663	-9.7676	54.3813
16312	98.5036	94.2290	12.0303	9.8934	28.6974
17590	98.4520	285.0370	77.1088	67.3643	35.2005
18695	98.4520	90.5147	4.1203	48.3731	16.1590
733	98.4520	217.4283	76.3852	35.0061	39.0491
	98.4004	61.5817	0.4070	84.3478	
12580	98.4004	62.9820	11.9219	19.4747	27.7086
20127	98.2972	93.0660	7.5880	30.6760	9.1851
21115	98.2972	231.9090	10.3353	102.9476	20.9299
13005	98.2972	39.8907	4.6011	18.4472	53.5277
16029	98.2972	81.3597	27.8106	13.8859	7.3766
12978 356	98.2972	174.3473	30.0006	78.0023	19.1912 51.9326
3561	98.2456	165.1347		10.00251	51 43261

GC ID	LDA Score	Mean Tox		Man N	
25761	98.2456	- · · · · · · · · · · · · · · · · · · ·		Mean Nontox	SD Nont
18597	98.1940		0.9103	10.3706	
14250	98.1940		56.3348	94.5047	63.0
23044	98.1940	475.3620	54.8318	145.1721	51.
17556	98.1424		72.5360	227.0935	51.
21653	98.0908	447.2547	4.5099	418.5919	269.8
4512	98.0908	271.2960	36.0854	116.2228	40.6
16030	98.0908	136.4383	56.5763	23.1132	27.3
17532	97.9876	46.1457	31.5041	-6.3851	16.6
20161	97.9360	166.7917	5.1276	264.8779	55.6
357	97.9360	231.1267	105.1007	36.2762	39.2
11203	97.9360	85.4477	19.1172	25.4313	18.0
24019	97.9360	94.6200	7.3173	50.3291	16.1
20614	97.8844	104.0047	17.2367	27.0516	25.4
244	97.8844	42.7467	1.2769	17.2406	214.8
10097		196.2470	29.2619	63.1635	44.1
16249	97.8844	71.4007	3.2167	118.9075	22.9
21683	97.8844	42.3113	4.1646	-4.0842	48.6
21657	97.8328	271.7527	92.8744	48.5984	33.9
9423	97.7812	1448.9427	42.7862	954.6483	229.3
25567	97.7812	477.6037	161.5233	167.2220	78.0
	97.7812	138.8263	11.4355	67.6319	35.7
1921	97.7812	181.9453	43.7093	81.4987	23.2
19085	97.7296	103.0713	12.4950	52.2006	14.0
5384	97.7296	329.6763	123.8702	42.1950	55.74
16197	97.7296	160.0660	0.8063	161.5913	52.3
18694	97.7296	85.3757	71.6381	-7.2428	25.7
6153	97.6780	184.3700	32.7761	622.7538	222.1
25072	97.6780	25.2017	6.0933	-6.1292	14.89
17336	97.6780	38.8513	6.0298	15.6028	7.69
21975	97.6264	509.6623	141.1960	180.4975	77.57
24674	97.6264	39.2367	0.4022	33.2995	26.82
1097	97.6264	113.2633	13.0527	303.5668	
17337	97.6264	274.9593	43.2507	141.9581	99.73 42.96
11483	97.5748	255.8617	50.3113	99.1670	
15353	97.5748	54.9167	15.7750	19.2374	43.75
2736	97.5748	211.0247	16.5303	358.5069	16.86 62.99
15640	97.5232	143.6827	1.3775	141.8909	
804	97.5232	135.3840	26.7548	52.3425	61.06 29.20
17301	97.5232	148.7857	39.6259	502.6110	
15570	97.5232	193.2387	49.8258	622.6698	155.57
1295	97.5232	27.4813	7.8249	75.2102	207.28
15003	97.4716	763.7743	241.5009	94.6028	19.21
19086	97.4716	157.9933	20.0631	75.1020	189.13
17658	97.4716	4.3310	3.7428	41.4360	28.14
15301	97.4200	275.7437	37.4354	100.2767	20.50
15002	97.3684	872.2577	263.0266	207.7934	84.48
25090	97.3684	441.3950	92.2155	140.5463	185.58
9240	97.3684	933.6183	14.9587		81.49
15192	99.9484	245.0187	6.7325	1170.9649	183.30
18472	99.8968	261.0007	4.7005	70.9741	40.19
3049	99.8968	1215.6133	12.3725	67.1399	41.949
15984	99.8452	492.0337	8.2519	248.1956 247.8687	126.689

nepoint(s): .GC ID	LDAG.		•	f. 44921-5090-01	
		Mean Tox	SD Tox	Mean Nontox	SD Nonto
15078	99.8452		1.8675		
6988	99.7420		21.8467	12.9282	
24200	99.7420	1831.3610	51.0588	650.5468	
6844	99.7420	-15.2123	3.7916	158.4966	
23424	99.6388	495.8370	8.8821	309.6446	89.872
13619	99.6388	260.5140	8.2960		63.270
13240	99.5872	384.1850	26.2196	135.0774	46.73
5943	99.5872	2.5757	7.2305	46.0984	41.10
14209	99.5872	95.2830	0.6904	117.6422	43.872
2348	99.5872	235.1720	0.4753	186.1088	61.093
22765	99.5356	111.5053	3.6676	280.7291	97.611
11467	99.5356	216.0630	2.1991	22.9075	22.691
23025	99.4840	-14.1163	0.4311	139.6584	38.003
23471	99.4840	283.3903	14.5924	27.1357	41.448
22381	99.4840	175.8840	6.3195	77.3412	35.079
22081	99.4840	94.4403		103.3030	23.748
4626	99.4324	91.5253	6.8233	229.1844	47.764
15157	99.4324	39.1553	4.1731	27.8457	26.423
13353	99.3808	116.6127	0.2282	65.6418	20.217
9059	99.3808	636.5220	5.6815	200.6327	32.270
4018	99.3808	27.1503	39.1324	271.8312	79.823
22152	99.3292	57.3433	4.5802	-11.2888	10.830
7315	99.3292		2.7280	-0.2891	20.207
15051	99.2776	214.7143 615.7103	34.5163	10.0917	25.318
5675	99.2776	1314.5897	141.6182	119.3141	105.811
2331	99.2260	1230.4933	174.2619	156.0669	123.353
11873	99.2260	964.7597	59.9098	389.0874	358.267
13266	99.2260	349.0043	160.1007	147.0140	109.619
11871	99.2260	3316.3687	67.6682	94.0862	43.1564
3050	99.1744		720.1954	43.1452	326.8880
2605	99.1744	615.6347	84.2415	87.5598	59.6096
21740	99.1228	36.3433	10.6257	302.2771	139.0916
6532	99.1228	697.6160	38.4674	276.3875	85.5203
12435	99.1228	933.6980	54.8957	449.2898	126.9559
3619	99.1228	116.6823	3.7442	229.7496	48.2511
23038	99.1228	46.3957	0.1635	57.9467	16.1863
2729	99.0712	155.3643	13.0636	20.6635	122.9799
9796	99.0712	193.8313	10.9173	480.0400	152.5689
5210	99.0712	48.0417	4.7084	6.8524	13.4118
10020	99.0712	52.3533	1.8222	96.2220	21.6672
15892	99.0196	290.1433	29.1231	117.2104	99.4120
6715	99.0196	334.6830	40.5811	58.3685	50.3007
15042	99.0196	96.9987	8.6659	42.9113	17.2734
9083	99.0196	147.0083	7.5527	44.1413	36.5945
16631		118.1750	6.7094	251.4949	62.4067
16976	99.0196	599.9867	112.2449	64.6549	72.3076
4797	99.0196	630.3390	110.0159	244.6155	67.7554
8477	98.9680	239.9153	2.9022	150.0514	44.9756
18473	98.9164	1373.4903	73.9002	595.5884	183.3453
	98.9164	502 5353	39 9997	204.2286	69.6891
24375	98.9164	168.6763	3.3642	109.8936	32.6563
19071	98.9164	175.4793	5.4536	67.1093	38.8081
3207	98.9164	-77.1093	28.2336	241.8528	97.3643

lenbuterolCo	re Tox Markers	Atty. Re	f. 44921-5090-01	-WO/2105485
LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
98.8648	1647.6060	76.4982		
98.8648				216.6497
98.8648				47.1111
98.8648				26.4536
98.8648	886.3967			156.2251
98.8132	475.8523			85.2827
98.8132	630.2727			91.2200 57.1698
98.7616	384.3923			73.8458
98.7100	110.4397			
98.7100	495.3427			15.6427 83.4252
98.7100	18.7610			19.0817
98.7100	139.3167			123.0551
98.7100	75.9110	17.8196		45.8238
	98.8648 98.8648 98.8648 98.8648 98.8648 98.8132 98.7100 98.7100 98.7100 98.7100 98.7100	LDA Score         Mean Tox           98.8648         1647.6060           98.8648         206.4873           98.8648         179.9300           98.8648         76.7463           98.8648         886.3967           98.8132         475.8523           98.8132         630.2727           98.7616         384.3923           98.7100         110.4397           98.7100         495.3427           98.7100         18.7610           98.7100         139.3167	6 hrs         Mean Tox         SD Tox           98.8648         1647.6060         76.4982           98.8648         206.4873         38.0144           98.8648         179.9300         10.9265           98.8648         76.7463         14.9592           98.8648         886.3967         192.5967           98.8132         475.8523         20.6543           98.8132         630.2727         103.1035           98.7616         384.3923         15.9078           98.7100         110.4397         11.4396           98.7100         495.3427         80.8484           98.7100         18.7610         0.4810           98.7100         139.3167         15.6944	6 hrs         LDA Score         Mean Tox         SD Tox         Mean Nontox           98.8648         1647.6060         76.4982         822.0337           98.8648         206.4873         38.0144         -18.9284           98.8648         179.9300         10.9265         101.8803           98.8648         76.7463         14.9592         408.5599           98.8648         886.3967         192.5967         312.3243           98.8132         475.8523         20.6543         247.4404           98.8132         630.2727         103.1035         224.5298           98.7616         384.3923         15.9078         156.3555           98.7100         110.4397         11.4396         42.1501           98.7100         495.3427         80.8484         160.3289           98.7100         18.7610         0.4810         43.1912           98.7100         139.3167         15.6944         399.3163

1.000011110	): 6, 48, 192 l	<u>irs</u>		ef. 44921-5090-0	3
LGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
10320	89.7810			80.2271	26.635
25752	89.4281		32.3077	-48.6677	50.368
4565			7,4914	43.5158	14.255
6535	88.9067	326.4850	26.2854	443.6589	71.121
4474	88.1246	83.1301	16.8788	38.9299	27.371
3430	87.9803	166.8932	45.6262	107.2888	28.377
17160	87.2263		246.2741	1700.7727	422.770
25600	86.6528	46.2684	8.1829	70.3570	19.569
25777	86.4964	318.4775	67.4468	233.5822	144.321
4235	86.2998	418.5075	36.8917	323.8966	67.876
20298	86.0632	-209.7280	224.0546	75.5678	98.810
25438	85.7263	36.9592	16.6537	71.6885	22.801
23215	85.7143	73.2627	9.3638	100.2808	26.845
17130	85.5178	157.2409	27.1432	121.4634	27.873
17350	85.3092	33.7344	14.9914	70.3727	23.611
16227	85.2691	-8.5485	40.6641	57.0384	38.309
4242	85.2170	354.5961	76.3555	238.4828	
298	84.9322	39.3249	7.5073	58.9297	64.273
9538	84.4870	139.5897	45.3819	246.1349	23.5384
25075	84.4229	-55.1296	123.6013	126.3349	56.4678 124.4803
17501	84.1101	47.8965	10.5383	30.7274	
21928	84.0058	24.0430	8.7688	40.1568	16.706
15573	84.0058	85.2547	7.1748	105.6006	12.3982
485	83.9416	26.1465	4.0048	30.0318	18.1901
20440	83.8213	15.0142	24.2204	51.5582	14.0485
18819	83.5365	9.6234	18.9771	47.3364	18.9648
4601	83.5085	124.2250	54.2512	64.3827	25.9806
25235	83.4202	21.0332	3.1490	28.7791	25.3876
1816	83.3801	63.6727	11.0712	36.9095	9.5164
21287	83.2478	663.9862	249.7618	437.6605	24.3261
15846	83.1716	28.2028	18.3707	68.2328	113.2092
22434	83.0553	75.1141	22.1786	158.0193	33.9342
21182	83.0392	446.7158	113.3050	273.5515	85.7508
14989	82.9871	1065.5044	242.9779	724.6623	73.8746
1894	82.8828	323.7673	130.9377	148.5104	151.5867
20928	82.8587	4.8148	9.5444	22.6804	74.7605
20864	82.7545	7.0454	5.2635	24.6889	14.0144
1170	82.5580	99.0908	23.3225	74.5513	14.9762
4684	82.4537	90.8723	14.6729	55.9466	20.4279
1879	82.2211	52.2070	12.8776		21.9963
24662	82.1810	160.5178	9.0516	70.6751	19.1321
16210	81.9082	344.3033	25.2730	177.7223	40.3160
1709	81.9082	42.6635	6.6617	309.6258	80.6548
21882	81.7639	67.8985	9.4656	60.1366	32.4778
492	81.7478	521.8128	359.0693	96.4214	28.1915
21440	81.6596	69.1262	6.7560	200.5845	132.3089
24597	81.6315	664.7450	113.9138	58.8514	29.7861
4622	81.5673	744.0142	80.0984	481.3343	107.1911
11454	81.5152	295.1553	62.6632	594.7047	97.8738
25737	81.4911	20.6926		209.1293	63.0907
16955	81.3829	917.9139	7.4353	33.0323	16.0955
25495	81.3588	179.2540	347.0575	528.0292	172.1319
		173.2040	16.6020	140.4145	34.0588

imepoint(s): 6, 48; 192 hrs  LGC ID LDA Score Mean Tox ISD Tox Mean Nontox ISD North							
20554	81.3468			Mean Nontox	SD Nontox		
9905	81.2665				36.72		
18468	81.2665			42.2181	22.76		
4362				95.0510	27.89		
17561	81.0981	31.5221	34.1067	35.6249	20.78		
25369	81.0219	181.7411	42.6801	286.7749	138.06		
20450	81.0219	18.4957	4.2567	26.8936	11.11		
16241	80.9818	46.5020	15.8107	72.8100	22.30		
919	80.9818	29.5792	3.7244	39.2193	9.57		
22583	80.9176	-8.1594	16.5029	28.3589	38.35		
200	80.8254	17.6804	3.1824	23.9761	5.78		
20225	80.8254	55.7341	11.1492	79.2127	22.57		
	80.7732	32.5332	10.4836	96.7807	57.48		
1108 14980	80.7331	16.5236	7.6479	33.0522	11.91		
1005	80.7211	30.2779	12.3506	13.1152	14.75		
23058	80.7211	48.6211	8.6610	32.9766	20.184		
	80.6569	216.2758	48.4577	282.9896	72.709		
619	80.5126	28.8201	3.2076	36.6183	8.673		
381	80.4083	17.2289	7.4306	29.1982	10.673		
20779	80.3160	165.3218	17.5305	124.0075	27.846		
15485	80.2759	30.7244	11.8598	14.1573	10.243		
1948	80.2639	135.8238	30.4102	82.4756	43.207		
21069	80.2519	35.4449	5.3390	49.5922	14.214		
17502	80.2238	285.0915	63.2148	193.0939	56.403		
20998	80.1315	524.4325	181.7060	279.3474	80.870		
20536	80.1195	38.3231	31.6941	11.8192	22.370		
17972	80.1075	27.8115	11.5342	42.8828	11.808		
18895	80.0032	114.9495	22.6815	163.3734	34.799		
19949	79.9751	131.3377	28.7340	82.5089	20.937		
17086	79.9390	157.1793	28.2946	209.2537	48.693		
20246	79.9230	4.4057	29.0201	46.5865	21.632		
912 17174	79.8709	514.3985	115.6418	380.2598	63.122		
	79.8187	88.9931	34.3390	44.8814	24.087		
25496	79.7425	201.9165	22.2101	157.5616	37.482		
22150 25659	79.6503	224.3901	48.0786	151.1148	44.511		
20021	79.6142	38.9102	12.7519	90.1269	61.218		
4412	79.5981	21.5031	62.2867	-68.4464	58.723		
20980	79.5861	505.8172	57.5353	391.7156	81.310		
18032	79.5741	34.7882	6.1143	49.3264	15.3112		
	79.5219	44.1663	19.4651	88.9932	44.5654		
15142 18655	79.4417	29.8871	10.2390	14.9828	11.7599		
8269	79.4016	48.4742	105.6019	156.9252	61.1346		
15408	79.3134	15.1508	3.8355	21.8943	9.4989		
18226	79.3014	201.3526	31.1048	267.5795	79.7365		
25705	79.2733	347.2062	41.3967	285.8516	55.2318		
1581	79.2452	529.9615	172.6778	359.4869	116.2552		
18098	79.2211	370.1620	43.9235	296.6924	61.2129		
23698	79.1570	43.4105	10.6774	58.5767	15.2037		
19928	79.1570	22.5660	4.4851	36.6734)	12.7716		
13802	95.5162	925.7691	133.5806	455.9207	201.3601		
2782	90.0417	82.1183	15.6432	139.6725	38.6296		
11563	89.6767	90.1382	18.5820	55.6441	44.4733		
11303	89.2717	223.4953	52.2880	116.1155	54.8260		

GLGC ID	): 6, 48, 192 I	110		ef. 44921-5090-0	
	LDA Score		SD Tox	Mean Nontox	SD Nontox
23545 5553			1280.6033	3900.7723	1027.45
				86.3451	
5969	87.8118	330.0040		426.2666	
461	87.4870		10.9837	99.8830	-
7715	87.3827	19.2980		33.8221	30.260
9286	87.3306	222.8223		310.6062	11.918
22771	87.2904	559.0163	58.8088	385.8688	67.979
2559	87.1220	284.6615	53.9835	411.3248	93.012
19283	87.0699	265.8252	85.8404	429.5856	89.197
15786	86.8733	156.4094	30.5506	89.4438	125.703
19093	86.2878	83.5065	38.2466	188.3403	41.803
5378	86.1835	320.8532	19.9846	373.9869	83.902
12805	86.0792	77.2402	22.4623	11.6043	86.189
7970	85.9349	104.6198	20.6103	152.3275	53.334
4151	85.9228	391.9504	84.6875	603.8739	31.056
11368	85.7383	60.7732	29.7627		163.244
23840	85.6862	89.0182	59.5736	12.0356 -30.0771	24.996
17261	85.6220	766.4824	84.1296		58.939
17796	85.5057	76.7958	16.8909	575.6093	138.960
3094	85.4135	39.5858	11.4552	147.3081	60.387
18854	85.2972	164.8416	20.7067	87.0693	51.025
19145	85.2691	475.8288	65.8220	191.7377	51.6309
13511	85.1528	210.4325	25.4688	361.1610	60.9836
2211	85.0485	-13.4862	33.9645	155.3516	35.9170
5111	84.9844	240.8116	43.9451	51.7761	39.4487
11337	84.8801	41.2845	12.0828	365.5485	128.5405
17089	84.8400	1402.3132	189.5788	65.7655	19.9522
16543	84.7999	53.5725	22.0423	1086.3912	401.2285
5740	84.7237	44.1492	12.5690	97.1162	25.0521
23337	84.7076	508.7272	176.7436	74.0108	26.5389
3191	84.6836	229.4547	29.9839	279.0357	100.2738
23464	84.6435	259.7548	64.2746	161.5617	44.6216
1182	84.6314	69.0456	16.7101	161.8276	51.8224
9876	84.2665	41.0540	22.0838	107.3778	26.4151
12804	84.2143	29.3941		93.3784	36.4615
17355	84.1622	539.2781	16.9388	62.1187	24.9069
4873	83.9256	727.1948	108.7013 252.9898	762.9939	169.7132
17492	83.8895	532.6638	131.2774	441.5460	110.5566
15084	83.7571	67.0725		802.8211	236.1699
22438	83.7451	-10.9127	57.5538	197.8258	77.3188
4626	83.6007	70.5967	12.3748	23.1043	29.0729
14337	83.5365	236.3598	26.6423	27.4654	26.1604
8627	83.4323	19.7490	30.3950	307.7315	50.7455
4975	83.3280	66.2334	10.6688	39.2932	14.3428
6458	83.2758	13.9457	15.4385	105.7459	29.5074
18337	83.2758	423.4050	5.6771	34.2500	21.6628
11268	83.2117	103.1452	86.0876	592.1076	120.7567
15904	83.1716	297.8010	22.8648	146.3976	40.9740
22911	83.1595	113.0401	53.1909	427.0825	92.9293
7044	83.1435	1676.3148	27 8182	171 0561	61.5415
3319	83.0793	14.5687	416.2079	1293.0095	246.6518
12356	83.0152	57.0170	17.0282	35.4199	15.6659
		37.0170	13.5032	99.2891	36.0694

Timepoint(s	<u>):  6, 48, 192 f</u>		, ady, ix	ef. 44921-5090-0	)1-WO/210548
			SD Tox	Mean Nontox	SD Nontox
7961 18680			13.8782	46.4652	
18610			11,7000	164.6098	
15924		.00.0200			00.1148
6658		10.0 17 2		98.2426	37.6253
4917	82.9109 82.9109		22.9474	134.7486	0020
4311	62.9109	14.4837	15.2375	61.1111	36.2076

Core Tox M		•		Ref. No. 44921-509	0-01-110721054
Fimepoint(s 3LGC ID	): 6, 48, 192 LDA Score	hrs	•	. * *	
10320		Mean Tox	SD Tox	Mean Nontox	SD Nontox
25752				80,2271	26.63
4565	89.4281			-48.6677	50.368
			7.4914	43.5158	14.255
6535	88.9067	326.4850	26.2854	443.6589	71.121
4474	88.1246	83.1301	16.8788	38.9299	27.371
3430	87.9803		45.6262	107.2888	28.377
17160	87.2263	2103.6017	246.2741	1700.7727	422.770
25600	86.6528	46.2684	8.1829	70.3570	19.569
25777	86.4964	318.4775	67.4468	233.5822	144.321
4235	86.2998	418.5075	36.8917	323.8966	
20298	86.0632	-209.7280	224.0546	75.5678	67.876
25438	85.7263	36.9592	16.6537	71.6885	98.810
23215	85.7143	73.2627	9.3638	100.2808	22.801
17130	85.5178	157.2409	27.1432	121.4634	26.845
24228	85.4897	327.6269	131.5678	158.3839	27.873
17350	85.3092	33.7344	14.9914	70.3727	46.245
16227	85.2691	-8.5485	40.6641	57.0384	23.611
4242	85.2170	354.5961	76.3555		38.309
298	84.9322	39.3249	7.5073	238.4828	64.273
22423	84.4991	191.4260	97.7415	58.9297	23.538
9538	84.4870	139.5897	45.3819	85.1822	50.768
25075	84.4229	-55.1296	123.6013	246.1349	56.467
17501	84.1101	47.8965	10.5383	126.3349	124.480
21928	84.0058	24.0430	8.7688	30.7274	16.706
15573	84.0058	85.2547	7.1748	40.1568	12.3982
485	83.9416	26.1465	4.0048	105.6006	18.190°
20440	83.8213	15.0142	24.2204	30.0318	14.048
18819	83.5365	9.6234	18.9771	51.5582	18.9648
4601	83.5085	124.2250	54.2512	47.3364	25.980
25235	83.4202	21.0332	3.1490	64.3827	25.3876
1816	83.3801	63.6727	11.0712	28.7791	9.5164
21287	83.2478	663.9862	249.7618	36.9095	24.3261
15846	83.1716	28.2028	18.3707	437.6605	113.2092
22434	83.0553	75.1141		68.2328	33.9342
21182	83.0392	446.7158	22.1786	158.0193	85.7508
14989	82.9871	1065.5044	113.3050	273.5515	73.8746
1894	82.8828	323.7673	242.9779	724.6623	151.5867
20928	82.8587	4.8148	130.9377	148.5104	74.7605
20864	82.7545	7.0454	9.5444	22.6804	14.0144
1170	82.5580	99.0908	5.2635	24.6889	14.9762
4684	82.4537	90.8723	23.3225	74.5513	20.4279
1879	82.2211	52.2070	14.6729	55.9466	21.9963
24662	82.1810	160.5178	12.8776	70.6751	19.1321
16210	81.9082	344.3033	9.0516	177.7223	40.3160
1709	81.9082	42.6635	25.2730	309.6258	80.6548
21882	81.7639	67.8985	6.6617	60.1366	32.4778
492	81.7478	521.8128	9.4656	96.4214	28.1915
21440	81.6596	69.1262	359.0693	200.5845	132.3089
24597	81.6315	664.7450	6.7560	58.8514	29.7861
4622	81.5673		113.9138	481.3343	107.1911
11454	81.5152	744.0142	80.0984	594.7047	97.8738
	01.0102	295.1553	62.6632	209.1293	63.0907

menoint/e	Core Tox Markers Timepoint(s): 6, 48, 192 hrs							
LGC ID	): 6, 48, 192 LDA Score	hrs Mean Tox	ICD Tour					
25737	81.4911				SD Nontox			
16955	81.3829				16.09			
25495	81.3588				172.13			
20554	81.3468				34.05			
9905		30.1092	19.3862		36.72			
18468	81.2665	3.2448		42.2181	22.76			
4362	81.2665	57.1878	30.4622	95.0510	27.89			
17561	81.0981	31.5221	34.1067	35.6249	20.78			
25369	81.0219	181.7411	42.6801	286.7749	138.06			
20450	81.0219	18.4957	4.2567	26.8936	11.11			
16241	80.9818	46.5020	15.8107	72.8100	22.30			
919	80.9818	29.5792	3.7244	39.2193	9.57			
22583	80.9176	-8.1594	16.5029	28.3589	38.35			
200	80.8254	17.6804	3.1824	23.9761	5.78			
20225	80.8254	55.7341	11.1492	79.2127	22.57			
	80.7732	32.5332	10.4836	96.7807	57.48			
1108	80.7331	16.5236	7.6479	33.0522	11.91			
14980	80.7211	30.2779	12.3506	13.1152	14.75			
1005	80.7211	48.6211	8.6610	32.9766	20.18			
25676	80.6810	75.3428	70.7945	167.8154	66.12			
23058	80.6569	216.2758	48.4577	282.9896	72.70			
619	80.5126	28.8201	3.2076	36.6183	8.67			
381	80.4083	17.2289	7.4306	29.1982	10.67			
20779	80.3160	165.3218	17.5305	124.0075	27.840			
15485	80.2759	30.7244	11.8598	14.1573	10.24			
1948	80.2639	135.8238	30.4102	82.4756	43.20			
21069	80.2519	35.4449	5.3390	49.5922	14.214			
17502	80.2238	285.0915	63.2148	193.0939	56.403			
15174	80.1837	257.3659	99.4323	167.1174	50.446			
20998	80.1315	524.4325	181.7060	279.3474	80.870			
20536	80.1195	38.3231	31.6941	11.8192	22.370			
17972	80.1075	27.8115	11.5342	42.8828	11.808			
18895	80.0032	114.9495	22.6815	163.3734	34.799			
19949	79.9751	131.3377	28.7340	82.5089	20.937			
17086	79.9390	157.1793	28.2946	209.2537	48.693			
20246	79.9230	4.4057	29.0201	46.5865	21.632			
21657	79.8709	1487.1038	441.9326	948.9767				
912	79.8709	514.3985	115.6418	380.2598	218.129			
17174	79.8187	88.9931	34.3390	44.8814	63.122			
25496	79.7425	201.9165	22.2101	157.5616	24.087			
22150	79.6503	224.3901	48.0786	151.1148	37.482			
25659	79.6142	38.9102	12.7519	90.1269	44.511			
20021	79.5981	21.5031	62.2867	-68.4464	61.218			
4412	79.5861	505.8172	57.5353	391.7156	58.723			
20980	79.5741	34.7882	6.1143	49.3264	81.310			
18032	79.5219	44.1663	19.4651	88.9932	15.311			
15142	79.4417	29.8871	10.2390	14.9828	44.565			
18655	79.4016	48.4742	105.6019		11.759			
8269	79.3134	15.1508	3.8355	156.9252	61.134			
15408	79.3014	201.3526	31.1048	21.8943	9.498			
19928	95.5162	925.7691	133.5806	267.5795 455.9207	79.736			
			เบบ.บดเกต	400 9707	201.360			

ABLE 5M: Cyclophosphamide Atty. Ref. No. 44921-5090-01-WO/210548 Atty. Ref. No. 44921-5090-01-WO/210548 Atty. Ref. No. 44921-5090-01-WO/210548 Atty. Ref. No. 44921-5090-01-WO/210548 Atty. Ref. No. 44921-5090-01-WO/210548							
LGC ID	LDA Score	Mean Tox.	SD Tox	Mean Nontox	SD Nontox		
2782	89.6767		18.5820		44.473		
11563			52.2880	116.1155	54.826		
23545				3900.7723			
5553	88.6861	24.6978	17.7864	86.3451			
5969	87.8118	600.5945		426.2666			
461	87.4870	59.9835	10.9837	99.8830			
7715	87.3827	19.2980	5.1869	33.8221	11.918		
9286	87.3306	222.8223	32.2374	310.6062	67.979		
22771	87.2904	559.0163	58.8088	385.8688	93.012		
2559	87.1220	284.6615	53.9835	411.3248	89.197		
19283	87.0699	265.8252	85.8404	429.5856	125.703		
15786	86.8733	156.4094	30.5506	89.4438	41.803		
19093	86.2878	83.5065	38.2466	188.3403	83.902		
5378	86.1835	320.8532	19.9846	373.9869	86.189		
12805	86.0792	77.2402	22.4623	11.6043	53.334		
7970	85.9349	104.6198	20.6103	152.3275	31.056		
4151	85.9228	391.9504	84.6875	603.8739	163.244		
11368	85.7383	60.7732	29.7627	12.0356	24.996		
23840	85.6862	89.0182	59.5736	-30.0771	58.939		
17261	85.6220	766.4824	84.1296	575.6093	138.960		
17796	85.5057	76.7958	16.8909	147.3081	60.387		
3094	85.4135	39.5858	11.4552	87.0693	51.025		
18854	85.2972	164.8416	20.7067	191.7377	51.630		
19145	85.2691	475.8288	65.8220	361.1610	60.983		
13511	85.1528	210.4325	25.4688	155.3516	35.917		
2211	85.0485	-13.4862	33.9645	51.7761	39.448		
5111	84.9844	240.8116	43.9451	365.5485	128.540		
11337	84.8801	41.2845	12.0828	65.7655	19.952		
17089	84.8400	1402.3132	189.5788	1086.3912	401.228		
16543	84.7999	53.5725	22.0423	97.1162	25.052		
5740	84.7237	44.1492	12.5690	74.0108	26.538		
23337	84.7076	508.7272	176.7436	279.0357	100.273		
3191	84.6836	229.4547	29.9839	161.5617	44.621		
23464	84.6435	259.7548	64.2746	161.8276	51.822		
1182	84.6314	69.0456	16.7101	107.3778	26.415		
9876	84.2665	41.0540	22.0838	93.3784	36.461		
12804	84.2143	29.3941	16.9388	62.1187			
17355	84.1622	539.2781	108.7013	762.9939	24.906		
4873	83.9256	727.1948	252.9898	441.5460	169.713		
17492	83.8895	532.6638	131.2774	802.8211	110.556 236.169		
15084	83.7571	67.0725	57.5538	197.8258	77.318		
22438	83.7451	-10.9127	12.3748	23.1043	29.072		
4626	83.6007	70.5967	26.6423	27.4654			
14337	83.5365	236.3598	30.3950	307.7315	26.160 50.745		
19257	83.5085	21.1983	35.8030	-27.3921	50.745		
8627	83.4323	19.7490	10.6688	39.2932	31.394 14.342		
4975	83.3280	66.2334	15.4385	105.7459			
6458	83.2758	13.9457	5.6771	34.2500	29.507		
18337	83.2758	423.4050	86.0876		21.662		
				592.1076	120.756		
11268	83.2117	103.1452	22.8648	146.3976	40.974		

Core Tox M	Cyclophosp arkers ): 6, 48, 192	Atty.	Ref. No. 44921-509	0-01-WO/2105485	
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
22911	83.1595		27.8182	171.0561	61.5415
7044	83.1435	1676.3148	416.2079	1293.0095	
3319	83.0793	14.5687	17.0282	35.4199	
12356	83.0152	57.0170	13.5032	99.2891	36.0694
7961	83.0152	21.9158	13.8782	46.4652	
18680	83.0152	117.5713	17,4993	164.6098	
18610	82.9630	469.9288	62,6292	375.7056	
15924	82.9229	40.8472	37.0034	98.2426	0 .0
6658	82.9109	93.6829		134.7486	31.5014
4917	82.9109	14.4837	15.2375	61.1111	36.2076

GLGC ID LDA Score   Mean Tox   SD Tox   Mean Nontox   SD Nontox   21666   99.2776   26.5160   0.5537   6.1908   11.8188   23651   99.1744   1189.0270   603.8436   41.0596   145.0774   7486   99.1744   38.6977   0.5324   87.5030   51.1809   18128   99.1228   97.7840   0.8931   136.4916   26.0286   16049   98.8132   62.2973   0.9762   88.2642   88.2297   16416   98.7100   84.5417   18.0022   38.6044   12.6402   12422   98.6068   128.8727   4.6111   79.9457   18.8585   25450   98.5552   71.5753   0.5908   100.0363   33.8216   20589   98.5036   705.7920   156.4907   148.0740   85.6816   24869   98.5036   89.4850   1.5779   155.9979   43.2849   17570   98.4004   219.0427   0.6782   209.9197   61.7961   14970   98.3488   36.4547   1.8231   80.6479   20.5629   11843   98.2456   125.3780   14.4234   73.8868   16.2415   243   98.0908   792.8837   10.8311   621.4805   114.4201   20913   97.8844   80.2733   0.2583   84.1934   19.2986   25249   27.8844   80.273		: EPINEPHE	RINE	Atty. Re	f. 44921-5090-01	-WO/2105485
21666 99.2776 26.5160 0.5537 6.1908 11.8188 23651 99.1744 1189.0270 603.8436 41.0556 145.0774 7486 99.1744 33.6977 0.5324 87.5030 51.1803 18128 99.1228 97.7840 0.8931 136.4916 26.0286 16049 98.8132 62.2973 0.9762 88.2642 88.2297 16416 98.7100 84.5417 18.0022 38.6044 12.6402 12422 98.6068 128.8727 4.6111 79.9457 18.8565 25450 98.5552 77.15753 0.5908 100.0363 33.8216 20589 98.5036 705.7920 156.4907 148.0740 85.6816 24869 98.5036 89.4850 1.5779 155.9979 43.2849 17570 98.4004 219.0427 0.6762 209.9197 61.7961 14970 98.3488 36.4547 1.8231 80.6479 20.5629 11843 98.2456 125.3780 14.4234 73.8868 16.2415 20313 97.8844 106.9910 1.1868 152.4929 40.5650 14034 97.8844 81.8490 0.6821 101.0746 25.2928 15913 97.7812 137.9433 40.1589 32.5121 22.2242 23219 97.7812 0.4467 1.5517 21.5528 23.5072 23219 97.7812 0.4467 1.5517 21.5528 23.5072 23219 97.7812 0.4467 1.5517 21.5528 23.5072 23219 97.7812 0.4467 1.5517 21.5528 23.5072 23219 97.7812 0.4467 1.5517 21.5528 23.5072 23219 97.7812 0.4467 1.5517 21.5528 23.5072 23288 97.5780 44.0570 0.9964 60.2613 30.0527 23488 97.5780 44.0570 0.9964 60.2613 30.0527 23488 97.5780 44.0570 0.9964 60.2613 30.0527 15884 97.5840 18.18507 0.9964 60.2613 30.0527 15884 97.5840 18.3527 0.9964 60.2613 30.0527 15884 97.5840 18.3527 0.9964 60.2613 30.0527 15888 97.5748 2836.0520 13.2871 22.82848 97.5848 97.5849 18.3527 0.9964 60.2613 30.0527 23488 97.5748 2836.0520 13.2871 22828 884 913.5317 15888 97.5748 183.5527 3.06395 68.5704 26.7822 16925 97.7810 40.5750 0.9964 60.2613 30.0527 23488 97.5964 34.2253 0.4176 42.8957 13.0247 15881 97.5748 183.5527 3.05395 63.5704 26.7822 16925 97.7810 40.5070 0.9964 60.2613 30.0527 23488 97.5964 34.2253 0.4176 42.8957 13.0247 15881 97.5748 183.5577 0.9964 60.2613 30.0527 24588 97.5984 183.5976 183.5777 5780 186.641 97.5522 59.7723 5.9776 31.5257 37.7707 1503 97.3684 97.5760 40.0570 0.9964 60.2613 30.0527 24533 97.6960 40.0570 0.9964 60.2613 30.0527 24548 97.5984 97.6869 40.9530 38.6955 97.7591 188.6559 97.7591 188.6559 97.7707 24548 97.5984 97.5984 97.5984 97.5984 97.5984 97.			Moon Tox			; · ·
23651   99.1744   1189.0277   603.8436   41.0596   145.0774   7486   99.1744   38.6977   0.5324   87.5030   51.1808   18128   99.1228   97.7840   0.8931   136.4916   26.0286   16049   98.8132   62.2973   0.9762   88.2642   88.2297   16416   98.7100   84.5417   18.0022   38.6044   12.6402   12422   98.6068   128.8727   4.6111   79.9457   18.8565   25450   99.5552   71.5753   0.5908   100.0363   33.8216   24869   98.5036   705.7920   156.4907   148.0740   85.6816   24.869   98.5036   89.4850   1.5779   155.9979   43.2849   17570   98.4468   36.4547   1.8231   80.6479   20.5629   11843   98.2456   125.3780   14.4234   73.8868   16.2415   243   98.0908   792.8837   10.8311   621.4805   114.4201   20913   97.8844   106.9910   1.1868   152.4929   40.5650   15913   97.8844   81.8490   0.6821   101.0746   26.2928   15913   97.7812   37.9433   40.1589   32.5121   22.2242   16925   97.7812   64.23187   46.1746   975.4178   177.5760   23219   97.7812   0.4077   0.2911   21.6317   7.7240   15629   97.8760   44.0570   0.9964   60.2613   30.0527   23488   97.5780   44.0570   0.9964   60.2613   30.0527   23488   97.5780   44.0570   0.9964   60.2613   30.0527   23488   97.5780   44.0570   0.9964   60.2613   30.0527   23488   97.5780   44.0570   0.9964   60.2613   30.0527   15839   97.8760   44.0570   0.9964   60.2613   30.0527   23488   97.5780   44.0570   0.9964   60.2613   30.0527   23488   97.5780   44.0570   0.9964   60.2613   30.0527   23488   97.5780   44.0570   0.9964   60.2613   30.0527   23488   97.5780   24.0530   33.8203   94.5369   88.4213   15903   97.8760   44.0570   0.9964   60.2613   30.0527   23488   97.5780   24.0530   33.8203   94.5369   88.4213   15903   97.8760   44.0570   0.9964   60.2613   30.0527   23488   97.5780   235.4777   235.4884   97.5232   59.7723   5.6778   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707   31.5257   37.7707						
T486						
18128						
16049   98.8132   62.2973   0.9762   88.2842   88.2297   16416   98.7100   84.5417   18.0022   38.6044   12.6402   12422   98.6068   128.8727   4.6111   79.9457   18.8585   25450   98.5552   71.5753   0.5908   100.0363   33.8216   28.899   98.5036   705.7920   156.4907   148.0740   85.6816   24869   98.5036   89.4850   1.5779   155.9979   43.2849   14970   98.4040   219.0427   0.6782   209.9197   61.7961   14970   98.4048   219.0427   0.6782   209.9197   61.7961   11843   98.2456   125.3780   14.4234   73.8868   62.4416   243   98.0908   792.8837   10.8311   621.4805   114.4201   14034   97.8844   106.9910   1.1868   152.4929   40.5650   140.344   169.910   1.1868   152.4929   40.5650   25249   97.8844   81.8490   0.6821   101.0746   26.2928   15913   97.7812   137.9433   40.1589   32.5121   22.2242   16925   97.7812   642.3187   46.1746   975.4176   177.5760   23219   97.6780   44.0570   0.9964   60.2613   30.0527   23488   97.5288   44.0570   0.9964   60.2613   30.0247   16883   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   13.2871   282.88884   97.5748   283.0520   33.969   65.5704   26.7822   34.5369   34.5						
16416   98.7100   84.5417   18.0022   38.6044   12.6402     12422   98.6068   128.8727   4.6111   79.9457   18.8585     25450   98.5552   71.5753   0.5908   100.0363   33.8216     20589   98.5036   705.7920   156.4907   148.0740   85.681     24869   98.5036   89.4850   1.5779   155.9979   43.2849     17570   98.4004   219.0427   0.6782   209.9197   61.7961     14970   98.3488   36.4547   1.8231   30.6479   20.5629     14980   98.2456   125.3780   14.4234   73.8868   16.2415     243   98.0908   792.8837   10.8311   621.4805   11.4805     243   98.0908   792.8837   10.8311   621.4805   11.4920     20913   97.8844   106.9910   1.1868   152.4929   40.5650     14034   97.8844   80.2733   0.2683   84.1934   19.2966     252249   97.8844   81.8490   0.6821   101.0746   26.2928     252249   97.8844   81.8490   0.6821   101.0746   26.2928     15913   97.7812   137.9433   40.1589   32.5121   22.2242     23219   97.7812   642.3187   46.1746   975.4178   177.5760     23219   97.6780   44.0570   0.9964   60.2613   30.0527     23488   97.6264   34.2253   0.4476   42.8957   31.0247     16844   97.5748   2836.0520   13.2871   2828.8884   91.35317     18883   97.5748   163.1527   30.6395   68.5704   26.7822     18881   97.5232   45.3447   6.3140   18.6079   80.4911     11114   97.5232   59.7723   5.9778   31.5257   37.7701     15003   97.4200   250.3110   33.9669   157.8583   23.8601     15003   97.4200   250.3110   33.9669   157.8583   23.8601     15004   97.3684   93.7643   34.923   625.9727   104.5680     14109   97.3684   737.1813   3.4232   625.9727   104.5680     2413   97.3684   737.1813   3.4232   625.9727   104.5680     15004   97.3684   737.1813   3.4232   625.9727   104.5680     15004   97.3684   737.1813   3.4232   625.9727   104.5680     15004   97.3684   737.1813   3.4232   625.9727   104.5680     15004   97.3684   737.1813   3.4232   625.9727   104.5680     15004   97.3684   737.1813   3.4232   625.9727   104.5680     15004   97.3684   100.15317   187.6777   538.064   143.4631     15004   97.3684   100.15317   1						26.0286
12422   98.6068   128.8727   4.61111   79.9457   18.8585   25450   98.5552   71.5753   0.5908   100.0363   33.8216   20569   98.5036   705.7920   156.4907   148.0740   85.6816   24869   98.5036   89.4850   1.5779   155.9979   43.2849   17570   98.4004   219.0427   0.6782   209.9197   61.7961   14970   98.3488   36.4547   1.8231   80.6478   20.5629   11843   98.2456   125.3780   14.4234   73.8868   61.2416   243   98.0908   792.8837   10.8311   621.4805   114.4201   20913   97.8844   106.9910   1.1868   152.4929   40.5650   14.034   97.8844   80.2733   0.2583   84.1934   19.2986   25249   97.8844   81.8490   0.6821   101.0746   26.2928   25249   97.7812   137.9433   40.1589   32.5121   22.2242   25245   97.7812   642.3187   46.1746   975.4178   177.5760   23219   97.6780   44.0570   0.9964   60.2613   30.6527   23488   97.6264   34.2253   0.4176   42.8957   13.0247   13883   97.5748   2636.0520   13.2871   282.8884   97.5748   2836.0520   13.2871   282.8884   97.5748   2836.0520   13.2871   282.8884   97.5748   2836.0520   13.2871   282.8884   97.5748   263.6352   13.2871   282.8884   97.5748   63.147   6.3140   18.6079   8.0491   1114   97.5232   45.3147   6.3140   18.6079   8.0491   1503   97.4820   25.3473   5.8073   143.6030   39.74200   215.3473   5.8073   143.6030   39.6125   1503   97.3684   97.5463   37.763   382.0366   45.569   37.7670   45.509   37.76384   27.76384   27.76384   27.7599   37.7670   37.884   27.76388   382.0336   94.5369   38.4213   1503   97.4200   255.3473   5.8073   143.6030   39.6125   37.7707   3684   37.76384   27.76384   27.7599   34.663   31.9264   27.7599   34.6641   34.9253   34.9269   37.884   37.6463   311.9264   207.5999   34.6641   34.9253   34.9253   34.9269   37.76384   37.76384   37.763   38.2256   97.7759   34.6630   31.8745   15.594   34.6630   39.74200   255.3473   5.8073   34.36030   39.6125   37.7707   36.64384   37.7636   36.256   97.7599   34.6643   37.7636   36.256   97.7599   34.6643   37.7636   36.256   97.7599   34.6643   37.7636   36.256   97.7599   34.6643						88.2297
25450 98.5552 71.5753 0.5908 100.0363 33.8216 20589 98.5036 705.7920 156.4907 148.0740 85.6816 24869 98.5036 89.4550 1.5779 155.9979 43.2849 17570 98.4004 219.0427 0.6782 209.9197 61.7961 14970 98.3488 36.4547 1.8231 80.6479 20.5629 11843 98.2456 125.3780 14.4234 73.868 16.2415 243 98.0908 792.8837 10.8311 621.4805 1114.4201 20913 97.8844 106.9910 1.1868 152.4929 40.5650 14034 97.8844 80.2733 0.2583 84.1934 19.2986 25249 97.8844 81.8490 0.6821 101.0746 26.2928 15913 97.7812 137.9433 40.1589 32.5121 22.2242 16925 97.7812 642.3187 46.1746 975.4178 177.5760 23219 97.6780 44.0570 0.9964 60.2613 30.0527 23488 97.6264 34.2253 0.4176 42.8957 13.0247 16844 97.5748 2836.0520 13.2871 2828.8884 913.5317 16849 97.5748 2836.0520 13.2871 2828.8884 913.5317 18881 97.5232 45.3147 6.3140 18.6079 8.0491 11114 97.5232 59.7723 5.9778 31.5257 37.7707 15003 97.4200 785.0383 382.0336 94.5369 188.4213 15503 97.4200 785.0383 382.0336 94.5369 188.4213 15503 97.3684 153.7763 8.8029 157.8583 23.8601 15503 97.4200 785.0383 382.0336 94.5369 188.4213 15503 97.4200 785.0383 382.0336 94.5369 188.4213 15503 97.4200 250.3110 33.9669 157.8583 23.8601 15503 97.3684 737.1813 3.4232 625.9727 104.5680 2413 97.3684 737.1813 3.4232 625.9727 104.5680 15503 97.3684 163.1527 6.8769 157.8583 23.8601 15009 97.3684 737.1813 3.4232 625.9727 104.5680 15503 97.4200 785.0383 382.0336 94.5369 188.4213 197.5364 73.1813 3.4232 625.9727 104.5680 1375 97.3684 737.1813 3.4232 625.9727 104.5680 1375 97.3684 737.1813 3.4232 625.9727 104.5680 1375 97.3684 737.1813 3.4232 625.9727 104.5680 13974 97.3168 1001.5317 187.6777 538.4064 143.4835 15639 97.3684 737.1813 3.4232 625.9727 104.5680 13974 97.3168 1001.5317 187.6777 538.4064 143.4835 14539 97.3684 737.813 3.4232 625.9727 104.5680 13974 97.3168 1001.5317 187.6777 538.4064 143.4835 14539 97.3168 1001.5317 187.6777 538.4064 143.4835 14539 97.3168 133.9577 65.7596 757.7591 158.9157 15839 97.3168 133.9577 65.7596 757.7591 158.9157 15839 97.104 11.22.2877 163.9331 577.3346 154.8930 15669 97.5688 40.1933 0.6364 30.8397 21.211						12.6402
20589   98.5036   705.7920   156.4907   148.0740   85.6816   24869   98.5036   89.4850   1.5779   155.9979   43.2849   17570   98.4004   219.0427   0.6782   209.9197   61.7961   14970   98.3488   36.4547   1.8231   80.6479   20.5629   11843   98.2456   125.3780   14.4234   73.8868   16.2415   20913   97.8844   106.9910   1.1868   152.4929   40.5650   140.034   97.8844   80.2733   0.2583   84.1934   19.2966   159.139   77.812   137.9433   40.1589   32.5121   22.2424   97.8844   81.8490   0.6821   101.0746   26.2928   15913   97.7812   137.9433   40.1589   32.5121   22.2422   23219   97.612   0.4667   1.3517   21.5528   23.5072   23219   97.612   0.4467   1.3517   21.5528   23.5072   23248   97.6780   14.1007   0.2911   216.317   7.7240   15629   97.6780   44.0570   0.9964   60.2613   30.0527   23488   97.6264   34.2253   0.4176   42.8957   13.0247   18883   97.5748   163.1527   30.6395   68.5704   26.7822   18881   97.5232   45.3147   6.3140   18.6079   8.0491   1114   97.5232   45.3147   6.3140   18.6079   8.0491   1114   97.5232   45.3147   6.3140   18.6079   8.0491   15003   97.4200   785.0383   382.0336   94.5369   184.4213   1808   97.4200   250.3110   33.9669   157.8583   23.8601   15002   97.3684   937.6463   311.9264   207.5909   84.6641   175.509   97.3684   97.5763   8.2227   22.7124   94.6434   207.5909   184.6641   17530   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   153.7763   8.8256   95.0549   23.9660   15002   97.3684   937.6463   311.9264   207.5909   184.6641   17530   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   153.7763   8.8256   95.0549   23.9660   13.974   97.3684   97.7662   12.7623   22.7744						18.8585
24869         98.5036         89.4650         1.5779         155.9979         43.2849           17570         98.4004         219.0427         0.6782         209.9197         61.7961           14970         98.3488         36.4547         1.8231         80.6479         20.5629           11843         98.2456         125.3780         14.4234         73.8868         162.415           243         98.0908         792.8837         10.8311         621.4805         114.4201           20913         97.8844         106.9910         1.1868         152.4929         40.5650           14034         97.8844         80.2733         0.2583         84.1934         19.2986           25249         97.8844         81.8490         0.6821         101.0746         26.2928           15913         97.812         642.3187         46.1746         975.4178         177.5760           23219         97.7812         642.3187         46.1746         975.4178         177.5760           23319         97.6780         14.1007         0.2911         21.6317         7.7240           23488         97.6264         34.2253         0.4176         42.8957         13.0247           18881						33.8216
17570						85.6816
14970						43.2849
11843 98.2456 125.3780 14.4234 73.8868 16.2415 243 98.0908 792.8837 10.8311 621.4805 114.4201 20913 97.8844 106.9910 1.1868 152.4929 40.5650 14034 97.8844 80.2733 0.2563 84.1934 19.2866 25249 97.8844 81.8490 0.6821 101.0746 26.2928 15913 97.7812 137.9433 40.1589 32.5121 22.2242 16925 97.7812 642.3187 46.1746 975.4178 177.5760 23219 97.7812 0.1467 1.3517 21.5528 23.5072 20318 97.6780 44.0570 0.9964 60.2613 30.0527 23488 97.6264 34.2253 0.4176 42.8957 13.0247 16844 97.5748 2836.0520 13.2871 2828.8884 913.5317 18883 97.5748 163.1527 30.6395 68.5704 26.7822 18881 97.5232 45.3147 6.3140 18.6079 8.0491 11114 97.5232 45.3147 6.3140 18.6079 8.0491 11114 97.5232 45.3147 6.3140 18.6079 8.0491 11114 97.5232 45.3147 6.3140 18.6079 8.0491 11114 97.5232 45.3147 6.3140 18.6079 8.0491 11114 97.5232 45.3147 6.3140 18.6079 8.0491 15003 97.4200 785.0383 382.0336 94.5369 188.4213 15003 97.4200 250.3110 33.9669 157.8583 23.8661 17530 97.3684 937.6463 311.9264 207.5909 188.4213 15002 97.3684 937.6463 311.9264 207.5909 184.6661 17530 97.3684 737.1813 3.4232 625.9727 104.5680 137.7 130.7						61.7961
243         98.0908         792.8837         10.8311         621.4805         114.4201           20913         97.8844         106.9910         1.1868         152.4929         40.5650           14034         97.8844         80.2733         0.2563         84.1934         19.2986           25249         97.8844         81.8490         0.6821         101.0746         26.2928           15913         97.7812         137.9433         40.1589         32.5121         22.2242           16925         97.7812         0.467         1.3517         21.5528         23.5072           23219         97.7812         0.467         1.3517         21.5528         23.5072           23318         97.6780         14.007         0.2911         21.6317         7.7240           15629         97.6780         44.0570         0.9964         60.2613         30.527           23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         283.60520         13.2871         2828.8884         913.517           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18841         9						20.5629
20913         97.8844         106.9910         1.1868         152.4929         40.5650           14034         97.8844         80.2733         0.2583         84.1934         19.2986           25249         97.8844         81.8490         0.6821         101.0746         26.2928           15913         97.7812         137.9433         40.1589         32.5121         22.2242           16925         97.7812         642.3187         46.1746         975.4178         177.5760           23219         97.6780         14.1007         0.2911         21.5528         23.5072           20318         97.6780         14.1007         0.2911         21.6317         7.7240           15629         97.6780         44.0570         0.9964         60.2613         30.0527           23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18883         97.5738         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           15003						16.2415
14034         97.8844         80.2733         0.2583         84.1934         40.5650           25249         97.8844         81.8490         0.6821         101.0746         26.2928           15913         97.7812         137.9433         40.1589         32.5121         22.2242           16925         97.7812         642.3187         46.1746         975.4178         177.5760           23219         97.6780         14.1007         0.2911         21.6317         7.7240           20318         97.6780         14.1007         0.2911         21.6317         7.7240           15629         97.6780         44.0570         0.9964         60.2613         30.0527           23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003						114.4201
25249         97.8844         81.8490         0.6821         101.0746         26.2928           15913         97.7812         137.9433         40.1589         32.5121         22.2242           16925         97.7812         642.3187         46.1746         975.4178         177.5760           23219         97.7812         0.1467         1.3517         21.5528         23.5072           20318         97.6780         14.1007         0.2911         21.6317         7.7240           15629         97.6780         14.0570         0.9964         60.2613         30.0527           23488         97.6786         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         215.3473         5.8073         143.6030         39.6125           18108						40.5650
15913         97.7812         137.9433         40.1589         32.5121         22.2242           16925         97.7812         642.3187         46.1746         975.4178         177.5760           23219         97.7812         0.1467         1.3517         21.5528         23.5072           23318         97.6780         14.1007         0.2911         21.6317         7.7240           15629         97.6780         44.0570         0.9964         60.2613         30.0527           23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         215.3473         5.8073         143.6030         39.6125           18108					84.1934	19.2986
16925         97.7812         642.3187         46.1746         975.4178         177.5760           23219         97.7812         0.1467         1.3517         21.5528         23.5072           20318         97.6780         14.1007         0.2911         21.6317         7.7240           15629         97.6780         44.0570         0.9964         60.2613         30.0527           23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.884         913.5317           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         215.3473         5.8073         143.6030         39.6125           18108					101.0746	26.2928
23219         97.7812         0.1467         1.3517         21.5528         23.5072           20318         97.6780         14.1007         0.2911         21.6317         7.7240           15629         97.6780         44.0570         0.9964         60.2613         30.0527           23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         757.750         8.8256         95.0549         23.6960           2413						22.2242
20318         97.6780         14.1007         0.2911         21.6317         7.7240           15629         97.6780         44.0570         0.9964         60.2613         30.0527           23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18881         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         225.3473         5.8073         143.6030         39.6125           18108         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413					975.4178	177.5760
15629         97.6780         44.0570         0.9964         60.2613         30.0527           23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         215.3473         5.8073         143.6030         39.6125           18108         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375 <td></td> <td></td> <td></td> <td></td> <td>21.5528</td> <td>23.5072</td>					21.5528	23.5072
23488         97.6264         34.2253         0.4176         42.8957         13.0247           16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0369         94.5369         188.4213           15503         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         87.1750         0.8159         105.0913         34.0323           1375         97.3684         87.1750         0.8159         105.0913         34.0323           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215					21.6317	7.7240
16844         97.5748         2836.0520         13.2871         2828.8884         913.5317           18883         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         215.3473         5.8073         143.6030         39.6125           18108         97.4200         2250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974 <td></td> <td></td> <td></td> <td></td> <td></td> <td>30.0527</td>						30.0527
18883         97.5748         2836.0520         13.2871         2828.8884         913.5317           18881         97.5748         163.1527         30.6395         68.5704         26.7822           11114         97.5232         45.3147         6.3140         18.6079         8.0491           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         215.3473         5.8073         143.6030         39.6125           18108         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           24413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         101.5317         187.6777         538.4064         143.4835 <t< td=""><td></td><td></td><td></td><td></td><td>42.8957</td><td>13.0247</td></t<>					42.8957	13.0247
18881         97.5748         163.1527         30.6395         68.5704         26.7822           18881         97.5232         45.3147         6.3140         18.6079         8.0491           11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215					2828.8884	
11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         215.3473         5.8073         143.6030         39.6125           18108         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2					68.5704	
11114         97.5232         59.7723         5.9778         31.5257         37.7707           15003         97.4200         785.0383         382.0336         94.5369         188.4213           15503         97.4200         215.3473         5.8073         143.6030         39.6125           18108         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         1133.9577         65.7596         757.7591         158.9157 <td< td=""><td></td><td></td><td></td><td></td><td>18.6079</td><td>8.0491</td></td<>					18.6079	8.0491
15503         97.4200         215.3473         5.8073         143.6030         39.6125           18108         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         18133.9577         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221					31.5257	37.7707
18108         97.4200         215.3473         5.8073         143.6030         39.6125           18108         97.4200         250.3110         33.9669         157.8583         23.8601           15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221 <t< td=""><td></td><td></td><td></td><td></td><td>94.5369</td><td>188.4213</td></t<>					94.5369	188.4213
15002         97.3684         937.6463         311.9264         207.5909         184.6641           17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.346         154.8930					143.6030	
17530         97.3684         153.7763         8.8256         95.0549         23.6960           2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           15682						23.8601
2413         97.3684         737.1813         3.4232         625.9727         104.5680           1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         123.1260         12.9143         212.0214         51.9488           15					207.5909	184.6641
2413         97,3684         737,1813         3.4232         625,9727         104,5680           1375         97,3684         87,1750         0.8159         105,0913         34,0323           786         97,3684         20,8183         0.4460         31,8745         11,5904           13974         97,3168         1001,5317         187,6777         538,4064         143,4835           15135         97,3168         1805,3227         222,7124         994,6434         216,5505           16215         97,3168         381,4167         68,5701         212,8355         44,1031           2109         97,3168         1133,9577         65,7596         757,7591         158,9157           24533         97,2652         121,7623         23,9496         272,2374         84,4221           16654         97,2136         22,0607         9,5395         6,3900         7,7609           13646         97,1620         1122,2877         163,9331         577,3346         154,8930           15829         97,1104         11,2407         0,4962         51,0544         73,5249           25629         97,1104         61,8770         0,9283         86,5926         34,0593           1523<					95.0549	
1375         97.3684         87.1750         0.8159         105.0913         34.0323           786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682				3.4232	625.9727	
786         97.3684         20.8183         0.4460         31.8745         11.5904           13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           2486					105.0913	
13974         97.3168         1001.5317         187.6777         538.4064         143.4835           15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         40.1933         0.6384         30.8397         21.2116           13					31.8745	
15135         97.3168         1805.3227         222.7124         994.6434         216.5505           16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         40.1933         0.6384         30.8397         21.2116           22940 <td></td> <td></td> <td></td> <td>187.6777</td> <td>538.4064</td> <td></td>				187.6777	538.4064	
16215         97.3168         381.4167         68.5701         212.8355         44.1031           2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         84.3060         1.6831         70.4649         20.4728           503					994.6434	216.5505
2109         97.3168         1133.9577         65.7596         757.7591         158.9157           24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034					212.8355	
24533         97.2652         121.7623         23.9496         272.2374         84.4221           16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034           23781         97.0072         0.44047         0.9373         63.6186         17.8034					757.7591	
16654         97.2136         22.0607         9.5395         6.3900         7.7609           13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         247.8743         1.7134         281.5172         59.2644           22940         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034           23781         97.0072         46.9083         0.9373         63.6186         17.8034					272.2374	
13646         97.1620         1122.2877         163.9331         577.3346         154.8930           15829         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         247.8743         1.7134         281.5172         59.2644           22940         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034           23781         97.0072         0.14047         0.9373         63.6186         17.8034					6.3900	
15629         97.1104         11.2407         0.4962         51.0544         73.5249           25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         247.8743         1.7131         281.5172         59.2644           22940         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034           23781         97.0072         0.14047         0.9683         0.9373         63.6186         17.8034					577.3346	
25629         97.1104         61.8770         0.9283         86.5926         34.0593           1523         97.1104         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         247.8743         1.7131         281.5172         59.2644           22940         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034           23781         97.0072         0.14.017         0.14.017         0.14.017         0.14.017         0.14.017					51.0544	
1523         97.1704         123.1260         12.9143         212.0214         51.9488           15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         247.8743         1.7131         281.5172         59.2644           22940         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034           23781         97.0072         0.0472         0.0472         0.0503         0.0503         0.0503         0.0503					86.5926	
15682         97.0588         76.4617         1.9705         118.7850         33.9263           24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         247 8743         1 7131         281.5172         59.2644           22940         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034           23781         97.0072         0.14047         0.5534         0.5634         0.6364         0.6364						
24868         97.0588         18.4540         0.4151         26.0513         12.4125           20127         97.0588         40.1933         0.6384         30.8397         21.2116           13369         97.0588         247.8743         1.7131         281.5172         59.2644           22940         97.0588         84.3060         1.6831         70.4649         20.4728           503         97.0072         46.9083         0.9373         63.6186         17.8034           23781         97.0072         0.14047         0.5636         17.8034					118.7850	
20127     97.0588     40.1933     0.6384     30.8397     21.2116       13369     97.0588     247.8743     1.7131     281.5172     59.2644       22940     97.0588     84.3060     1.6831     70.4649     20.4728       503     97.0072     46.9083     0.9373     63.6186     17.8034       23781     97.0072     91.4047     0.95373     63.6186     17.8034				0.4151	26.0513	
13369     97.0588     247 8743     1 7131     281.5172     59.2644       22940     97.0588     84.3060     1.6831     70.4649     20.4728       503     97.0072     46.9083     0.9373     63.6186     17.8034       23781     97.0072     01.4047     0.9373     63.6186     17.8034					30.8397	
22940     97.0588     84.3060     1.6831     70.4649     20.4728       503     97.0072     46.9083     0.9373     63.6186     17.8034       23781     97.0072     01.4047     07.0072     01.4047						
503 97.0072 46.9083 0.9373 63.6186 17.8034 23781 97.0072 01.4047 07.0073						
23/81 97 0072 04 4047 05 0045						
	23/81	97.0072	91.4017	25.3615		

-GC ID II	DA Score	Mean Tox	SD Tox	Mean Nontox	en Marie
22321	96.9556	507.3317	93.8041		SD Nontox
15446	96.9556	404.0587	6.9877	173.3048	
17215	96.9040	83.5970	10.4867	304.1873	73.11
18798	96.8524	107.5180	1.3541	168.0604	43.61
18572	96.8524	908.0947	3.9575	138.4193	28.29
21975	96.8524	257.9910	7.7455	1003.6540	145.84
20032	96.8008	17.5237	1.7078	181.2767	79.84
25899	96.7492	15.5163	0.2316	43.4604	15.22
23731	96.7492	263.6543	18.5718	20.5485	7.18
619	96.7492	22.4083	1.7778	159.9061	45.06
20770	96.6976	156.8697	23.4808	36.5577	8.64
1801	96.6976	120.4320	15.6344	56.2296	41.23
24536	96.6976	1355.7977	41.0844	76.8255	18.71
10015	96.6460	420.5977	68.7205	998.6555	188.85
25359	96.5944	33.1293	0.4272	217.8729	63.78
15253	96.5944	237.1250	24.9522	43.7954	14.75
11849	96.5944	1458.8320	107.8285	108.3637	47.02
12400	96.5428	48.3297	12.2020	940.8786	195.54
16552	96.4912	92.8863	24.4873	24.2917	8.70
18357	96.4912	323.6223	3.3133	38.9750	18.77
15513	96.4912	166.9317	2.7130	319.9372	82.78
18054	96.4396	83.6250	2.1335	189.9391	42.31
7050	96.4396	67.4593	1.1035	126.2777	31.62
22675	96.3880	87.7107		60.3158	24.30
24814	96.3880	125.6697	18.4663 30.0655	30.8168	20.88
20518	96.3364	175.7517	3.1089	71.9543	16.45
13151	96.3364	3338.0793	190.6440	226.4270	41.254
25816	96.2848	17.6030	0.4452	2187.6161	569.219
22555	96.2332	29.4340	3.0467	25.6224	8.593
5622	96.2332	406.5067	100.2078	12.0415	8.103
16218	96.2332	1127.6243	21.3959	206.3462	60.927
22552	96.1816	715.1360	22.1595	845.7607	365.879
4327	96.1816	157.7943	47.5454	452.2379	173.437
6100	96.1816	3273.6163	299.3398	91.5411	27.797
11454	96.1816	286.6350	5.8844	2108.3253	503.604
25529	96.1300	38.6000	0.7893	210.0435	63.779
2853	96.0784	150.4390	47.4404	38.3339	74.349
343	96.0784	58.3073	4.3074	80.3220	24.731
1478	96.0268	23.1500	0.6358	53.2117	43.878
18148	96.0268	59.9527	2.7085	37.8936	24.943
487	95.9752	28.8640	0.7488	98.7423	29.386
1540	95.9752	50.0800	14.4963	41.7508	11.985
492	95.9236	118.3757	2.8412	16.6814	13.456
25547	95.9236	191.8723	8.0536	205.1486	142.362
12118	95.9236	1192.9273	298.6520	356.1624	129.216
15185	95.9236	1429.2477	152.1055	544.6224	298.797
1168	95.9236	21.1347	3.0824	931.2553	186.785
19661	95.8720	6.7690		6.1562	6.621
3527	99.8452	12.9287	1.0521	28.3817	15.590
3931	99.4324	107.6857	0.0487	24.7505	21.011
7036	99.2776	101.0093	0.2150	127.5319	30.512
12324	99.1228	35.7033	0.1155	113.8784	21.482
<del></del>		00.7000	6.6789	-35.6344	38.662

TABLE 5N: EPINEPHRINE Atty. Ref. 44921-5090-01-WO/2						
	LDA Score		SD Tox	Mean Nontox	SD Nonto	
13717			0.9743	112.0620		
21509	98.9164		27.5886			
24135	98.9164	380.8940	1.7808	259.5384		
11644	98.8648		20.1340	224.8430		
22026	98.8132	3518.2023	8.7712	3305.1771	82.15	
11166	98.7616	228.4097	13.3451	124.5399	1100.94	
3211	98.7100	136.1203	47.1696		35.41	
4049	98.6584	757.4380	272.8084	6.0020	17.23	
4048	98.6584	331.6660	154.6004	42.0070	124.28	
24270	98.5552	238.9863	2.3146	18.3030	75.15	
22592	98.5552	836.2727	287.0068	170.0291	58.40	
23326	98.5036	111.8597	0.4384	201.6477	133.26	
1506	98.4520	336.9553	11.6236	126.6552	27.45	
3165	98.4004	33.5920	0.3715	239.0523	37.04	
17106	98.2972	49.6850	0.6158	30.7942	25.05	
23435	98.2972	27.0300	1.9148	75.5109	26.20	
13929	98.2456	331.9700		-34.1479	49.13	
10970	98.2456	42.4007	89.3004	110.4635	47.96	
21771	98.2456	1064.0957	1.1561	84.6732	32.65	
16062	98.2456	1259.5520	7.2340	920.3425	230.42	
4207	98.2456	291.3373	34.4070	841.6006	186.68	
23511	98.1940	124.6603	74.6083	122.4612	41.640	
13915	98.1424		2.0103	76.6181	30.87	
3832	98.1424	61.3407	0.3722	68.1771	16.957	
13702	97.9876	57.6423	0.5583	78.0201	35.229	
894	97.9876	24.4990	0.7311	49.7110	21.541	
4969	97.9360	409.7137	21.2847	213.4587	79.853	
2765	97.8844	113.4747	56.9545	-18.6405	48.154	
5228	97.8844	165.9460	2.0674	115.4260	33.718	
18581	97.8844	172.1703	63.8689	17.5026	45.083	
2125	97.8328	309.6860	8.9991	224.5213	58.770	
5760	97.8328	458.4750	239.1954	110.1359	89.711	
10310		166.8853	2.3547	125.9282	28.026	
8347	97.8328	468.2403	34.3944	773.8072	151.824	
16971	97.8328 97.7296	125.8373	71.4582	33.1032	24.262	
10096		604.9870	2.2495	625.9080	110.195	
4490	97.7296	45.2850	0.7088	67.9757	27.815	
15004	97.7296	350.7433	99.1027	71.4423	77.370	
11634	97.6780	1513.7483	676.9818	333.7069	264.877	
6606	97.6780 97.6780	63.2070	1.0015	104.1398	33.624	
14945		4957.6607	591.8675	1868.8558	759.088	
19396	97.6780	201.9357	4.8148	312.2025	284.670	
9808	97.6780	77.0060	0.5804	64.5836	22.018	
9546	97.6264	21.9317	0.2473	28.2164	12.746	
21252	97.6264	248.0543	3.4682	348.8435	71.553	
8058	97.6264	21.4473	0.3102	27.0436	17.6819	
	97.6264	502.7917	51.4777	316.4540	55.8210	
4945	97.6264	48.4333	2.8325	114.2217	62.8329	
24089	97.6264	383.9677	11.7182	215.7464	102.1879	
2531	97.5748	232 7287	19 4053	128.3824	43.799	
4475	97.5232	121.5643	1.2526	98.1603	24.626	
6098	97.5232	62.4710	5.0207	104.3365	21.8370	
24040	97.5232	858.5613	317.0292	373.3416	133.6995	

Timepoint	l: EPINEPHF t(s): 24 hrs		Atty. Re	f. 44921-5090-01	I-WO/2105485
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
21166	97.5232	678.6667	202.1629	312.2661	87.1282
1901	97.4716	01.0100	3.4812		
11995		58.4227	0.5425	67.8725	
18198		223.5667	0.9721	230.7480	
9218	3.1.200		0.8715		31.9428
23097	97.4200	133.0247	18.6534	70,5065	23.7675
10053	97.4200	49.2487	0.7590	66.8934	38.0980
18848		16.4617	0.3413	27.1611	11.3058
10028	97.3684	205.4137	3.2177	278.2003	56.9774
21796	97.3684	623.4527	184.6330	267.9207	90.6188

TABLE 50: Epi Timepoint(s): 2	inephrine—Cor 24 hrs	e Tox Markers	Atty.	Ref. 44921-5090	-01-WO/2105485
GLGC ID	LDA Score		SD Tox	Mean Nontox	SD Nontox
21666	99.2776			6.1908	11.8188
23651	99.1744	1189.0270	603.8436	41.0596	145.0774
7486	, 99.1744	38.6977	0.5324	87.5030	51.1809
18128	99.1228	97.7840	0.8931	136.4916	26.0286
16049	98.8132	62.2973	0.9762	88.2642	88.2297
16416	98.7100	84.5417	18.0022	38.6044	12.6402
12422	98.6068	128.8727	4.6111	79.9457	18.8585
25450	98.5552	71.5753	0.5908	100.0363	33.8216
20589	98.5036	705.7920	156.4907	148.0740	85.6816
24869	98.5036	89.4850	1.5779	155.9979	43.2849
17570	98.4004	219.0427	0.6782	209.9197	61.7961
14970	98.3488	36.4547	1.8231	80.6479	20.5629
11843	98.2456	125.3780	14.4234	73.8868	
243	98.0908	792.8837	10.8311	621.4805	16.2415
20913	97.8844	106.9910	1.1868	152.4929	114.4201
14034	97.8844	80.2733	0.2583	84.1934	40.5650
25249	97.8844	81.8490	0.6821	101.0746	19.2986
15913	97.7812	137.9433	40.1589	32.5121	26.2928
16925	97.7812	642.3187	46.1746	975.4178	22.2242
23219	97.7812	0.1467	1.3517	21.5528	177.5760
20318	97.6780	14.1007	.0.2911	21.6317	23.5072
15629	97.6780	44.0570	0.9964	60.2613	7.7240
23488	97.6264	34.2253	0.4176	42.8957	30.0527
16844	97.5748	2836.0520	13.2871	2828.8884	13.0247
18883	97.5748	163.1527	30.6395	68.5704	913.5317
1892	97.5232	2524.4427	258.3548	1211.4688	26.7822
18881	97.5232	45.3147	6.3140		391.7182
11114	97.5232	59.7723	5.9778	18.6079	8.0491
15003	97.4200	785.0383	382.0336	31.5257	37.7707
385	97.4200	-2.5247	4.4773	94.5369	188.4213
15503	97.4200	215.3473	5.8073	45.8836	22.7615
18108	97.4200	250.3110	33.9669	143.6030	39.6125
15002	97.3684	937.6463	311.9264	157.8583	23.8601
17530	97.3684	153.7763		207.5909	184.6641
2413	97.3684	737.1813	8.8256 3.4232	95.0549	23.6960
1375	97.3684	87.1750		625.9727	104.5680
786	97.3684	20.8183	0.8159	105.0913	34.0323
13974	97.3168	1001.5317	0.4460	31.8745	11.5904
15135	97.3168	1805.3227	187.6777	538.4064	143.4835
16215	97.3168	381.4167	222.7124	994.6434	216.5505
2109	97.3168	1133.9577	68.5701	212.8355	44.1031
24533	97.2652		65.7596	757.7591	158.9157
16654	97.2136	121.7623	23.9496	272.2374	84.4221
13646	97.1620	22.0607	9.5395	6.3900	7.7609
15829	97.1104	1122.2877	163.9331	577.3346	154.8930
25629	97.1104	11.2407	0.4962	51.0544	73.5249
1523	97.1104	61.8770	0.9283	86.5926	34.0593
15682	97.0588	123.1260	12.9143	212.0214	51.9488
24868	97.0588	76.4617	1.9705	118.7850	33,9263
20127	97.0588	18.4540	0.4151	26.0513	12,4125
13369	97.0588	40.1933	0.6384	30.8397	21.2116
22940	97.0588	247.8743	1.7131	281.5172	59.2644
	91.0000	84.3060	1.6831	70.4649	20.4728

CID	LDA Score	Mean Toy	SD Tox	184000 11	
503				Mean Nontox	
23781	97.0072			63.6186	17.80
22321	96.9556				16.78
17734	96.9556				95.639
15446				1047.1352	499.36
17215		404.0587		304.1873	73.114
18798	96.8524	83.5970 107.5180		168.0604	43.61
18572	96.8524			138.4193	28.29
21975	96.8524	908.0947		1003.6540	145.84
11531	96.8008	257.9910	7.7455	181.2767	79.84
20032	96.8008	1110.7257	227.5568	408.4068	295.31
10016	96.8008	17.5237	1.7078	43.4604	15.22
25899	96.7492	404.6877	66.9408	201.8223	61.93
23731	96.7492	15.5163	0.2316	20.5485	7.18
619	96.7492	263.6543	18.5718	159.9061	45.06
20770		22.4083	1.7778	36.5577	8.64
1801	96.6976	156.8697	23.4808	56.2296	41.23
24536	96.6976	120.4320	15.6344	76.8255	18.71
10015	96.6976	1355.7977	41.0844	998.6555	188.85
25359	96.6460	420.5977	68.7205	217.8729	63.78
15253	96.5944	33.1293	0.4272	43.7954	14.75
11849	96.5944	237.1250	24.9522	108.3637	47.02
12400	96.5944	1458.8320	107.8285	940.8786	195.540
17736	96.5428	48.3297	12.2020	24.2917	8.700
16552	96.4912	1642.5653	546.3408	621.3711	360.157
18357	96.4912	92.8863	24.4873	38.9750	18.774
16017	96.4912	323.6223	3.3133	319.9372	82.782
15513	96.4912	74.2610	4.5885	117.0576	30.074
11530	96.4912	166.9317	2.7130	189.9391	42.319
18054	96.4396	601.3107	161.2935	210.8034	173.760
	96.4396	83.6250	2.1335	126.2777	31.627
7050	96.4396	67.4593	1.1035	60.3158	24.308
22675	96.3880	87.7107	18.4663	30.8168	20.889
24814	96.3880	125.6697	30.0655	71.9543	16.459
20518	96.3364	175.7517	3.1089	226.4270	41.254
13151	96.3364	3338.0793	190.6440	2187.6161	569.219
25816	96.2848	17.6030	0.4452	25.6224	8.593
22555	96.2332	29.4340	3.0467	12.0415	8.103
5622	96.2332	406.5067	100.2078	206.3462	60.927
16218	96.2332	1127.6243	21.3959	845.7607	365.879
22552	96.1816	715.1360	22.1595	452.2379	173.437
4327	96.1816	157.7943	47.5454	91.5411	27.797
6100	96.1816	3273.6163	299.3398	2108.3253	503.604
11454	96.1816	286.6350	5.8844	210.0435	63.779
25529	96.1300	38.6000	0.7893	38.3339	74.349
2853	96.0784	150.4390	47.4404	80.3220	24.731
343	96.0784	58.3073	4.3074	53.2117	43.878
1478	96.0268	23.1500	0.6358	37.8936	24.943
18148	96.0268	59.9527	2.7085	98.7423	29.386
3527	99.8452	12.9287	0.0487	24.7505	21.011
3931	99.4324	107.6857	0.2150	127.5319	30.512
7036	99.2776	101.0093	0.1155	113.8784	21.4829
12324	99.1228	35.7033	6.6789	-35.6344	38.6620

ID	24 hrs LDA Score	Moon T	10 - E	<u> </u>	
		Mean Tox		Mean Nontox	SD Nontox
13717 21509				112.0620	23.
24135				445.5429	136.
11644				259.5384	91.
22026	98.8648	510.5817	20.1340	224.8430	82.
		3518.2023	8.7712	3305.1771	1100.
11166	98.7616	228.4097	13.3451	124.5399	35.
24209	98.7616	130.9367	14.5426	3.0070	41.
3211	98.7100	136.1203	47.1696	6.0020	17.
4049	98.6584	757.4380	272.8084	42.0070	124.
4048	98.6584	331.6660	154.6004	18.3030	75.
24270	98.5552	238.9863	2.3146	170.0291	58.
22592	98.5552	836.2727	287.0068	201.6477	133.
23326	98.5036	111.8597	0.4384	126.6552	27.
1506	98.4520	336.9553	11.6236	239.0523	37.
3165	98.4004	33.5920	0.3715	30.7942	25.
17106	98.2972	49.6850	0.6158	75.5109	26.
23435	98.2972	27.0300	1.9148	-34.1479	49.
13929	98.2456	331.9700	89.3004	110.4635	47.
10970	98.2456	42.4007	1.1561	84.6732	32.
21771	98.2456	1064.0957	7.2340	920.3425	230.
16062	98.2456	1259.5520	34.4070	841.6006	186.
4207	98.2456	291.3373	74.6083	122.4612	41.
23511	98.1940	124.6603	2.0103	76.6181	30.
13915	98.1424	61.3407	0.3722	68.1771	16.9
3832	98.1424	57.6423	0.5583	78.0201	35.2
13702	97.9876	24.4990	0.7311	49.7110	21.
894	97.9876	409.7137	21.2847	213.4587	
4969	97.9360	113.4747	56.9545	-18.6405	79.8
2765	97.8844	165.9460	2.0674	115.4260	48.
5228	97.8844	172.1703	63.8689	17.5026	33.7
18581	97.8844	309.6860	8.9991	224.5213	45.0
2125	97.8328	458.4750	239.1954	110.1359	58.7
5760	97.8328	166.8853	2.3547	125.9282	89.7
10310	97.8328	468.2403	34.3944	773.8072	28.0
8347	97.8328	125.8373	71.4582	33.1032	151.8
16971	97.7296	604.9870	2.2495	625.9080	24.2
10096	97.7296	45.2850	0.7088	67.9757	110.1
4490	97.7296	350.7433	99.1027	71.4423	27.8
15004	97.6780	1513.7483	676.9818	333.7069	77.3
11634	97.6780	63.2070	1.0015	104.1398	264.8
6606	97.6780	4957.6607	591.8675	1868.8558	33.6
14945	97.6780	201.9357	4.8148	312.2025	759.0
19396	97.6780	77.0060	0.5804	64.5836	284.6
9808	97.6264	21.9317	0.2473	28.2164	22.0
9546	97.6264	248.0543	3.4682		12.7
21252	97.6264	21.4473	0.3102	348.8435	71.5
8058	97.6264	502.7917	51.4777	27.0436	17.6
4945	97.6264	48.4333	2.8325	316.4540	55.8
24089	97.6264	383 9677	11 7182	114.2217	62.8
2531	97.5748	232.7287	19.4053	215.7464	102.1
4475	97.5232	121.5643	1.2526	128.3824	43.7
6098	97.5232	62.4710	5.0207	98.1603 104.3365	24.6

TABLE 50: Ep	ABLE 50: EpinephrineCore Tox Markers Atty. Ref. 44921-5090-01-WO/2105485							
Timepoint(s): 2	24 hrs 🔞	7.0		1.027 0000	*0 14VVC/2 100400			
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox			
24040	97.5232	858.5613	317.0292	373.3416	133.6995			
21166	97.5232	678.6667	202.1629	312.2661	87.1282			
1901	97.4716	51.5103	3.4812	72.1035				
11995	97.4716	58.4227	0.5425	67.8725				
18198	97.4200	223.5667	0.9721	230.7480				
9218	97.4200	47.6807	0.8715	71.3801	31.9428			
23097	97.4200		18.6534	70.5065				
5227	97.4200	284.8487	20.7484	153.0970				
10053	97.4200	49.2487	0.7590	66.8934				
18848	97.3684	16.4617	0.3413	27.1611	11.3058			
10028	97.3684	205.4137	3.2177	278.2003				
21796	97.3684	623.4527	184.6330	267.9207	90.6188			

Timepoint(s	EPINEPHRIN s): 3, 6 hrs	E	Atty. R	ef. 44921-5090-01	I-WO/2105485
GLGC ID		Mean Tox	SD Tox	Mean Nontox	SD Nontox
21682	99.7415	170.2108	17.8746		54.1422
24716	99.3795	83.0638	44.2356		9.6679
2628	99.3795	101.2262	21.4093	9.7733	13.5113
4512	99.0176	100.1628		23.0663	27.6873
1475	98.9659	2131.2934	1187.2397	99.1846	
18349	98.9142	419.5130	34.5782	174.2737	236.0731
4407	98.9142	183,4034	28.3841	76.5220	61.4315
21238	98.8625	110.8422	41.3186	-25.5080	20.5864
22625	98.8625	288.1454	124.1975	64.9472	25.5893
20161	98.7590	283.5106	45.0052		26.9144
16318	98.7590	194.4522	99.2263	35.6024	36.8795
21683	98.7073	187.7900	12.6924	39.8236	20.4925
18259	98.7073	383.5616	293.5490	48.5710	35.0644
23872	98.6556	555.1498		93.0553	39.5025
12978	98.6556	329.5664	216.9557	52.3884	68.5290
10181	98.6556	604.7244	109.3731	77.0005	48.5301
2629	98.6039	164.3506	207.4892	125.0557	110.9162
18059	98.6039		51.0557	20.7590	13.2840
16312	98.5522	259.6754	203.7536	28.0897	34.0609
567		269.9038	57.0820	66.9923	34.2802
23871	98.5522	135.7288	56.5042	11.7060	36.0499
	98.5522	162.5520	44.4375	41.5533	21.0213
23869	98.5522	376.3680	133.3922	41.0667	56.3412
11113	98.5522	74.9128	5.2741	36.0679	19.5003
24431	98.5005	579.7786	203.5851	74.1401	65.8132
357	98.5005	111.4196	22.3553	25.1729	17.2240
18597	98.3454	410.7850	196.9638	93.4415	58.4374
17908	98.3454	247.8356	89.2240	43.3927	31.2296
356	98.3454	229.7986	49.0958	40.7630	43.8095
25730	98.3454	513.9482	88.0797	223.3287	70.4308
13930	98.2937	541.6812	170.7749	109.4264	59.3881
223	98.2937	178.8056	84.6612	12.7804	23.9861
16122	98.2937	201.4534	44.7091	64.5007	26.8626
23868	98.2420	1389.5956	403.1165	212.1732	214.4325
355	98.2420	116.8578	31.5423	9.6020	28.0037
923	98.2420	154.5252	82.8649	16.6897	16.1037
20169	98.2420	277.0936	95.7389	72.8978	72.7922
11483	98.1903	331.7654	63.7991	98.4505	41.2669
21663	98.1386	1165.2894	270.7719	378.5087	180.0980
804	98.1386	189.0236	66.4419	51.8934	27.6155
46	98.1386	313.5256	74.0148	120.9001	39.0253
20193	98.1386	57.2454	16.2227	12.5417	12.8705
5297	98.0869	636.1846	281.5152	204.1140	87.4082
20433	98.0352	184.8048	32.5754	65.0037	
5384	97.9835	384.9230	132.8474	41.3148	33.9370
15829	97.9835	422.2494	148.8760	49.0116	52.1603
15083	97.9835	171.2682	27.3645		67.9183
354	97.9835	645.3834	325.2897		26.4706
15708	97.9835	68.0462	26.7231	161.4268	73.4115
12797	97.9317	101.6880		5.2693	17.7616
352	97.8800	192.5686	13.3643	47.5052	17.5608
23679	97.8283		39.9891	60.2376	41.0027
15301	97.7766	86.3938 572.5163	11.8022	37.7964	14.1923
10001	51.1100	572.5162	219.7328	98.3793	76.7665

GC ID	s): 3, 6 hrs	The state of the s	<u> </u>		1-WO/21054
	LDA Score		SD Tox	Mean Nontox	SD Nontox
21239	97.7766			117.8727	59.56
363	97.7249	100.00 10	36.2308		19.87
21653	97.6732		56.6963	115.9132	
3455	97.6732		41.5154	138.5602	11100
1742	97.6732	118.7334	36.8921	32.6240	42.10
1609	97.6215	1636.9828	249.3978	870.5481	21.38
17765	97.6215	2256.6424	206.1313	1392.1893	286.66
16123	97.6215	356.9620	118.1274	104.5867	281.39
3454	97.6215	159.1384	24.8517	67.3493	44.39
19086	97.5181	189.6412	55.5297	74.7669	29.63
19	97.5181	509.6354	72.6219	322.9745	27.10
15300	97.4664	940.0314	379.0212		72.99
16080	97.4664	103.3676	18.5126	241.4715	130.27
22412	97.4147	213.8002	101.9986	16.6288	40.928
18396	97.4147	142.5440	59.4536	92.0753	29.768
17401	97.3630	1642.7358		42.1700	30.778
3404	97.3630	316.6988	584.4295	603.1921	226.660
15082	97.3630	191.4824	21.2199	210.0892	45.223
4133	97.3113	64.0094	43.5429	48.8199	46.636
16025	97.3113	53.0716	4.7748	103.9881	20.921
11940	97.3113		4.6147	104.1006	29.216
16074	97.3113	48.1170	6.9000	25.1038	8.476
4318	97.1562	115.4958	11.8207	186.5315	30.313
17589	97.0527	20.0936	9.9767	3.5640	4.506
9815		21.7392	1.4012	6.2329	8.912
16081	97.0010	121.5864	6.2765	78.7610	20.011
18713	96.8976	208.6630	38.2141	87.3138	66.789
1581	96.7942	375.9924	80.3421	221.3549	52.520
399	96.6908	487.9414	68.3975	296.6913	60.032
	96.6391	21.2000	5.2149	8.9482	4.913
1844	96.6391	210.7696	6.9139	161.9336	34.834
21723	96.5874	58.5174	2.8000	99.0297	32.496
1745	96.3806	67.6086	16.1516	27.6620	13.501
1061	96.3806	17.0476	4.4648	73.7109	45.160
16026	96.3806	73.2400	12.3368	158.9491	46.887
22499	96.2771	50.3252	8.1201	20.7980	
24219	96.2771	500.8952	77.0303	295.5761	11.980
5758	96.1737	1258.2172	121.1144	728.8533	84.189
21120	96.1220	237.1964	12.0230	152.8194	206.439
25279	96.1220	442.4454	35.8349	292.9163	43.988
17764	95.7601	2977.1100	324.5606	1942.9901	67.199
20625	95.6567	456.8968	51.0519	1082.0410	394.548
19646	95.6567	39.9698	21.4456	149.1969	486.704
15711	95.5533	179.5744	33.3786		60.196
16499	95.5533	-5.5418	21.9029	89.3327	33.102
21147	95.5016	35.6852	3.2769	57.5645	33.515
904	95.4498	32.7976	4.1948	18.0286	11.222
3799	95.3464	649.1842	137.6624	64.3982	18.246
15414	95.3464	-5.7218		381.4697	114.159
19031	99.4312	982.6658	12.5874	23.8691	11.5189
7751	98.9142		120.6744	258.9055	111.5534
23567	98.8108	55.7776	3.6708	26.6190	11.5282
19184	98.7590	227.4204	26.5291	45.3472	63.3799
.0.04	30.7380	147.1298	47.5142	18.3058	24.0398

mepoint(s): 3, 6 hrs  Atty. Ref. 44921-5090-01-WO/2105								
LGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nonto			
12999	98.7073			330.9860				
6054 12979	98.7073			53.3184	92.2			
	98.7073		169.5989	312.8437				
2331	98.6556	2163.9720	213.8867	382.5205	193.9			
18350	98.6556	291.0254	8.7395	140.0944	338.0			
7516	98.6556	889.7998	438.7596	50.3085	60.6			
22667	98.6556	192.7286	17.4709	58.4133	173.9			
19012	98.5522	932.2302	108.1775	455.2176	40.2			
13633	98.5522	1017.1960	159.6258	340.8687	113.5			
14763	98.5005	515.9030	145.4453	24.0301	103.97			
22681	98.5005	719.6722	146.8975	300.2426	99.86			
13634	98.4488	1880.3100	310.7357	819.1229	83.87			
11873	98.4488	547.9730	130.6466		207.26			
6532	98.4488	871.9112	84.2306	147.4777	115.18			
16124	98.4488	689.2324	105.9491	448.6074	126.22			
3808	98.4488	1608.7652	223.2933	229.3567	89.44			
22765	98.3971	141.9492	37.6784	559.1888	207.25			
16053	98.3971	395.9836	63.5918	22.5669	21.47			
16136	98.3971	331.5860	111.5788	117.6825	86.17			
8759	98.3454	459.3384	173.1906	109.1438	39.24			
14117	98.3454	568.3832	116.5057	35.6491	56.06			
21579	98.3454	245.2786		1162.3826	221.75			
5675	98.3454	621.6554	54.3629	95.5227	33.16			
23314	98.2937	1539.4846	119.1463	157.2537	135.26			
17506	98.2937	169.7166	620.7748	80.2665	200.85			
19011	98.2420	1208.2564	50.5107	51.4166	25.81			
8053	98.1903	310.3878	183.0800	601.0513	123.888			
22958	98.1903	445.7316	22.4150	161.7129	45.387			
11088	98.1903	40.7278	55.1817	232.5878	63.309			
15212	98.1386	286.4968	11.0571	113.6213	33.635			
10182	98.1386	376.9936	137.2593	55.7180	36.318			
12969	98.1386	259.9774	167.7702	31.6820	100.464			
19075	98.1386	230.6110	9.3908	157.8627	44.262			
23626	98.1386	226.7950	57.9787	113.1016	25.630			
11021	98.0869	644.2628	99.5140	72.8989	32.682			
8314	98.0869		48.0691	325.7648	108.094			
3817	98.0869	140.9914 311.6976	51.7258	49.2117	24.829			
7471	98.0352		25.8985	180.3736	60.320			
6217	97.9835	398.5200	92.0347	198.9423	49.984			
15051	97.9835	196.6190	114.6867	58.2228	22.130			
19723	97.9317	303.7946	68.2762	119.9003	108.766			
16314	97.9317	293.6122	49.7000	109.3153	54.231			
. 30 1-7	31.8311	295.3764	66.9849	63.9732	47.299			

	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
21682	99.7415	170.2108			
24716	99.3795	83.0638			54.142
2628	99.3795	101.2262			9.667
4512	99.0176	100.1628		23.0663	13.511
1475	98.9659	2131.2934		23.0663	27.687
18349	98.9142	419.5130	34.5782	99.1846	236.073
4407	98.9142	183.4034	28.3841	174.2737	61.431
21238	98.8625	110.8422	41.3186	76.5220	20.586
22625	98.8625	288.1454	124.1975	-25.5080	25.589
20161	98.7590	283.5106	45.0052	64.9472	26.914
16318	98.7590	194.4522	99.2263	35.6024	36.879
21683	98.7073	187.7900	12.6924	39.8236	20.492
18259	98.7073	383.5616	293.5490	48.5710	35.064
23872	98.6556	555.1498		93.0553	39.502
12978	98.6556	329.5664	216.9557	52.3884	68.529
10181	98.6556	604.7244	109.3731	77.0005	48.530
2629	98.6039	164.3506	207.4892	125.0557	110.916
18059	98.6039		51.0557	20.7590	13.284
16312	98.5522	259.6754	203.7536	28.0897	34.060
567	98.5522	269.9038	57.0820	66.9923	34.280
23871	98.5522	135.7288	56.5042	11.7060	36.049
23869	98.5522	162.5520	44.4375	41.5533	21.021
11113	98.5522	376.3680	133.3922	41.0667	56.3412
24431	98.5005	74.9128	5.2741	36.0679	19.500
357		579.7786	203.5851	74.1401	65.8132
21654	98.5005	111.4196	22.3553	25.1729	17.2240
18597	98.3454	551.3256	137.5534	203.2898	71.3742
17908	98.3454	410.7850	196.9638	93.4415	58.4374
356	98.3454	247.8356	89.2240	43.3927	31.2296
25730	98.3454	229.7986	49.0958	40.7630	43.8095
13930	98.3454	513.9482	88.0797	223.3287	70.4308
223	98.2937	541.6812	170.7749	109.4264	59.3881
	98.2937	178.8056	84.6612	12.7804	23.986
16122	98.2937	201.4534	44.7091	64.5007	26.8626
23868	98.2420	1389.5956	403.1165	212.1732	214.4325
355	98.2420	116.8578	31.5423	9.6020	
923	98.2420	154.5252	82.8649	16.6897	28.0037
20169	98.2420	277.0936	95.7389	72.8978	16.1037
11483	98.1903	331.7654	63.7991	98.4505	72.7922
21663	98.1386	1165.2894	270.7719	378.5087	41.2669
804	98.1386	189.0236	66.4419	51.8934	180.0980
46	98.1386	313.5256	74.0148	120.9001	27.6155
20193	98.1386	57.2454	16.2227	12.5417	39.0253
5297	98.0869	636.1846	281.5152	204.1140	12.8705
20433	98.0352	184.8048	32.5754		87.4082
5384	97.9835	384.9230	132.8474	65.0037	33.9370
15829	97.9835	422.2494	148.8760	41.3148	52.1603
353	97.9835	484.9402	257.6271	49.0116	67.9183
15083	97.9835	171.2682		115.1804	63.5617
354	97.9835	645.3834	27.3645	67.0638	26.4706
15708	97.9835	68.0462	325.2897	161.4268	73,4115
12797	97.9317	101.6880	26.7231	5.2693	17.7616
352	97.8800	192.5686	13.3643	47.5052	17.5608

imepoint(s):	3, 6 nrs	, i		i i	990-01-WO/210548
LGC ID	LDA Score	Mean:Tox	SD Tox	Mean Nontox	SD Nontox
23679	97.8283	86.3938		37.7964	14.192
15301	97.7766	572.5162		98.3793	76.766
21239	97.7766	419.1316		117.8727	59.566
363	97.7249	105.5316		44.6670	19.878
17734	97.6732	3246.6368	927.5498	1040.2773	478.849
17736	97.6732	2289.5822	894.5995	615.9135	340.720
21653	97.6732	269.1608	56.6963	115.9132	40.031
3455	97.6732	281.7104	41.5154	138.5602	42.105
1742	97.6732	118.7334	36.8921	32.6240	21.383
1609	97.6215	1636.9828	249.3978	870.5481	286.668
17765	97.6215	2256.6424	206.1313	1392.1893	281.397
16123	97.6215	356.9620	118.1274	104.5867	44.393
3454	97.6215	159.1384	24.8517	67.3493	29.636
20461	97.6215	39.3302	3.5153	86.2453	45.3078
11531	97.5698	1657.1368	674.6719	404.1289	281.164
19086	97.5181	189.6412	55.5297	74.7669	27.109
19	97.5181	509.6354	72.6219	322.9745	72.991
11530	97.4664	1141.9942	494.4777	207.2001	158.962
15300	97.4664	940.0314	379.0212	241.4715	130.271
16080	97.4664	103.3676	18.5126	16.6288	40.9284
22412	97.4147	213.8002	101.9986	92.0753	29.7683
18396	97.4147	142.5440	59.4536	42.1700	30.7788
17401	97.3630	1642.7358	584.4295	603.1921	226.660
3404	97.3630	316.6988	21.2199	210.0892	45.223
15082	97.3630	191.4824	43.5429	48.8199	
4133	97.3113	64.0094	4.7748	103.9881	46.6366 20.9217
16025	97.3113	53.0716	4.6147	104.1006	
11940	97.3113	48.1170	6.9000	25.1038	29.2162
16074	97.3113	115.4958	11.8207	186.5315	8.4766 30.3132
19710	97.2596	132.0752	32.6093	48.2437	
4318	97.1562	20.0936	9.9767	3.5640	22.2772 4.5068
17589	97.0527	21.7392	1.4012	6.2329	
9815	97.0010	121.5864	6.2765	78.7610	8.9129
16081	96.8976	208.6630	38.2141	87.3138	20.0110
18713	96.7942	375.9924	80.3421	221.3549	66.7896
1581	96.6908	487.9414	68.3975	296.6913	52.5204
399	96.6391	21.2000	5.2149	8.9482	60.0325
1844	96.6391	210.7696	6.9139	161.9336	4.9132
21723	96.5874	58.5174	2.8000	99.0297	34.8342
1745	96.3806	67.6086	16.1516	27.6620	32.4967
1061	96.3806	17.0476	4.4648	73.7109	13.5013
16026	96.3806	73.2400	12.3368	158.9491	45.1607
22499	96.2771	50.3252	8.1201	20.7980	46.8871
24219	96.2771	500.8952	77.0303	295.5761	11.9808
5758	96.1737	1258.2172	121.1144	728.8533	84.1890
21120	96.1220	237.1964	12.0230	152.8194	206.4390
25279	96.1220	442.4454	35.8349	292.9163	43.9886
10071	95.9669	534.8884	105.5033	264.8235	67.1991
19031	99.4312	982,6658	120.6744	258.9055	107.4576
7751	98.9142	55.7776	3.6708	26.6190	111.5534
23567	98.8108	227.4204	26.5291	45.3472	11.5282
19184	98.7590	147.1298	47.5142	18.3058	63.3799 24.0398

GC ID :	3, 6 hrs LDA Score	Mean Tox	SD Tox	Mean Nontox	ISD No.
12999	98.7073				SD Nontox
6054	98.7073	654.2018			
12979	98.7073	1116.3096			
2331	98.6556	2163.9720	213.8867		
18350	98.6556	291.0254	8.7395		338.06
7516	98.6556	889.7998	438.7596	. 10.0077	60.60
22667	98.6556	192.7286	17.4709	50.3085	173.95
19012	98.5522	932.2302	108.1775	58.4133	40.21
13633	98.5522	1017.1960			113.51
22605	98.5005	298.9122	159.6258	340.8687	103.97
14763	98.5005	515.9030	86.8134	46.8640	36.53
22681	98.5005	719.6722	145.4453	24.0301	99.86
13634	98.4488	1880.3100	146.8975	300.2426	83.87
11873	98.4488	547.9730	310.7357	819.1229	207.26
6532	98.4488	871.9112	130.6466	147.4777	115.18
16124	98.4488	689.2324	84.2306	448.6074	126.22
3808	98.4488	1608.7652	105.9491	229.3567	89.44
22765	98.3971	141.9492	223.2933	559.1888	207.25
16053	98.3971	395.9836	37.6784	22.5669	21.47
16136	98.3971	331.5860	63.5918	117.6825	86.172
8759	98.3454	459.3384	111.5788	109.1438	39.243
14117	98.3454	568.3832	173.1906	35.6491	56.060
21579	98.3454	245.2786	116.5057	1162.3826	221.756
5675	98.3454	621.6554	54.3629	95.5227	33.167
12695	98.2937	104.4010	119.1463	157.2537	135.264
23314	98.2937	1539.4846	32.7881	1.3002	31.219
17506	98.2937		620.7748	80.2665	200.859
19011	98.2420	169.7166	50.5107	51.4166	25.810
8053	98.1903	1208.2564	183.0800	601.0513	123.888
22958	98.1903	310.3878	22.4150	161.7129	45.387
11088	98.1903	445.7316	55.1817	232.5878	63.309
15212	98.1386	40.7278	11.0571	113.6213	33.635
10182	98.1386	286.4968	137.2593	55.7180	36.318
12969	98.1386	376.9936	167.7702	31.6820	100.464
19075	98.1386	259.9774	9.3908	157.8627	44.262
6585	98.1386	230.6110	57.9787	113.1016	25.630
2459	98.1386	2421.0914	359.2627	736.8839	413.833
23626	98.1386	1898.8080	723.9863	121.3918	267.624
11021	98.0869	226.7950	99.5140	72.8989	32.682
8314	98.0869	644.2628	48.0691	325.7648	108.094
3817	98.0869	140.9914	51.7258	49.2117	24.829
7471	98.0352	311.6976	25.8985	180.3736	60.3209
6217	97.9835	398.5200	92.0347	198.9423	49.9844
15051	97.9835	196.6190	114.6867	58.2228	22.1304
19723	97.9337	303.7946	68.2762	119.9003	108.7666
16314	97.9317	293.6122	49.7000	109.3153	54.2319
• •	01.8011	295.3764	66.9849	63.9732	47.2996

meponice	): 6, 192 hrs		•	ef. 44921-5090-01	: 110/21004
	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
20065	93.6486	64.5336	15.5144	28.3182	
22773	92.3077	284.2659			29.009
23491	90.0208	64.4093		116.5459	
10540	89.9584	79.6845			34.537
2143	88.4615	205.6064	19.3914	22.9667	23.968
3910	87.9418	117.9722	6.1754	261.7126	54.918
15884	87.8274	428.9210		145.6334	35.486
2324	87.7859	100.4435	71.0840	724.7975	186.763
8599	87.2557	161.8975	5.4519	81.7793	29.388
15638	87.1622	563.8050	28.0984	100.2554	36.868
3244	87.1622	194.1251	83.5590	932.5900	306.978
9528	87.0062		7.6588	175.9356	33.848
20092		39.5442	1.7304	38.7435	25.033
20902	86.6944	37.2246	5.1645	34.0494	18.037
2133	86.6424	136.3531	6.7880	158.2420	30.057
	86.5385	46.9168	4.5796	34.4053	13.430
15623	86.3306	245.5920	54.3446	418.3828	140.463
634	86.2578	233.1804	64.6370	95.2150	54.320
23569	86.0707	150.4479	7.7162	126.2006	
17764	86.0603	2515.6902	214.7747	1942.4118	23.962
18654	86.0083	104.5548	44.7109	218.9800	398.290
1016	85.9667	130.3715	17.5267	94.4053	64.688
18031	85.9148	331.9946	28.2218		45.594
23033	85.9148	382.1855	34.8056	387.7143	97.911
18957	85.8524	1133.3488	53.5900	526.8407	135.440
20518	85.8108	184.9967		910.3338	163.599
635	85.3222	173.9367	10.9456	226.6997	41.271
25619	85.2807	737.8122	53.8127	93.8402	42.085
25525	85.2703	185.5478	95.7001	572.0521	115.169
20601	85.1351		54.7659	78.6183	46.6012
20876	85.1247	60.9161	6.8553	83.8053	29.293
25237	85.0312	1477.8560	94.3479	1188.7541	225.8488
25066		36.8579	15.2615	80.7048	36.152
187	84.7713	236.0595	50.3392	163.9011	83.2976
10888	84.7609	138.2698	29.4137	54.9629	47.4598
	84.7609	63.2809	6.7913	52.5103	31.2517
1291	84.7089	349.3815	44.9135	256.0730	55.9576
17936	84.3971	42.1342	7.8386	28.8558	10.6646
16607	84.3555	161.5580	11.0476	140.6459	36.4500
17868	84.3035	91.0739	16.4840	137.3277	
409	84.2516	53.9426	2.9469	62.5564	44.9267
20972	84.1892	685.9562	126.8069	1004.5982	12.5587
17379	84.0333	566.0024	52.1466	437.6768	223.9314
2012	84.0333	51.4565	7.7452		98.7187
1827	83.9397	24.3368	15.2526	73.9695	17.2172
20762	83.8877	73.8346	9.2642	75.2777	47.8439
25445	83.8877	33.1559		91.5686	17.0952
24874	83.8358	36.3819	6.2801	33.1519	27.0709
25569	83.7318	51.7451	4.0736	38.2723	18.4138
25070	83.7214		9.8328	34.5213	17.6905
18061	83.6694	210.4100	28.7273	159.6915	36.5691
16081	83.6590	159.2217	21.0681	115.9734	32.9274
18967		145.6088	47.3785	87.3385	67.1593
20960	83.6071	393.5761	85.9385	203.7180	105.0874
20300	83.5655	691.0195	61.2470	520.7054	116.1343

mehomité	s): 6, 192 hrs	<u>. ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;</u>	•	ef. 44921-5090-01	110/21004
LGC ID		Mean Tox	SD Tox	Mean Nontox	SD Nontox
17765		1741.1042	178.9719	1393.0553	
20959	83.5135	306.9811	36.5119	218.9331	62.07
16219	83.4719	484.5323	119.0956	789.5112	258.34
16099	83.4200	374.8630	21.6957	430.6596	
21239	83.3992	221.4428	46.3566	118.3619	62.59
25618	83.3576	777.8311	87.4808	624.9041	62.86
14542	83.2640	30.6546	6.1426	21.3064	128.56
15875	83.1081	1422.4221	65.2450	1569.9365	17.09
15849	83.0977	497.5558	92.3428	271.6573	300.79
18057	83.0977	25.4141	2.6996	20.2121	141.43
9391	83.0561	2201.7503	129.6568	2047.1440	9.47
11202	83.0457	69.4587	10.5124	47.7518	419.55
4402	82.9938	267.3028	36.0275	194.1380	15.893
20619	82.9938	4.0962	6.6296	22.2013	60.374
22783	82.9522	609.1080	69.8339	472.5891	13.26
1824	82.9002	87.3108	10.0804		166.69
9541	82.8378	555.4538	91.6877	112.6497	25.937
18729	82.7963	14.1671	11.8544	402.8147	108.519
1338	82.7339	51.0268	15.7818	42.3843	27.779
18317	82.7339	1103.1219	189.3486	26.4355	18.181
2577	82.6299	163.8201	10.2165	630.0896	288.170
19505	82.5780	29.6876	6.2768	127.8969	39.182
13731	82.5260	137.1868	20.1514	49.9631	16.370
25104	82.5260	293.0527	38.8201	192.5144	41.463
623	82.4844	110.7857	25.1048	173.1177	90.217
2735	82.4740	28.9793	6.0732	165.3757	60.291
10743	82.4324	127.0427	17.4009	18.2200	15.877
15886	82.3701	283.3204	46.2343	164.5138	43.021
16084	82.3285	23.4277		407.5226	96.152
338	82.3285	9.6305	5.1613 10.6024	34.5399	14.685
15864	82.2765	42.2848		41.6928	35.982
5358	82.2765	30.1691	9.5215	64.2521	21.749
20161	82.2557	72.3282	9.1089	52.8179	32.349
16675	82.2245	6.4648	30.7027	36.5091	40.886
20509	82.2245	41.7443	9.8542	23.9162	17.486
24234	82.2141	110.0508	3.8443	35.8325	15.148
15037	82.2141	158.7025	21.1288	77.0101	32.669
17960	82.1726	115.5419	43.1588	251.0986	68.695
15412	82.0478	72.9889	19.4553	135.9037	33.894
12253	82.0166	17.9676	28.1407	38.9881	25.507
25854	81.9127	35.6123	4.2628	23.8982	22.798
7395	81.9127	3223.9060	7.9702	50.3945	16.5373
1295	81.9023	49.4074	176.7481	3550.2689	741.6043
24033	81.9023	99.2837	14.2289	75.3296	19.245
15640	81.8087		18.7151	146.7463	37.671
1596	81.7464	96.0308 84.1073	14.7136	142.3732	61.0904
15829	81.7256		5.6887	102.3077	17.1709
19388	81.7048	178.6291	111.9201	49.6041	71.8434
23152	95.8940	47.1590	13.9443	30.9755	45.9566
3584	94.7505	1335.9175	118.1675	867.9193	203.9039
21713	93.2952	14.2293	5.4921	60.6882	32.4469
15538	93.1393	582.7896	69.9045	872.7586	176.6252
	00.1080	536.0414	54.6891	365.6804	104.8045

SLGC ID	): 6, 192 hrs			ef, 44921-5090-01	•
	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontoy
21229	93.0353		11.0545	27.1504	
2803	92.4116		21.4838	176.3510	
4782	92.2037		15.8476		
23437	91.7879	236.7137	41.3343	139.6025	
11173	91.5281	243.0114	58.0247	535.3317	
14582	91.2682	127.6744	21.5199	224.2760	167.992
10115	91.2682	29.6057	13.6555		70.220
5982	90.9563	330.2865	56.5047	90.3885	44.523
24220	90.8004	75.6789	14.2419	504.3480	103.619
23608	90.8004	504.9734	53.1811	48.9576	26.710
17761	90.3326	628.0054	52.1838	370.6369	85.374
22431	90.1767	43.1080	22.9255	454.0933	117.296
4445	89.2412	496.0604	33.5495	110.5954	42.071
11399	89.0852	86.8469	15.6233	649.1682	124.361
6121	88.9293	21.1135	4.1346	155.1791	51.781
18438	88.9293	634.1819		11.2633	8.440
4285	88.6071	187.1363	51.5064	470.5666	122.591
22451	88.5551	69.9633	42.6328	304.2508	62.905
11585	88.5135	428.5571	16.1178	151.1270	54.680
18890	88.5135	622.3692	54.5189	583.7686	113.308
562	88.4615	351.8821	39.7606	834.6452	207.652
2195	88.3992	37.4029	19.9393	443.1682	93.776
11413	88.1497	41.8912	12.5528	12.5809	11.0479
6974	88.0457	465.5023	13.2820	116.6002	69.4703
10918	88.0353	249.3467	57.8721	672.4599	169.8077
10549	88.0249	76.7015	44.9415	394.0465	82.6490
18162	87.9938		27.5227	25.7768	13.2437
22899	87.8794	672.9671	157.9230	1379.7346	622.7619
2607	87.8378	99.8766	31.4158	44.2337	33.3480
16124	87.7235	210.1685	36.9080	309.7591	77.6187
4330	87.5260	349.2498	69.2475	230.5006	94.8320
15959	87.5156	291.9245	58.6099	457.8991	140.3640
3650	87.2141	166.1477	35.3812	284.1650	68.3560
2146	87.1102	27.5894	7.3449	47.3570	16.8362
9668	87.0374	112.9026	7.9507	83.1270	69.9111
13977		294.4770	103.1179	104.9414	48.2427
5482	86.9543	324.9940	47.9945	473.8557	139.7205
22691	86.7879	131.7752	46.1137	262.4037	74.2493
17223	86.6944	610.5659	137.7533	925.4717	241.2703
11550	86.6840	1740.5481	162.7909	1385.7345	197.6986
8004	86.5800	53.8907	15.8747	24.7288	17.1509
26254	86.4865	51.9950	8.1689	33.3889	24.2458
24229	86.4345	62.2933	6.7403	43.5870	16.5093
19480	86.3306	40.4595	25.6329	102.7587	67.3230
8036	86.3202	1082.1691	173.5370	1683.1091	376.5196
9746	86.3098	134.7036	31.9390	73.2170	22.4198
	86.2786	152.0881	23.8073	109.2433	
23313	86.1642	193.6157	31.1318	300.9419	62.9276
6691	86.1227	96.9943	24.9702	158.1074	73.0184
2708	86.1227	523.6743	46.8008	660.4570	51.5964
11017	86.0707	44.1708	21.1458	104.5216	128.0638
14430 2422	86.0707	-4.2543	7.5839	23.7641	47.2598
フハンツ	86.0707	131.8345	17.6804	20./041	26.1542

TABLE 5R:	EPIRUBICIN	5 3 EV	Attv. Re	ef. 44921-5090-01	-MO/240540
GLGC ID	s): 6, 192 hrs LDA Score	184 com T	•		-vv0/210548
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
665		655.9712		561.4934	112.5356
5070	85.9667	85.7730	10.6372	52.6396	36.2695
22711	85.9148	180.0290	22.1305	230.2369	
6522	85.9044	450.1290	145.1702	835.3920	47.3605
6502	85.8628	159.2748	22.1170	232.6916	230.1413
17243	85.8628	207.4676	55.0211		70.0673
6166	85.8524	165.8695	54.9624	347.7619	112.2982
7528	85.7588	95.4966	8.9508	322.5498	92.7068
7740	85.6965	416.2965		63.3362	27.7343
3996	85.6445	87.6525	59.9352	299.4983	66.7080
13453	85.5509	201.6490	14.7965	59.6366	16.0125
4716	85.5405		33.7731	300.0235	81.7371
21755	85.4990	170.1268	17.6057	125.1288	30.6648
4907	85.4990	438.1096	78.0876	628.7300	162.3387
22536		136.2406	13.5281	173.5136	37.6766
13181	85.3950	710.5183	98.6998	1051.4300	301.1097
18439	85.3846	43.2573	10.9705	19.9964	14.0652
	85.3846	356.3238	37.3752	258.2394	67.8627
11445	85.3846	157.7293	42.6245	285.6630	83.7123

imepoint(s):	6 hrs	E V	Atty. Ref. 44921-5090-01-WO/210548			
LGC ID L		Mean Tox	SD Tox	Mean Nontox	ICO N	
15087	98.7590	156.8356			SD Nonto	
1884	98.1903	212.7678			48.5	
17336	97.7766	38.8984		146.8696	33.4	
13339	97.1562	621.0880	36.3859	15.5544	7.6	
10544	97.0527	579.5536		418.4784	87.1	
25964	96.8976	10.3804	26.8199	430.2195	65.2	
10248	96.8459	560.9118	1.5050	30.7610	28.7	
20801	96.8459	124.0848	75.9608	306.7008	83.5	
17959	96.6908	196.1464	9.9768	78.3221	18.5	
1316	96.3806	194.5946	32.6060	103.5609	35.1	
15253	96.1737	213.1780	3.0724	220.5001	67.6	
21065	95.9152		15.3416	108.2212	47.0	
21170	95.7084	64.0334	6.5672	32.7124	16.7	
4748	95.5016	23.4838	3.1293	4.4235	16.1	
15494	95.2430	80.0904	8.0144	44.1474	44.7	
8385		30.1844	11.4627	1.2506	13.16	
22149	95.1913	65.6368	3.4862	120.7273	53.38	
19022	95.1913	102.1954	21.5573	44.6483	21.6	
	95.1913	166.9424	17.2286	106.2918	27.33	
1570	95.1913	188.7068	22.2973	128.2530		
4391	95.1913	964.1682	28.6948	748.8637	34.54	
692	95.1396	226.4920	31.5708	136.7682	167.16	
1048	94.9845	34.4978	1.3618	32.2165	35.65	
5758	94.8811	1126.7468	67.5204	729.5331	23.43	
5618	94.8811	20.6124	0.6174		208.06	
18713	94.7777	337.1688	47.9403	16.1073	12.49	
25741	94.7777	316.6112	28.7189	221.5557	53.19	
23042	94.7777	168.7624	7.8811	204.9095	55.10	
25435	94.7260	4.4656	4.8069	106.7368	46.26	
13359	94.6743	67.3408		40.9287	21.51	
17868	94.6743	223.1472	14.1570	20.7383	20.71	
23344	94.5191	312.8444	24.4925	136.4057	44.62	
17326	94.4674	103.0512	8.5720	258.7436	47.12	
15510	94.4157	193.4632	25.6833	42.3484	24.42	
1943	94.3640	106.5466	17.2712	281.2604	54.43	
15560	94.3640		18.1488	62.4307	19.56	
23061	94.3123	19.8352	2.6627	38.4841	17.54	
1521	94.2606	50.6234	0.7799	56.6232	17.46	
18190	94.2606	133.3518	17.4480	68.3514	34.506	
1921		104.4614	3.4337	142.4649	35.877	
23310	94.2089	130.4758	22.4579	81.5571	23.697	
945	94.1572	121.0986	7.7792	79.1103	28.425	
18946	93.9504	34.0030	9.4963	-12.4155	31.008	
24106	93.7435	30.7076	3.0945	13.8638	10.513	
	93.6401	48.1790	5.6697	27.1419	10.694	
21656	93.6401	20.8806	2.4819	39.6907	13.386	
18957	93.5367	785.0618	16.6500	913.2878		
23892	93.4850	63.0390	7.1285	43.9236	164.550	
20762	93.4333	69.1156	3.7502	91.5013	10.139	
15446	93.3816	425.6222	30.8100	303.8692	17.091	
18209	93.3299	123.0876	5.5037		72.852	
22385	93.2782	234.0026	17.9207	88.5967	32.075	
18820	93.2265	88.4046	3.8870	148.7964	70.909	
17589	93.1748	23.0494	6.7302	94.9261	46.615	

ABLE 5S: HYDRALAZINE Atty. Ref. 44921-5090-01-WO/21054							
LGC ID	LDA Score		SD Tox	Mean Nontox	IOD N		
16601	93.1748				SD Nontox		
1928	93.0714	612.9376	1.2193 10.0815	27.1258			
17957	93.0196	100.3830		573.3866			
14066	92.9679	82.6706	12.8643	66.2742	17.507		
436	92.8645	91.0144	2.6372	111.0196	31.376		
16955	92.8645	351.1696	12.4145	58.2971	17.278		
727	92.8128	351.1696	24.0086	534.1851	180.897		
25711	92.7611	250.8246	5.8409	222.3852	33.121		
18043	92.7094	60.4372	5.8554	27.9624	21.921		
11152		100.0874	16.5917	62.8439	21.718		
24283	92.6060	336.3804	36.5219	214.4555	89.473		
	92.5543	56.7636	4.8815	84.0133	26.769		
12848	92.4509	46.4060	9.3354	26.6783	13.169		
3900	92.4509	30.1638	6.7989	8.1642			
22407	92.3992	145.0898	36.4334	262.9633	13.250		
16342	92.3992	56.6232	6.2416	34.9010	69.495		
20714	92.3992	36.3614	2.6050	7.0023	12.490		
482	92.3475	41.2860	4.8405	109.9989	32.309		
25257	92.3475	103.9680	11.1885		77.878		
20921	92.3475	89.1870	13.7751	70.6630	18.251		
17658	92.3475	20.4468	3.4186	49.6330	23.924		
20083	92.3475	13.0912		41.4294	20.574		
3762	92.3475	60.4542	3.5158	40.5189	21.601		
1581	92.3475	381.3852	2.8419	42.2743	16.755		
23950	92.2958	81.2448	18.7110	297.2422	61.430		
17158	92.2958		11.7875	58.9087	13.0678		
16026	92.2441	692.2852 237.9962	19.4813	744.8099	211.2131		
21104	92.1923	475.0962	30.8417	158.0972	46.9047		
20741	92.0889	175.6340	9.9545	126.3519	35.6131		
19749	92.0889	195.6502	31.8691	123.0799	39.9077		
11454		62.3318	4.5405	42.0015	13,4042		
5033	92.0889	258.2222	10.1641	210.0320	63.8915		
11843	92.0889	758.2678	14.0368	683.2052	151.6138		
	91.9855	89.5282	3.4154	73.9656	16.4826		
21103	91.9338	382.6494	64.5228	269.4251	66.5565		
25543	91.9338	35.7336	1.2476	40.1607	16.7910		
20246	91.7787	27.9992	6.3133	46.1156			
11959	91.7270	37.8310	5.1631	65.3994	22.2777		
13595	91.6236	124.2288	5.6409		19.8840		
25276	91.6236	-19.5760	13.2759	96.4356	18.2726		
11455	91.6236	127.6180	11.4570	95.0678	96.0023		
1920	91.5719	329.6462	22.8902	85.5654	31.9573		
3929	91.5202	0.8188		255.1135	63.6334		
16663	91.5202	28.6692	6.1616	21.7883	12.2968		
21905	91.4685	83.4162	1.1725	23.2420	10.2207		
11709	91.4685	251.7840	1.6888	94.6712	16.8457		
5257	91.4685		16.1910	167.6742	56.0592		
15980	91.4168	109.8050	7.3292	74.9256	23.9694		
517	91.4168	108.6496	9.3997	76.9870	21.0493		
1024		63.0800	8.9266	102.9841	33.5337		
8124	91.3650	30.9232	1.2299	44.3473	19.0074		
15988	98.8625	95.3660	7.7097	40.2143	17.6130		
14904	98.2937	558.6684	65.8687	241.6226	86.0058		
the statement	98.1903	112.3884	1.2288	83.6469	20.3510		
19271	97.7766	513.5628	37.1821	301.9994	73.4440		

Timepoint(s	HYDRALAZIN s): 6 hrs	E	Atty. F	Ref. 44921-5090-0	1-WO/210548
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
23015		153.2294	30.5337		
5007	97.5181	1227.9742	164.0440		
23471	97.3113	189.1040		77.4026	
12398	97.3113	399.6760		280.6130	
6828	97.1562	671.4382			66.774
17236	97.0010	778.2720		327.2167	123.597
26075	97.0010	924.5460	22.1006	428.0899	134.217
14342	96.7425	59.0536		1301.2541	323.329
2788	96.6908	243.0384	1.1919	83.3173	28.182
23673	96.6908	209.5468	1.5378	223.5537	41.081
21311	96.5874	252.0194	7.9002	360.8423	128.926
22677	96.5874		18.5667	173.1230	35.704
3979	96.5874	426.8144	74.5008	154.5159	88.332
19082	96.4840	116.0628	24.6605	49.4074	22.113
6888		289.2080	11.0645	223.3971	34.529
3953	96.4323	1068.6526	93.9476	691.3709	176.116
5953	96.3806	201.1584	13.2141	118.9865	36.844
	96.3289	169.6634	17.2572	290.3810	71.832
8303	96.3289	92.3654	8.0782	50.7243	18.031
21973	96.3289	94.0224	1.4839	84.8166	31.202
2687	96.2771	62.2784	2.6128	100.0773	25.542
2042	96.1737	320.1662	58.4861	142.4172	69.325
23998	96.1220	83.0044	19.9299	37.4956	13.932

GLGC ID	6 hrs			Ref. 44921-5090-0	
	LDA Score	Mean Tox	SD Tox	Mean Nontox	105 11
3601			14.3187		SD Nonto
13083		49.1638			
15087		156.8356	5.1580		
20735		261.2344	24.8554		48.55
25567	98.6556	230.1810	33.0818	101.1277	47.47
20734	98.3454	247.5826	38.2069	67.0123	33.95
1884	98.1903	212.7678	15.4227	94.2223	46.89
3430	98.1386	189.1080	13.1173	146.8696	33.49
17336	97.7766	38.8984	6.0547	107.6670	28.92
19894	97.7249	446.0524		15.5544	7.62
13339	97.1562	621.0880	124.8880	189.3509	64.35
10544	97.0527	579.5536	36.3859	418.4784	87.15
25964	96.8976	10.3804	26.8199	430.2195	65.22
10248	96.8459	560.9118	1.5050	30.7610	28.772
20801	96.8459	124.0848	75.9608	306.7008	83.568
1571	96.8459	290.1124	9.9768	78.3221	18.502
17959	96.6908	196.1464	33.2546	172.0863	53.633
25379	96.6391	314.9680	32.6060	103.5609	35.197
22411	96.6391	183.1822	26.0216	190.4498	49.617
1316	96.3806	194.5946	16.2164	92.2423	37.297
4749	96.3289		3.0724	220.5001	67.681
23419	96.2771	273.3598	7.2158	198.2721	80.471
15253	96.1737	347.5576	37.7552	207.3125	56.491
20740	95.9152	213.1780	15.3416	108.2212	47.019
21065	95.9152	780.8648	98.8353	449.8457	143.181
21170	95.7084	64.0334	6.5672	32.7124	16.712
18897	95.6567	23.4838	3.1293	4.4235	16.179
4748	95.5016	66.4808	4.7508	159.2470	64.755
15494	95.2430	80.0904	8.0144	44.1474	44.773
8385	95.1913	30.1844	11.4627	1.2506	13.1609
22149	95.1913	65.6368	3.4862	120.7273	53.3853
19022	95.1913	102.1954	21.5573	44.6483	21.6509
1570	95.1913	166.9424	17.2286	106.2918	27.3335
4391	95.1913	188.7068	22.2973	128.2530	34.5486
692	95.1396	964.1682	28.6948	748.8637	167.1622
1048	94.9845	226.4920	31.5708	136.7682	35.6521
5758	94.8811	34.4978	1.3618	32.2165	23.4399
5618	94.8811	1126.7468	67.5204	729.5331	208.0611
18713	94.7777	20.6124	0.6174	16.1073	12.4939
25741	94.7777	337.1688	47.9403	221.5557	53.1969
23042	94.7777	316.6112	28.7189	204.9095	55.1017
25435	94.7260	168.7624	7.8811	106.7368	46.2615
13359	94.6743	4.4656	4.8069	40.9287	21.5174
17868		67.3408	14.1570	20.7383	
1031	94.6743 94.6225	223.1472	24.4925	136.4057	20.7125
17468		110.6578	6.0793	73.9500	44.6227
23344	94.6225	41.4512	2.5169	59.0650	19.1861
17326	94.5191	312.8444	8.5720	258.7436	10.9062
15510	94.4674	103.0512	25.6833	42.3484	47.1229
1943	94.4157	193.4632	17.2712	281.2604	24.4297
15560	94.3640	106.5466	18.1488	62.4307	54.4386
23061	94.3640	19.8352	2.6627	38.4841	19.5604
23001	94.3123	50.6234	0.7799	56.6232	17.5475 17.4678

imepoint(s): LGC ID		188		Ref. 44921-5090-0	.,
		Mean Tox	SD Tox	Mean Nontox	SD Nonto
1521	94.2606	133.3518	17.4480	68.3514	
18190 13420	94.2606	104.4614	3,4337	142.4649	
	94.2089	643.8456	55.5188	449.4092	
1921	94.2089	130.4758	22.4579	81.5571	
23310	94.1572	121.0986	7.7792		23.6
945	93.9504	34.0030	9.4963	79.1103	28.4
18946	93.7435	30.7076	3.0945	-12.4155	31.0
24106	93.6401	48.1790	5.6697	13.8638	10.5
21656	93.6401	20.8806	2.4819	27.1419	10.6
18957	93.5367	785.0618	16.6500	39.6907	13.3
23892	93.4850	63.0390	7.1285	913.2878	164.5
20762	93.4333	69.1156	3.7502	43.9236	10.1
15446	93.3816	425.6222		91.5013	17.09
18209	93.3299	123.0876	30.8100	303.8692	72.8
22385	93.2782	234.0026	5.5037	88.5967	32.07
18820	93.2265	88.4046	17.9207	148.7964	70.90
17589	93.1748	23.0494	3.8870	94.9261	46.61
16601	93.1748	14.8828	6.7302	6.2261	8.89
1928	93.0714	612.9376	1.2193	27.1258	12.94
17957	93.0196		10.0815	573.3866	132.11
14066	92.9679	100.3830	12.8643	66.2742	17.50
436	92.8645	82.6706	2.6372	111.0196	31.37
16955	92.8645	91.0144	12.4145	58.2971	17.27
727	92.8128	351.1696	24.0086	534.1851	180.89
25711	92.7611	250.8246	5.8409	222.3852	33.12
18043	92.7094	60.4372	5.8554	27.9624	21.92
11152	92.6060	100.0874	16.5917	62.8439	21.71
24283	92.5543	336.3804	36.5219	214.4555	89.47
12848	92.4509	56.7636	4.8815	84.0133	26.76
3900	92.4509	46.4060	9.3354	26.6783	13.169
22407	92.3992	30.1638	6.7989	8.1642	13.250
16342	92.3992	145.0898	36.4334	262.9633	69.495
20714	92.3992	56.6232	6.2416	34.9010	12.490
482	92.3475	36.3614	2.6050	7.0023	32.309
25257		41.2860	4.8405	109.9989	77.878
20921	92.3475	103.9680	11.1885	70.6630	18.251
17658	92.3475	89.1870	13.7751	49.6330	23.924
20083	92.3475	20.4468	3.4186	41.4294	
3762	92.3475	13.0912	3.5158	40.5189	20.574
1581	92.3475	60.4542	2.8419	42.2743	21.601
23950	92.3475	381.3852	18.7110	297.2422	16.755
17158	92.2958	81.2448	11.7875	58.9087	61.430
16026	92.2958	692.2852	19.4813	744.8099	13.067
	92.2441	237.9962	30.8417	158.0972	211.213
21104 20741	92.1923	175.6340	9.9545	126.3519	46.904
19749	92.0889	195.6502	31.8691	123.0799	35.613
	92.0889	62.3318	4.5405		39.907
11454	92.0889	258.2222	10.1641	42.0015	13.4042
5033	92.0889	758.2678	14.0368	210.0320	63.891
21351	99.4829	80.6988	6.2490	683.2052	151.6138
11728	99.3278	753.1340	68.6619	12.1389	20.9150
9551	99.2761	796.8730	49.0184	380.7892	93.2638
13270	99.1727	476.3998	65.5985	498.5805	85.2638

6548 8124 2416 6562 5258 15885 8745	98.8625 98.8625 98.7590	Mean Tox 694.7628	SD Tox	Mean Nontox :	SD Nontox
8124 2416 6562 5258 15885 8745	98.8625 98.7590	694.7628	400 400		
2416 6562 5258 15885 8745	98.7590			213.2618	77.093
6562 5258 15885 8745		95.3660		40.2143	17.613
5258 15885 8745		501.2280		346.1962	87.937
15885 8745	98.7073	47.5550	3.1216	81.4447	17.673
8745	98.7073	664.1520	45.8208	402.7573	69.966
	98.6556	280.7466		145.7606	36.639
	98.6556	215.8620		107.9325	39.442
7299	98.6039	773.1158	120.8460	251.5905	113.140
11726	98.5005	533.5082	40.5515	286.8237	89.802
11727	98.5005	604.3898	48.0730	319.2727	85.660
22464	98.5005	278.9364	40.1997	124.1771	46.790
5129	98.4488	169.9756	12.3029	86.1985	
23035	98.3971	245.7036	21.6546	123.3464	28.246
15988	98.2937	558.6684	65.8687	241.6226	34.781
5292	98.2420	376.7596	113.5796	91.9099	86.005
14904	98.1903	112.3884	1.2288		69.346
12303	98.1903	112.7144	15.4871	83.6469	20.351
3050	98.0869	228.8394	38.5682	28.6056	39.041
15841	98.0352	85.1580	5.2567	88.4676	65.811
23110	98.0352	344.7718	15.4324	50.2158	13.628
2378	97.9835	129.8426	19.3748	210.0800	56.477
6936	97.9317	198.0056	27.9364	56.7000	19.645
22614	97.8800	156.9550		98.0114	30.921
3003	97.8283	417.5536	73.5855	45.3235	24.081
19271	97.7766	513.5628	106.1557	70.3467	60.2634
15212	97.6732	116.1712	37.1821	301.9994	73.4440
23015	97.6215	153.2294	20.9712	56.5987	40.6347
7867	97.6215	248.1136	30.5337	77.7618	21.742
13966	97.5698		37.4367	97.2828	44.8662
7615	97.5698	194.0216	33.4736	104.6886	27.0718
8495	97.5698	91.9202	11.3562	29.7933	25.0687
5007	97.5181	192.2230	8.3247	131.8170	29.8504
11331	97.4147	1227.9742	164.0440	736.2918	160.4563
14955	97.4147	140.2186	14.3519	87.0803	18.9431
3941	97.3630	181.0944	80.5659	-178.9106	195.8687
23471		380.7426	47.4343	180.8175	67.4454
12398	97.3113	189.1040	51.5207	77.4026	35.9134
7220	97.3113	399.6760	9.1169	280.6130	66.7741
6560	97.2596	51.8602	0.7886	76.1486	29.3080
	97.1562	432.4062	30.2947	282.7162	57.5640
6828	97.1562	671.4382	59.8131	327.2167	123.5972
17903	97.1044	244.5414	29.1343	137.7887	38.4653
9658	97.1044	244.7306	62.7510	99.7752	47.9401
17236	97.0010	778.2720	64.5047	428.0899	134.2179
5531	97.0010	172.8490	10.8200	102.8946	
3049	97.0010	498.4446	86.8179	249.9030	29.5049
26075	97.0010	924.5460	22.1006	1301.2541	136.4987
22958	96.8976	375.6922	31.5155	232.9499	323.3296
6094	96.7942	223.6600	29.8316		64.3866
23230	96.7425	162.8192	9.7664	112.4906	42.5031
14342	96.7425	59.0536	1.1919	252.2847	53.4630
4725	96.7425	239.6758	67.2939	83.3173	28.1826
2788	96.6908	243.0384	1.5378	87.1054 223.5537	101.4360 41.0819

rimepoint(s):	6 hrs 🥖	IOD Town		1-WO/210548	
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
23673		209.5468	7.9002	360.8423	
13029		435.5570	85.3821	201.6063	
21311	96.5874	252.0194	18.5667	173.1230	
22677	96.5874	426.8144	74.5008	154.5159	
3979	96.5874	116.0628	24.6605	49.4074	22.1134
22666	96.5357	125.0378	7.3520	78.9438	
3615	96.4840	575.8332	43.2667	305.7159	136.9796
19082	96.4840	289.2080	11.0645	223.3971	34.5298
6888	96.4323	1068.6526	93.9476	691.3709	176.1165
12098	96.3806	90.9948	33.1508	-8.9047	39.2096
3953	96.3806	201.1584	13.2141	118.9865	36.8447
18673	96.3806	237.2430	27.7351	143.5021	35.7604
6053	96.3289	36.2648	5.1090	11.4704	11.8845
4432	96.3289	116.5428	21.4180	46.0566	26.6820
5953	96.3289	169.6634	17.2572	290.3810	71.8326
8303	96.3289	92.3654	8.0782	50.7243	18.0310
21973	96.3289	94.0224	1.4839	84.8166	31.2021
2687	96.2771	62.2784	2.6128	100.0773	25.5429
2729	96.2254	276.0500	17.5150	480.2069	152.8510
2042	96.1737	320.1662	58.4861	142.4172	69.3252
23998	96.1220	83.0044	19.9299	37.4956	13.9322

michoniti	): 48, 144 hrs	. :	•	44921-5090-01	110/2/004
SLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nonto
1632	93.9252			49.1647	
4010			23.0504	36.4157	
1780			5.7305	49.4382	46.91
20734	92.3676	144.9521		94.5444	25.55
8587	92.3157	20.8803			48.04
25790	92.2638	35.6152	5.7390	41.8238	16.94
16708	91.8484	88.5919	17.8854	59.4251	16.38
20224	91.7965	26.1801	4.6261	157.9072	40.99
14543	91.5369	48.5444	13.3595	54.4380	23.60
18596	91.2773	10.5340	2.2310	5.1087	27.442
4338	91.2253	69.7044		21.6064	8.729
1827	91.2253	16.2629	4.9022	93.0153	21.272
24844	90.9657	6.6279	9.8338	75.3003	47.774
16260	90.4465		6.2995	54.7281	38.884
695	90.2908	45.4320	8.2771	79.8531	24.030
1904	90.2908	53.2826	3.7848	69.0072	17.908
305		47.5752	5.7608	84.8968	39.315
25306	90.1350	22.3219	9.1616	53.6244	26.016
16272	90.1350	-11.1511	13.4777	24.5808	23.845
	90.0312	25.6340	8.0024	50.4168	16.972
20232	89.9792	12.6166	3.2958	27.4022	10.948
20509	89.9273	20.0840	3.0939	36.0410	15.076
16610	89.7715	499.3631	73.4028	756.9499	181.840
24697	89.5119	105.8682	9.8884	155.6203	
16899	89.4600	32.9150	4.8111	20.0086	42.971
25262	89.1485	28.4856	3.1939	42.4705	13.372
385	89.1485	11.8336	5.9556	46.0511	14.536
2881	88.9927	252.2559	62.0365	398.2385	22.748
20313	88.8370	8.0980	9.4173		92.626
12022	88.8370	23.3220	5.1564	29.3879	10.893
1463	88.3697	637.2336	174.0208	49.3675	23.771
20073	88.2658	2.9439	8.0267	362.0256	132.666
5159	87.9543	336.6101	76.6035	40.0215	19.470
348	87.6947	47.5134		172.3420	76.1563
15380	87.6428	1163.6321	9.5651	81.4591	28.9767
1265	87.4870	13.2800	88.1712	936.7430	371.079
15777	87.4870	15.1453	9.0537	32.1539	11.5110
17709	87.3832		5.2606	35.8179	18.4377
25290	87.1236	131.6908	17.2177	181.8362	42.2679
17226	87.1236	587.7248	84.2770	388.4657	110.4809
19326	86.8640	269.8507	29.5324	190.1852	46.8537
2832		69.1733	6.3079	55.9080	24.3541
1765	86.8120	120.5140	13.6626	150.9123	24.0289
11113	86.8120	47.8216	9.6220	83.6380	31.6316
15776	86.7082	14.1942	9.7635	36.4740	19.6053
24643	86.7082	151.7243	22.4822	244.3187	74.2967
	86.6044	215.9132	50.8641	69.3391	74.1356
25365	86.3967	9.7790	7.4931	47.8117	33.8018
1808	86.3448	5.7119	5.3248	97.1407	156.9111
11218	86.3448	38.1513	30.2508	128.0294	
19795	86.3448	34.0938	13.5264	68.0481	49.1823
167	86.3448	345.9002	83.9734		27.3656
2947	86.2928	24.4228	9.0045	587.3977 51.3409	174.9745
21652	86.2409	16.3704		01.34091	20.3344

	): 48, 144 hrs	•			-WO/21054
SLGC ID	LDA Score		SD Tox	Mean Nontox	100 11
6577	86.2409			400 40 40	
938	86.2409	9.6093	3.2930	123.4940	
25765	86.2409	33.1944	8.5889	21.0064	
20210	86.1890	24.6803		65.7206	
24597	86.1890	561.1767	11.0628	56.1610	
1249	86.1371	41.7076	51.1917	483.0641	109.42
25571	86.1371	36.6171	8.2689	60.5223	14.32
20732	86.1371	12.7066	8.0319	54.8128	15.11
15727	86.1371	16.3477	4.1574	23.3332	9.08
16947	86.0332	50.5529	7.4304	39.3159	13.59
16962	85.9813	6.9492	10.1535	76.5861	22.002
23069	85.9294			28.2084	13.764
2153	85.7736	31.9091	4.3861	44.3683	10.890
10544	85.7736	289.2098	43.1231	220.9612	123.110
20450	85.7736	353.9149	29.0669	431.7080	65.784
23665	85.7217	52.3184	7.1360	72.6463	22.443
15310		34.9232	7.1230	51.8690	12.900
2413	85.6698	38.2432	6.9779	56.7156	15.212
25770	85.6179	752.3984	55.8953	625.1376	104.235
58	85.6179	69.4238	33.3087	160.7589	60.197
17693	85.5659	97.7782	5.3308	91.3499	24.667
20536	85.5140	61.2944	7.7884	44.4666	18.238
	85.5140	35.1599	9.6132	11.9589	22.682
21866	85.3583	113.1301	31.5776	217.3893	93.296
455	85.3583	3398.0386	634.4508	4996.0023	1069.395
19423	85.3063	57.2618	11.3319	97.6164	39.048
1356	85.3063	37.6693	8.3923	20.4105	11.370
24522	85.3063	8.8614	7.9366	27.5777	12.262
17427	85.2025	323.6780	57.0555	221.4037	65.871
17303	85.2025	33.7866	2.8455	41.9456	
162	84.9429	20.8002	17.6035	42.5670	9.1403
10108	84.8910	91.7666	10.7510	63.6700	23.7219
22355	84.7871	16.5914	5.3296	31.9805	27.1232
3799	84.6833	248.9998	58.6310	384.0977	12.8094
1025	84.5275	10.6336	5.2061	33.1574	115.4912
2464	84.5275	32.8120	3.7668	39.8959	21.1802
1024	84.4237	21.5096	7.3160		13.1058
10510	84.4237	231.8057	17.9081	44.4910	18.9310
18315	84.2679	752.9110	151.6886	245.7739	69.5059
18582	84.2679	338.0744	29.3245	1144.1357	341.8948
18360	84.2160	279.0253	73.8143	250.5000	55.4897
17997	84.2160	25.9506	5.2089	410.2238	103.7573
983	84.2160	84.9207	11.7220	38.3192	11.5819
942	84.2160	10.7322	6.7701	119.6201	32.5343
15507	84.2160	11.5281	3.6762	24.4656	9.1480
2401	84.1121	19.7984		20.9932	6.5180
14066	84.0602	83.1214	18.8561	54.8464	22.2599
1118	84.0602	20.3108	8.6258	111.1332	31.3829
10248	84.0083	373.7648	7.7863	51.3574	21.9794
3390	96.5213	98 0716	49.7422	307.3939	85.4952
11375	95.9502	47.0950	16 5306	13.2468	32.8732
5422	95.9502		6.7258	101.4006	31.7853
5549	95.6906	255.9669	15.3339	447.6795	137.3423
	00.0000	171.8383	14.2889	272.7479	88.2184

nuchonide	): 48, 144 hrs		٠.	f. 44921-5090-01	10040
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	100 11
6276	95.6386				SD Nontox
12796	95.6386				
2962	95.5348		. 11.2001	41.7692	
2424	95.4829	744.0810	0.00,0	117.4927	
23288	95.3271	162.0457		456.9711	109.419
14594	95.2233	37.3820		272.3246	62.054
5710	95.1194	64.4711	25.3448	-20.8144	26.616
2657	94.9117	404.4319	7.2831	115.7780	29.501
4954	94.8079	75.8566	47.1948	214.9007	86.218
8712	94.7560	93.8463	48.3559	300.5078	120.210
10070	94.7040		20.1516	10.3414	49.358
5433	94.6521	34.6609	9.5241	79.8852	30.340
3952	94.3406	48.3568	7.0044	97.6852	36.022
12426	94.2368	142.5596	15.2222	220.9986	49.2334
15108		36.4587	34.9450	-53.9307	40.685
5890	94.2368	33.5728	7.3179	75.1760	24.193
7447	94.0810	144.1226	16.6702	237.2963	56.8326
7698	93.8733	54.7359	9.9771	104.1249	30.759
16335	93.6656	74.4883	11.5063	149.5131	47.2443
	93.6137	88.6708	40.5413	266.6131	136.8408
4779	93.5618	40.2461	5.2003	66.4230	17.3590
3352	93.5099	721.7098	75.5300	447.0117	
10171	93.5099	91.0491	22.1459	180.0318	132.9273
8103	93.4579	-7.6890	9.1160	54.2286	47.2872
15160	93.3541	87.2868	16.4703	213.1044	37.7280
16034	93.3541	109.7919	25.9816	218.6182	92.6222
3899	93.3022	60.4683	21.0169	-11.5877	58.2329
21364	93.1983	72.5470	39.8668	262.2539	35.8785
9521	93.1464	55.8598	9.0144	91.8144	123.5654
2075	93.0426	44.3953	8.3172		22.2810
19214	92.8349	127.8322	22.3277	89.0395	28.0498
14842	92.7830	49.3027	12.6519	37.8946	63.3805
22187	92.7830	409.4556	129.1747	102.6669	39.3891
21782	92.6791	38.6721	27.8222	867.5699	267.7624
9352	92.6791	378.4376	53.4050	122.8371	47.2701
8039	92.6791	68.3052	18.3267	552.6199	96.8881
10453	92.6272	53.9392		140.0283	49.5285
11408	92.6272	32.4582	16.4808	132.5562	49.1075
5095	92.6272	416.0853	18.6918	129.4645	55.9234
9554	92.5753	40.4331	28.8365	567.1313	110.1052
3265	92.4714	41.5882	14.8696	97.1900	33.8327
3637	92.3676		12.8118	98.6859	36.9127
22405	92.3157	15.1582	7.5334	41.6123	22.4054
7264	92.2638	133.8187	32.5703	238.9619	59.6023
16686	92.2118	27.2209	10.8354	72.6050	. 47.7981
6737	92.1080	118.8172	33.9194	234.5096	69.1124
2526	92.1080	177.6041	46.8049	85.4628	68.4928
8557	92.1080	236.0059	26.3307	326.7278	58.8308
10690		124.4789	33.6220	298.5563	128.6680
22480	92.1080	26.9454	4.5462	6.3091	18.2157
5990	92.1080	67.8894	14.8504	144.3945	51.0405
6496	92.0561	483.3228	40.6774	361.6884	71.5924
21889	92.0042	91.6501	25.0566	188.0613	55.0460
21009	91.9522	72.4361	17.2609	128.0111	31.2454

SLGC ID	): 48, 144 hrs LDA Score	Mean Tox	CD T		<u>* </u>
				Mean:Nontox	SD Nontox
23092	9::0000			396.4401	70.107
5726	-	47.5982	14.2846		28.661
8158	91.8484	213.3934	48.7506	403.2356	114.786
10277	91.8484	25.4588	9.4491	82.9826	
3781	91.7445	-8.0857	12.0879	30.3861	42.347
4750	91.6926	129.3269	39.4346	255.8295	26.314
17552	91.6926	54.2706	13.2305	100.7306	84.718
22708	91.6926	165.1820	16.0246		33.800
19159	91.6407	347.2374	57.9407	252.7250	71.839
12805	91.6407	46.1116	10.1198	243.3276	58.790
2492	91.5888	191.2070		12.1679	53.711
22308	91.5888	311.2068	34.7816	110.1686	42.634
5595	91.5369		57.2959	130.6294	104.9578
5370	91.5369	133.1074	12.8488	188.8985	46.4980
0070	91.0309	44.2783	20.8570	134.8288	63.6771

CID	48, 144 hrs			lef. 44921-5090-0	
Ç ID	LDA Score	Mean Tox	SD Tox		SD Nontox
16448		52.2061	15.1149	282.8893	
25517	96.9886	47.0090	5.5888	164.7448	
18907	96.0540	43.0038	37.5571	445.5213	
6654	95.9502	66.3403	7.8424	32.6269	
25468	95.4829	1301.8949	1387.7861	6101.7220	13.774
25469	94.7560	1031.8324	1010.7518	4514.6746	2467.741
1632	93.9252	21.9256	4.7059	49.1647	1818.471
1684	93.6137	1779.0361	1757.4448	6747.6461	16.398
4010	92.7310	83.0657	23.0504	36.4157	2993.079
1780	92.4195	35.5666	5.7305	49.4382	46.912
20734	92.3676	144.9521	23.4277	49.4382	25.552
8587	92.3157	20.8803	4.2288	94.5444	48.044
25790	92.2638	35.6152	5.7390	41.8238	16.946
16708	91.8484	88.5919	17.8854	59.4251	16.380
20224	91.7965	26.1801	4.6261	157.9072	40.995
14543	91.5369	48.5444	13.3595	54.4380	23.604
18596	91.2773	10.5340		5.1087	27.442
4338	91.2253	69.7044	2.2310	21.6064	8.729
1827	91.2253	16.2629	4.9022	93.0153	21.272
24844	90.9657	6.6279	9.8338	75.3003	47.774
9501	90.9138	152.3356	6.2995	54.7281	38.884
16260	90.4465	45.4320	11.4546	118.4492	23.489
695	90.2908	53.2826	8.2771	79.8531	24.030
1904	90.2908	47.5752	3.7848	69.0072	17.908
1845	90.1869	-39.5333	5.7608	84.8968	39.315
305	90.1350	-39.5333	15.8480	50.2903	75.501
25306	90.1350	22.3219	9.1616	53.6244	26.016
16272	90.0312	-11.1511	13.4777	24.5808	23.845
20232	89.9792	25.6340	8.0024	50.4168	16.972
20509	89.9273	12.6166	3.2958	27.4022	10.948
16610	89.7715	20.0840	3.0939	36.0410	15.076
24697	89.5119	499.3631	73.4028	756.9499	181.840
16899	89.4600	105.8682	9.8884	155.6203	42.971
25262	89.1485	32.9150	4.8111	20.0086	13.3720
385	89.1485	28.4856	3.1939	42.4705	14.5360
2881	88.9927	11.8336	5.9556	46.0511	22.7486
20313	88.8370	252.2559	62.0365	398.2385	92.6266
12022	88.8370	8.0980	9.4173	29.3879	10.8937
1463		23.3220	5.1564	49.3675	23.7717
20073	88.3697	637.2336	174.0208	362.0256	132.6660
956	88.2658 88.2658	2.9439	8.0267	40.0215	19.4706
4011		109.0921	25.9296	220.8949	96.5220
5159	88.0062	26.8526	6.8641	15.2646	19.2039
348	87.9543	336.6101	76.6035	172.3420	76.1563
15380	87.6947	47.5134	9.5651	81.4591	28.9767
1265	87.6428	1163.6321	88.1712	936.7430	371.0795
15777	87.4870	13.2800	9.0537	32.1539	11.5110
	87.4870	15.1453	5.2606	35.8179	18.4377
17709	87.3832	131.6908	17.2177	181.8362	42.2679
25290	87.1236	587.7248	84.2770	388.4657	110.4809
17226	87.1236	269.8507	29.5324	190.1852	
19326	86.8640	69.1733	6.3079	55.9080	46.8537
2832	86.8120	120.5140	13.6626	150.9123	24.3541 24.0289

23303         86.3967         9.7790         7.4931         47.8117           1808         86.3448         5.7119         5.3248         97.1407         1           11218         86.3448         38.1513         30.2508         128.0294           19795         86.3448         34.0938         13.5264         68.0481           167         86.3448         345.9002         83.9734         587.3977         1           2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223           25571         86.1371         12.7066         4.1574         23.3332	31.6316 19.6053 74.2967 74.1356 33.8018 56.9111 49.1823 27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
1765         86.8120         47.8216         9.6220         83.6380           11113         86.7082         14.1942         9.7635         36.4740           15776         86.7082         151.7243         22.4822         244.3187           24643         86.6044         215.9132         50.8641         69.3391           25365         86.3967         9.7790         7.4931         47.8117           1808         86.3448         5.7119         5.3248         97.1407         1           11218         86.3448         38.1513         30.2508         128.0294           19795         86.3448         34.0938         13.5264         68.0481           167         86.3448         345.9002         83.9734         587.3977         1           2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597<	31.6316 19.6053 74.2967 74.1356 33.8018 56.9111 49.1823 27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
11113         86.7082         14.1942         9.7635         36.4740           15776         86.7082         151.7243         22.4822         244.3187           24643         86.6044         215.9132         50.8641         69.3391           25365         86.3967         9.7790         7.4931         47.8117           1808         86.3448         5.7119         5.3248         97.1407         1           11218         86.3448         38.1513         30.2508         128.0294           19795         86.3448         34.0938         13.5264         68.0481           167         86.3448         345.9002         83.9734         587.3977         1           2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597<	19.6053 74.2967 74.1356 33.8018 56.9111 49.1823 27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
15776         86.7082         151.7243         22.4822         244.3187           24643         86.6044         215.9132         50.8641         69.3391           25365         86.3967         9.7790         7.4931         47.8117           1808         86.3448         5.7119         5.3248         97.1407         1           11218         86.3448         38.1513         30.2508         128.0294           19795         86.3448         34.0938         13.5264         68.0481           167         86.3448         345.9002         83.9734         587.3977         1           2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1      <	74.2967 74.1356 33.8018 56.9111 49.1823 27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
24643         86.6044         215.9132         50.8641         69.3391           25365         86.3967         9.7790         7.4931         47.8117           1808         86.3448         5.7119         5.3248         97.1407         1           11218         86.3448         38.1513         30.2508         128.0294           19795         86.3448         34.0938         13.5264         68.0481           167         86.3448         345.9002         83.9734         587.3977         1           2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223	74.1356 33.8018 56.9111 49.1823 27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
25365         86.3967         9.7790         7.4931         47.8117           1808         86.3448         5.7119         5.3248         97.1407         1           11218         86.3448         38.1513         30.2508         128.0294           19795         86.3448         34.0938         13.5264         68.0481           167         86.3448         345.9002         83.9734         587.3977         1           2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223           25571         86.1371         36.6171         8.0319         54.8128	33.8018 56.9111 49.1823 27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
1808         86.3448         5.7119         5.3248         97.1407         1           11218         86.3448         38.1513         30.2508         128.0294           19795         86.3448         34.0938         13.5264         68.0481           167         86.3448         345.9002         83.9734         587.3977         1           2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223           25571         86.1371         36.6171         8.0319         54.8128           20732         86.1371         12.7066         4.1574         23.3332	56.9111 49.1823 27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
11218       86.3448       38.1513       30.2508       128.0294         19795       86.3448       34.0938       13.5264       68.0481         167       86.3448       345.9002       83.9734       587.3977       1         2947       86.2928       24.4228       9.0045       51.3409         21652       86.2409       16.3704       19.2389       25.6408         6577       86.2409       150.3376       9.2802       123.4940         938       86.2409       9.6093       3.2930       21.0064         25765       86.2409       33.1944       8.5889       65.7206         20210       86.1890       24.6803       11.0628       56.1610         24597       86.1890       561.1767       51.1917       483.0641       1         1249       86.1371       41.7076       8.2689       60.5223         25571       86.1371       36.6171       8.0319       54.8128         20732       86.1371       12.7066       4.1574       23.3332         15727       86.1371       16.3477       7.4304       39.3159	49.1823 27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
19795         86.3448         34.0938         13.5264         68.0481           167         86.3448         345.9002         83.9734         587.3977         1           2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223           25571         86.1371         36.6171         8.0319         54.8128           20732         86.1371         12.7066         4.1574         23.3332           15727         86.1371         16.3477         7.4304         39.3159	27.3656 74.9745 20.3344 11.2378 35.7175 10.0987
167         86,3448         345,9002         83,9734         587,3977         1           2947         86,2928         24,4228         9,0045         51,3409           21652         86,2409         16,3704         19,2389         25,6408           6577         86,2409         150,3376         9,2802         123,4940           938         86,2409         9,6093         3,2930         21,0064           25765         86,2409         33,1944         8,5889         65,7206           20210         86,1890         24,6803         11,0628         56,1610           24597         86,1890         561,1767         51,1917         483,0641         1           1249         86,1371         41,7076         8,2689         60,5223           25571         86,1371         36,6171         8,0319         54,8128           20732         86,1371         12,7066         4,1574         23,3332           15727         86,1371         16,3477         7,4304         39,3159	74.9745 20.3344 11.2378 35.7175 10.0987
2947         86.2928         24.4228         9.0045         51.3409           21652         86.2409         16.3704         19.2389         25.6408           6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223           25571         86.1371         36.6171         8.0319         54.8128           20732         86.1371         12.7066         4.1574         23.3332           15727         86.1371         16.3477         7.4304         39.3159	20.3344 11.2378 35.7175 10.0987
21652       86.2409       16.3704       19.2389       25.6408         6577       86.2409       150.3376       9.2802       123.4940         938       86.2409       9.6093       3.2930       21.0064         25765       86.2409       33.1944       8.5889       65.7206         20210       86.1890       24.6803       11.0628       56.1610         24597       86.1890       561.1767       51.1917       483.0641       1         1249       86.1371       41.7076       8.2689       60.5223         25571       86.1371       36.6171       8.0319       54.8128         20732       86.1371       12.7066       4.1574       23.3332         15727       86.1371       16.3477       7.4304       39.3159	11.2378 35.7175 10.0987
6577         86.2409         150.3376         9.2802         123.4940           938         86.2409         9.6093         3.2930         21.0064           25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223           25571         86.1371         36.6171         8.0319         54.8128           20732         86.1371         12.7066         4.1574         23.3332           15727         86.1371         16.3477         7.4304         39.3159	35.7175 10.0987
938     86.2409     9.6093     3.2930     21.0064       25765     86.2409     33.1944     8.5889     65.7206       20210     86.1890     24.6803     11.0628     56.1610       24597     86.1890     561.1767     51.1917     483.0641     1       1249     86.1371     41.7076     8.2689     60.5223       25571     86.1371     36.6171     8.0319     54.8128       20732     86.1371     12.7066     4.1574     23.3332       15727     86.1371     16.3477     7.4304     39.3159	10.0987
25765         86.2409         33.1944         8.5889         65.7206           20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223           25571         86.1371         36.6171         8.0319         54.8128           20732         86.1371         12.7066         4.1574         23.3332           15727         86.1371         16.3477         7.4304         39.3159	
20210         86.1890         24.6803         11.0628         56.1610           24597         86.1890         561.1767         51.1917         483.0641         1           1249         86.1371         41.7076         8.2689         60.5223           25571         86.1371         36.6171         8.0319         54.8128           20732         86.1371         12.7066         4.1574         23.3332           15727         86.1371         16.3477         7.4304         39.3159	
24597     86.1890     561.1767     51.1917     483.0641     1       1249     86.1371     41.7076     8.2689     60.5223       25571     86.1371     36.6171     8.0319     54.8128       20732     86.1371     12.7066     4.1574     23.3332       15727     86.1371     16.3477     7.4304     39.3159	19.4755
1249     86.1371     41.7076     8.2689     60.5223       25571     86.1371     36.6171     8.0319     54.8128       20732     86.1371     12.7066     4.1574     23.3332       15727     86.1371     16.3477     7.4304     39.3159	17.5939
25571     86.1371     36.6171     8.0319     54.8128       20732     86.1371     12.7066     4.1574     23.3332       15727     86.1371     16.3477     7.4304     39.3159	09.4266
20732 86.1371 12.7066 4.1574 23.3332 15727 86.1371 16.3477 7.4304 39.3159	14.3267
15727 86.1371 16.3477 7.4304 39.3159	15.1105
10.0477 7.4304 39.3159	9.0825
160///1 06 03201 50 5500/	13.5947
16962 95 0942 00.1030 76.5861	22.0020
23060 95 0204 0.5052 0.2045 28.2084	13.7644
2153 95 7720 900000 44.3083	10.8900
10544 95 7720 250.250 45.1231 220.9612 1	23.1106
29.0009 431.7080	65.7848
7.1300	22.4439
15310 95 6000 7.1250 51.8690	12.9006
2412 95 0470 0.9779 56.7156	15.2127
05770 05000 025.1376 1	04.2356
50 05 5050 33.3067 100.7589	60.1974
17602 05 5140 07.7702 5.5508 91.3499	24.6679
30530 61.2944 7.7884 44.4666	18.2384
20330 65.5140 35.1599 9.6132 11.9589	22.6823
<u>21808</u> 85.3583 113.1301 31.5776 217.3893	93.2963
455 85.3583 3398.0386 634.4508 4996.0023 106	39.3956
13423 65,3063 57.2618 11.3319 97.6164	39.0480
37.6693 8.3923 20.4105	11.3700
24522 85.3063 8.8614 7.9366 27.5777	12.2626
17427 85.2025 323.6780 57.0555 221.4037 6	35.8713
17303 85.2025 33.7866 2.8455 41.9456	9.1403
162 84.9429 20.8002 17.6035 42.5670	23.7219
10108 84.8910 91.7666 10.7510 63.6700 3	27.1232
22355 84.7871 16.5914 5.3296 31.9805	12.8094
3799 84.6833 248.9998 58.6310 384.0977 1	5.4912
1025 84.5275 10.6336 5.2061 33.1574	21.1802
2464 84.5275 32.8120 3.7668 39.8959	3.1058
1024 84.4237 21.5096 7.3160 44.4910	8.9310
10510 84.4237 231.8057 17.9081 245.7739 6	9.5059
8515 98.3385 195 2183 33.1208 516 7584 13	9.8226
1831 97.3001 61.1163 13.5200 103.4300	5.5834
26150 97.0924 239.4870 199.4131 3011.7153 108	3.3834
1687 97.0405 641.7103 593.6589 4468.7838 177	11.661

in pointe(s).	48, 144 hrs	1.5	f. 44921-5090-01-WO/21054		
GC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
19358		378.9000	312.7266		
3390		98.0716			947.31
1689		1657.4481	1651.1974	9093.2905	32.87
17832		753.9386	718.7494	5637.5942	4046.84
7120		3.4607	7.5661		2321.10
11375	95.9502	47.0950	6.7258	52.6522	27.15
5422	95.9502	255.9669	15.3339	101.4006	31.78
5549	95.6906	171.8383	14.2889	447.6795	137.34
6276	95.6386	16.9686	15.6448	272.7479	88.21
12796	95.6386	-12.9629	11.2831	103.0190	46.18
2962	95.5348	59.8316		41.7692	26.88
8612	95.5348	0.2689	8.6970	117.4927	32.22
2424	95.4829	744.0810	6.9976	46.0127	28.39
23288	95.3271	162.0457	64.6463	456.9711	109.41
14594	95.2233	37.3820	22.1140	272.3246	62.05
5710	95.1194		25.3448	-20.8144	26.61
17892	94.9637	64.4711	7.2831	115.7780	29.50
2657	94.9117	74.1322	32.9001	496.0090	309.03
23096	94.8598	404.4319	47.1948	214.9007	86.218
4954	94.8079	303.9404	28.8283	106.0388	116.08
8712	94.7560	75.8566	48.3559	300.5078	120.210
10070		93.8463	20.1516	10.3414	49.358
17917	94.7040	34.6609	9.5241	79.8852	30.340
5433	94.6521	94.8277	47.9334	-207.1858	165.704
1830	94.6521	48.3568	7.0044	97.6852	36.022
3952	94.5483	21.8907	8.9622	91.8654	47.123
12426	94.3406	142.5596	15.2222	220.9986	49.233
	94.2368	36.4587	34.9450	-53.9307	40.685
15108	94.2368	33.5728	7.3179	75.1760	24.193
5890	94.0810	144.1226	16.6702	237.2963	56.832
7447	93.8733	54.7359	9.9771	104.1249	
7698	93.6656	74.4883	11.5063	149.5131	30.759
16335	93.6137	88.6708	40.5413	266.6131	47.244
4779	93.5618	40.2461	5.2003	66.4230	136.840
3352	93.5099	721.7098	75.5300	447.0117	17.359
10171	93.5099	91.0491	22.1459		132.927
8103	93.4579	-7.6890	9.1160	180.0318	47.287
15160	93.3541	87.2868	16.4703	54.2286	37.728
16034	93.3541	109.7919	25.9816	213.1044	92.622
3899	93.3022	60.4683	21.0169	218.6182	58.232
21364	93.1983	72.5470	39.8668	-11.5877	35.878
6176	93.1983	38.5042		262.2539	123.565
9521	93.1464	55.8598	16.9291	124.2971	49.3222
2075	93.0426	44.3953	9.0144	91.8144	22.2810
19214	92.8349	127.8322	8.3172	89.0395	28.0498
14842	92.7830		22.3277	37.8946	63.380
22187	92.7830	49.3027	12.6519	102.6669	39.3891
21782	92.6791	409.4556	129.1747	867.5699	267.7624
9352	92.6791	38.6721	27.8222	122.8371	47.2701
8039	92.6791	378.4376	53.4050	552.6199	96.8881
10453		68.3052	18.3267	140.0283	49.5285
11408	92.6272	53.9392	16.4808	132.5562	49.1075
5095	92.6272	32.4582	18.6918	129.4645	55.9234
2093	92.6272	416.0853	28.8365	567.1313	110.1052

iiiiepoint(s):	sphamideCore 48, 144 hrs		Alty. F	Ref. 44921-5090-0	1-WO/21054
LGC ID	LDA Score	Mean Tox	SD Tox		SD Nontox
9554	92.5753	10.7001	14.8696		33.83
3265		41.5882		98.6859	36.912
3637	92.3676	15.1582	7.5334	41.6123	22.40
1685	92.3157	3767.8787	3620.3845	16237.8222	9744.370
22405	92.3157	133.8187	32.5703	238.9619	
7264	92.2638	27.2209	10.8354	72.6050	59.602
16686	92.2118	118.8172	33.9194	234.5096	47.798
6737	92.1080	177.6041	46.8049	85.4628	69.112
2526	92.1080	236.0059	26.3307	326.7278	68.492
8557	92.1080	124.4789	33.6220	298.5563	58.830
10690	92.1080	26.9454	4.5462		128.668
22480	92.1080	67.8894	14.8504	6.3091	18.215
5990	92.0561	483.3228	40.6774	144.3945	51.040
6496	92.0042	91.6501	25.0566	361.6884	71.592
21889	91.9522	72.4361	17.2609	188.0613	55.046
23092	91.9003	276.9497	35.3796	128.0111	31.245
5726	91.8484	47.5982	14.2846	396.4401	70.107
8158	91.8484	213.3934		92.5981	28.661
10277	91.8484	25.4588	48.7506	403.2356	114.786
3781	91.7445	-8.0857	9.4491	82.9826	42.347
4750	91.6926	129.3269	12.0879	30.3861	26.314
17552	91.6926	54.2706	39.4346	255.8295	84.718
22708	91.6926	165.1820	13.2305	100.7306	33.800
19159	91.6407		16.0246	252.7250	71.8390
12805	91.6407	347.2374	57.9407	243.3276	58.7902
2492	91.5888		10.1198	12.1679	53.7118
22308	91.5888	191.2070	34.7816	110.1686	42.634
5595	91.5369	311.2068	57.2959	130.6294	104.9578
5370		133.1074	12.8488	188.8985	46.4980
0070	91.5369	44.2783	20.8570	134.8288	63.6771

99.2761 99.2244 99.0693 98.2420 98.0869	242.5684		Mean Nontox 553.2170	SD Nontox
99.2244 99.0693 98.2420 98.0869	242.5684			
99.0693 98.2420 98.0869				108.973
98.2420 98.0869	1262 3600			26.236
98.0869			38.3062	
	364.6776		726,0715	
	686.0406		147.0226	81.717
97.9835	61.2730	11.9914	142.6882	
97.7249	191.1688	54.1307	61.7710	35.495
97.2079	109.6054	9.1395	202.5150	37.390
97.1562	93.4938	32.8141		51.977
	2107.4202	138,5598	1374 1080	17.526
	2286.4682	205.9736		298.224
	438.1068			242.075
				121.646
96.8459				348.745
96.8459	660.1966			273.4053
96.7425				184.9369
96.7425				180.1810
			537.7136	142.781
	43 1530			182.4209
				7.9904
				132.1563
				23.1224
				53.8512
		6.8639		17.6908
				390.8094
96 3289				77.0161
96 3280	1195 6250			62.0223
	3600 5440			157.0759
96 1220				595.1392
	1000.2712		994.3579	218.0367
				130.9204
	1151.5/24		559.6657	202.5750
	1612.5846		1149.1016	189.6771
			176.4112	33.5751
95.9152		187.6344	1018.6373	243.3853
			1308.2477	293.8709
		161.8414		225.7358
		7.0280		36.0667
		15.3955		21.8637
		4.6504		28.4901
		17.2852		51.8349
		1.2320		21.6870
		83.5885		155.8400
		18.4361		45.8032
	1127.9196			
	42.7394			152.9382
95.5533	91.0126			9.6285
95.5016	1825.4132			29.1854
95.4498				257.0082
95.4498				32.1467
95.3981				97.2775
95.3981				266.3647
				195.1788
	97.0527 97.0010 97.0010 96.8459 96.8459 96.8459 96.7425 96.7425 96.6908 96.6391 96.6391 96.4840 96.4823 96.3806 96.3289 96.3289 96.3289 96.3289 96.1220 96.1220 96.1220 96.1220 96.1620 95.7601 95.7601 95.7601 95.7601 95.7601 95.7601 95.7084	97.0527 2107.4202 97.0010 2286.4682 97.0010 438.1068 96.8459 2397.1246 96.8459 660.1966 96.7425 1309.2228 96.7425 950.2598 96.6908 841.4074 96.6391 1006.5474 96.4840 168.2388 96.4840 76.8508 96.3806 2701.6484 96.3806 253.3670 96.3289 77.1716 96.3289 1185.6356 96.2254 3600.5110 96.1220 1291.4320 96.1220 1291.4320 96.1220 1291.4320 96.1220 1151.5724 96.0186 1612.5846 96.0186 120.3262 95.9152 1572.3148 95.7601 2047.7910 95.7601 1918.3926 95.7601 1918.3926 95.7084 111.4202 95.7084 76.1978 95.7084 76.1978 95.5533 1127.9196 95.5533 91.0126 95.5533 91.0126 95.553981 193.3960 95.4498 193.3960 95.4498 193.3960 95.4498 193.3960 95.4498 193.3960 95.4498 193.3960	97.0527 2107.4202 138.5598 97.0010 2286.4682 205.9736 97.0010 438.1068 58.9423 96.8459 2397.1246 164.5055 96.8459 2430.0154 191.4842 96.8459 660.1966 91.9345 96.7425 1309.2228 111.2494 96.7425 950.2598 158.6988 96.6908 841.4074 37.9755 96.6391 43.1530 7.8137 96.6391 1006.5474 52.0540 96.4840 168.2388 26.2737 96.4840 76.8508 7.7156 96.3806 2701.6484 298.5475 96.3289 77.1716 18.0621 96.3289 1185.6356 179.4987 96.2254 3600.5110 873.6649 96.1220 1536.2712 135.8295 96.1220 1291.4320 87.5453 96.1220 1151.5724 181.5847 96.0186 1612.5846 102.2626 96.0186 120.3262 8.1327 95.9152 1572.3148 187.6344 95.7601 2047.7910 178.7334 95.7601 1918.3926 161.8414 95.7601 2047.7910 178.7334 95.7601 123.1492 7.0280 95.7084 76.1978 4.6504 95.7084 76.1978 4.6504 95.5533 1127.9196 97.1354 95.5533 1127.9196 97.1354 95.5533 91.0126 16.1662 95.59152 1572.3148 18.4361 95.5533 1127.9196 97.1354 95.5533 1127.9196 97.1354 95.5533 91.0126 16.1662 95.5016 1825.4132 196.0255 95.4498 193.3960 50.6143 95.4498 411.4880 45.1926 95.3981 2157.4994 150.2386 95.3981 2157.4994 150.2386 95.3981 1409.5814 104.8654	97.0527 2107.4202 138.5598 1374.1089 97.0010 2286.4682 205.9736 1515.4745 97.0010 438.1068 58.9423 701.2188 96.8459 2397.1246 164.5055 1484.6920 96.8459 660.1966 91.9345 1097.4267 96.7425 1309.2228 111.2494 796.0881 96.7425 950.2598 158.6988 537.7136 96.6391 43.1530 7.8137 18.5638 96.6391 1006.5474 52.0540 717.8472 96.4840 168.2388 26.2737 99.2782 96.4840 76.8508 7.7156 39.3922 96.3806 2701.6484 298.5475 1656.8293 96.3289 77.1716 18.0621 197.3083 96.3289 17.566.712 135.8295 994.3579 96.1220 1536.2712 135.8295 994.3579 96.0186 1612.5846 102.2626 1149.1016 96.0186 120.3262 8.1327 176.4112 95.7601 2047.7910 178.7334 1308.2477 95.7601 123.1492 7.0280 183.1607 95.7533 1127.9106 17.2852 212.2060 95.7533 1127.9106 17.2852 212.2060 95.5533 1127.9196 97.1354 18.4361 39.1802 95.5533 91.0126 16.1662 154.1554 95.5981 114.0984 193.3960 21.5775 95.5533 91.0126 16.1662 155.5959 95.3981 14.0986 45.1926 602.8949 95.3981 14.0986 15.2366 15.2366 15.2498 95.5981 14.0986 15.2366 15.2366 15.2498 95.5981 11.400.5814 104.8654 970.9436

GCID	LDA Score	Mean Tox	SD Tox	Moon Nonte	000
14959	95.2947	1152.2914			SD Nontox
10109	95.2947	1758.3110			
21377	95.1913	166.6046		1264.7123	
18387	95.1913	1591.3322		99.7410	31.394
1876	95.1396	48.7360	135.0484	2366.1538	453.006
17374	95.1396	211.4694	3.7356	82.1938	24.382
17303	95.0879	28.4336	5.6650	273.8754	58.566
3027	95.0362	2264.5632	1.5918	41.9396	9.106
17815	94.9845	25.1606	150.9679	1608.7857	296.60
17217	94.9845	335.5012	7.0400	6.0317	8.29
18250	94.9328	2294.3592	7.1145	405.3749	80.932
1143	94.9328	83.5102	147.3030	1649.1933	321.130
23854	94.8294	1140.2992	5.9807	128.6649	30.269
2812	94.8294		146.7358	709.1314	172.454
20810	94.7777	57.9592 3017.1464	3.3591	89.9564	24.883
7593	94.7777		362.7701	2018.4821	406.702
1728	94.7777	107.9794	13.5568	65.6747	22.402
15052	94.7260	1063.3382	64.9909	1491.8039	266.120
23606	94.7260	4286.7688	739.8015	2732.5401	638.068
23783	94.7260	446.1930	36.8473	640.8500	109.27
4459	94.7260	296.0890	15.7047	404.1912	68.244
22	94.6743	23.8026	3.2653	43.7754	15.83
15303	94.6225	23.2500	8.8763	108.2320	102.499
21	94.5191	121.2882	11.3289	215.2800	56.666
24814	94.5191	25.0396	2.4980	62.7119	52.789
2008	94.5191	104.1916	8.7462	71.9542	16.631
18319	94.5191	40.3384	1.9517	62.5625	33.958
15202	94.5191	558.4844 1683.4932	27.1746	864.7216	243.374
17494	94.5191		138.6406	1015.8598	357.108
19244	94.4674	165.2608	10.1135	247.6753	54.033
21575	94.4674	2381.5768	137.5725	1810.0884	305.164
15486	94.3640	185.8712	7.1711	142.3836	30.579
10498	94.3640	15.8234 1997.8460	0.7048	26.0108	16.051
16023	94.3123		323.6599	1376.3590	271.747
15468	94.2606	1098.3534 1764.6184	62.6343	1591.1177	334.184
18305	94.2606	3179.0632	146.7957	1309.5903	219.738
20178	94.2606		379.2372	2113.8723	463.918
15626	94.2089	24.0734	5.5628	-2.6341	30.958
18606	94.2089	2696.1736	223.2380	1808.3848	402.071
18386	94.2089	1187.2666	93.6190	822.6851	177.205
11384	94.2089	1463.4778	250.1575	2274.2335	449.128
15201	94.1055	30.5094	0.8177	33.3866	11.048
12058	94.1055	3246.1558	357.7373	2274.4849	449.278
15335	94.0538	129.6848	4.0030	101.1381	38.158
21840	94.0538	890.1394	89.1651	618.3418	136.274
20582		369.6284	22.7713	525.3803	122.981
5049	93.8469	325.5276	35.9961	493.2211	97.770
15136	93.8469	509.5548	31.1298	737.5654	170.586
19456	93.7435	1629.6028	243.9665	1070.6605	271.541
22592	99.0693	298.1502	177.2594	1.7645	27.091
	98.9659	758.3822	153.9430	200.7379	132.343
4048	98.8108	683.6852	414.7907	15.8348	54.817
4049	98.6556	1077.9050	555.8633	38.8703	101.879

Timepoint(s): 24 hrs Atty. Ref. 44921-5090-01-WO/2105								
4207		Mean Tox	SD Tox	Mean Nontox	SD Nontox			
2296	98.3454			122,1165				
11893	98.2937			119.8422				
	98.0352			3.6850				
2125	97.9317		244.5406					
16753	97.9317	228.0646	109.3065		0010			
7650	97.8800	336.5038	126.0327	104.0033	64.203			
16394	97.8283	1953.5320	301.7161	776.7555	39.0348			
24040	97.7766	978.5796	315.0650	371.7175	285.1212			
8058	97.7249	518.1870	64.7283	315.9890	128.616			
4232	97.7249	507.8808	143.7363	185.4600	54.8417			
21500	97.6732	302.2368	83.4080		77.570			
22556	97.5181	73.0724	20.5771	88.8370	88.7562			
22223	97.4147	52.9336	7.9327	20.3416	14.8252			
6691	97.4147	347.9868	74.7675	223.7111	108.7679			
4967	97.3630	88.9172	20.1806	156.4936	49.8047			
4491	97.3113	153.5246	56.1239	36.4109	41.2124			
14776	97.3113	288.4110		46.1077	27.4902			
13539	97.3113	183.1240	18.9884 55.3367	444.9225	80.9918			
3903	97.2596	34.9996		74.3225	25.9366			
17826	97.0010	41.9274	41.3641	-126.2066	69.6649			
23498	97.0010	224.7006	21.5602	4.8398	9.9495			
16203	96.9493	78.9488	18.7019	366.4700	165.6921			
18	96.9493	163.0158	12.7853	139.5266	48.7555			
3505	96.9493	201.4542	11.9147	87.7965	33.5906			
24038	96.8976	512.3702	43.7494	-34.7538	122.1253			
18296	96.8976		127.4492	214.5274	78.1911			
2888	96.7942	264.4690	9.2486	176.4902	54.0493			
14960	96.7425	572.6298	56.5113	985.9715	212.4677			
10269	96.4840	2827.0198	325.2308	1623.3914	445.4860			
20845	96.4323	3223.7554	534.9910	1981.1927	399.6866			
8339	96.3806	756.6490	199.2139	283.6651	204.3095			
8729	96.2771	67.1254	3.5227	109.8235	26.8107			
4670	96.2254	37.7988	23.4009	-26.2680	25.5023			
16496	96.2254	651.6486	37.0112	968.8950	197.5406			
19778	96.2254	1007.5318	80.5526	662.3587	140.2810			
16584		162.7704	19.4915	96.6441	28.4757			
7213	96.1737	206.5866	43.5278	99.5119	41.5816			
19458	96.1220	982.3286	81.0719	596.6911	156.4134			
13934	96.1220	175.6176	45.8215	81.8809	28.5183			
2173	96.0703	-9.7620	18.9704	108.1365	52.0482			
11157	96.0703	6108.5984	663.8294	3420.8716	1129.3754			
23173	96.0186	1426.7052	70.8267	1973.4101	332.9831			
6808	96.0186	2830.0816	416.7392	1561.9613	463.9543			
21927	96.0186	633.8266	119.9903	355.8146	97.7043			
	95.9669	986.1244	93.9318	636.1205	133.3608			
10919	95.9152	2262.2648	491.2299	842.8495				
18507	95.8635	845.7300	91.6336	509.8879	664.3673			
19379	95.8635	483.4050	16.0720	371.4526	133.9074			
20046	95.8118	36.0804	13.2519	9.6159	67.5500			
11864	95.8118	53.4336	6.5507	86.2261	8.6421			
22171	95.7601	459.3624	3.3321	481.9651	22.5507			
4858	95.7601	26.0362	6.4666	-26.1668	81.2899 33.6523			

imepoint(s): SLGC ID	24 hrs		Atty. Ref. 44921-5090-01-WO/21054			
	LDA Score	Mean Tox	SD Tox		SD Nontox	
1977	99.2761		19.9468			
17383	99.2244		60,2422	9.3550	100.07	
23651	99.0693	1262.3600	965.5064	38.3062	20.20	
18308	98.2420	364.6776	43.3971	726.0715		
20589	98.0869	686.0406	217.7915	147.0226		
18190	97.9835	61.2730	11.9914	142.6882	81.71	
20869	97.7249	191.1688	54.1307		35.49	
12118	97.6215	1593.8502	366.4674	61.7710	37.39	
15003	97.2079	499.7730	126.9177	541.2085	291.01	
20862	97.2079	109.6054	9.1395	94.5838	190.89	
15002	97.1562	640.5422	115.1965	202.5150	51.97	
25801	97.1562	93.4938	32.8141	207.6172	187.09	
20872	97.0527	2107.4202	138.5598	34.2978	17.52	
15876	97.0010	2286.4682	205.9736	1374.1089	298.224	
20855	97.0010	438.1068	58.9423	1515.4745	242.075	
815	96.8459	2397.1246		701.2188	121.646	
24886	96.8459	2430.0154	164.5055	1484.6920	348.745	
20856	96.8459	660.1966	191.4842	1650.1080	273.405	
22321	96.7425	579.0476	91.9345	1097.4267	184.936	
9620	96.7425	1309.2228	242.9531	172.2432	91.830	
13974	96.7425	950.2598	111.2494	796.0881	180.181	
9240	96.6908	841.4074	158.6988	537.7136	142.781	
18881	96.6391	42.4500	37.9755	1171.9326	182.420	
25702	96.6391	43.1530	7.8137	18.5638	7.990	
17586	96.4840	1006.5474	52.0540	717.8472	132.156	
15867	96.4840	168.2388	26.2737	99.2782	23.122	
17481	96.4323	76.8508	7.7156	39.3922	53.851	
16918	96.3806	44.0366	6.8639	8.6432	17.690	
468	96.3806	2701.6484	298.5475	1656.8293	390.809	
18307	96.3289	253.3670	4.6985	335.6019	77.016	
2109	96.3289	77.1716	18.0621	197.3083	62.022	
18569	96.2254	1185.6356	179.4987	756.7138	157.0759	
20743		3600.5110	873.6649	1593.1738	595.1392	
15135	96.2254	103.6790	6.8918	155.0261	28.0319	
4222	96.1220	1536.2712	135.8295	994.3579	218.0367	
13647	96.1220	1291.4320	87.5453	980.3590	130.9204	
5667	96.1220	1151.5724	181.5847	559.6657	202.5750	
3244	96.0186	1612.5846	102.2626	1149.1016	189.6771	
16847	96.0186	120.3262	8.1327	176.4112	33.5751	
17159	95.9152	1577.3310	112.3690	1115.1014	190.3333	
17100	95.9152	1572.3148	187.6344	1018.6373	243.3853	
17729	95.7601	2047.7910	178.7334	1308.2477	293.8709	
18025	95.7601	1918.3926	161.8414	1323.1157	225.7358	
23888	95.7601	123.1492	7.0280	183.1607	36.0667	
21076	95.7084	111.4202	15.3955	56.8814	21.8637	
	95.7084	76.1978	4.6504	123.0470		
1523	95.7084	122.9916	17.2852	212.2060	28.4901	
15510	95.6567	189.7192	13.2887	281.2798	51.8349	
690	95.6567	44.4970	1.2320	43.1497	54.4113	
13646	95.6050	946 2256	83 5885	577.1178	21.6870	
14966	95.6050	116.9316	18.4361		155.8400	
15387	95.5533	1127.9196	97.1354	39.1802	45.8032	
7594	95.5533	42.7394	8.6206	765.4720	152.9382	

imepoint(s):				00-01-WO/210548	
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
20056 24885	95.5533	91.0126		154.1554	29.185
	95.5016	1825.4132		1170.4232	257.008
23889	95.4498	193.3960		94.2180	
17380	95.4498		45.1926	602.8949	97.277
20839	95.3981	2157.4994	150.2386	1521.6955	266.364
25686	95.3981	1409.5814	104.8654	970.9436	195.1788
17379	95.3981	300.4482	20.9956	439.7134	98.9308
14959	95.2947	1152.2914	74.7831	802.2623	158.5034
10109	95.2947	1758.3110	118.9654	1264.7123	227.5776
21377	95.1913	166.6046	15.3011	99.7410	31.3940
18387	95.1913	1591.3322	135.0484	2366.1538	453.0061
1892	95.1396	2186.4372	487.7466	1210.5009	391.5950
1876	95.1396	48.7360	3.7356	82.1938	24.3829
17374	95.1396	211.4694	5.6650	273.8754	58.5667
17303	95.0879	28.4336	1.5918	41.9396	9.1066
3027	95.0362	2264.5632	150.9679	1608.7857	296.6061
17815	94.9845	25.1606	7.0400	6.0317	8.2944
17217	94.9845	335.5012	7.1145	405.3749	80.9328
18250	94.9328	2294.3592	147.3030	1649.1933	321.1304
1143	94.9328	83.5102	5.9807	128.6649	30.2698
23854	94.8294	1140.2992	146.7358	709.1314	172.4544
2812	94.8294	57.9592	3.3591	89.9564	24.8832
20810	94.7777	3017.1464	362.7701	2018.4821	406.7029
7593	94.7777	107.9794	13.5568	65.6747	22.4021
1728	94.7777	1063.3382	64.9909	1491.8039	266.1204
15052	94.7260	4286.7688	739.8015	2732.5401	638.0684
23606	94.7260	446.1930	36.8473	640.8500	109.2710
23783	94.7260	296.0890	15.7047	404.1912	68.2440
4459	94.7260	23.8026	3.2653	43.7754	15.8319
22	94.6743	23.2500	8.8763	108.2320	102.4995
15303	94.6225	121.2882	11.3289	215.2800	56.6663
21	94.5191	25.0396	2.4980	62.7119	52.7892
24814	94.5191	104.1916	8.7462	71.9542	16.6319
2008	94.5191	40.3384	1.9517	62.5625	33.9581
18319	94.5191	558.4844	27.1746	864.7216	243.3743
15202	94.5191	1683.4932	138.6406	1015.8598	357.1087
17494	94.5191	165.2608	10.1135	247.6753	54.0337
19244	94.4674	2381.5768	137.5725	1810.0884	305.1647
21575	94.4674	185.8712	7.1711	142.3836	
15486	94.3640	15.8234	0.7048	26.0108	30.5794 16.0510
10498	94.3640	1997.8460	323.6599	1376.3590	271.7471
16023	94.3123	1098.3534	62.6343	1591.1177	
15468	94.2606	1764.6184	146.7957	1309.5903	334.1844
18305	94.2606	3179.0632	379.2372	2113.8723	219.7387
20178	94.2606	24.0734	5.5628	-2.6341	463.9186
15626	94.2089	2696.1736	223.2380	1808.3848	30.9588
18606	94.2089	1187.2666	93.6190	822.6851	402.0718
าชีวี86	94.2089	1463.4778	250.1575	2274.2335	177.2054
19456	99.0693	298.1502	177.2594	1.7645	449.1281
22592	98.9659	758.3822	153.9430	200.7379	27.0914
4048	98.8108	683.6852	414.7907	15.8348	132.3437 54.8179
4049					

GLGC ID	24 hrs LDA Score	Mean Tox	Atty. Ref. 44921-5090-01-WO/21054			
4207			SD Tox	Mean Nontox	SD Nontox	
2296	98.3454 98.2937				40.9110	
11893				119.8422	39.066	
2125	98.0352	180.3784		3.6850	39.7708	
16753	97.9317	488.2134		109.2617	87.0160	
7650	97.9317	228.0646	109.3065	-5.2427	64.2031	
16394	97.8800	336.5038		104.0033	39.0348	
24040	97.8283	1953.5320	301.7161	776.7555	285.1212	
8058	97.7766	978.5796	315.0650	371.7175	128.6161	
4232	97.7249	518.1870	64.7283	315.9890	54.8417	
21500	97.7249	507.8808	143.7363	185.4600	77.5704	
6606	97.6732	302.2368	83.4080	88.8370	88.7562	
22556	97.5181	5040.9788	864.8078	1862.0365	743.3288	
22223	97.5181	73.0724	20.5771	20.3416	14.8252	
6691	97.4147	52.9336	7.9327	223.7111	108.7679	
4967	97.4147	347.9868	74.7675	156.4936	49.8047	
	97.3630	88.9172	20.1806	36.4109	41.2124	
4491	97.3113	153.5246	56.1239	46.1077	27.4902	
14776	97.3113	288.4110	18.9884	444.9225		
13539	97.3113	183.1240	55.3367	74.3225	80.9918	
15004	97.2596	972.5216	213.6666	334.0647	25.9366	
3903	97.2596	34.9996	41.3641	-126.2066	270.6975	
4074	97.0527	-0.9616	3.5722	63.0220	69.6649	
17826	97.0010	41.9274	21.5602	4.8398	44.5968	
23498	97.0010	224.7006	18.7019	366.4700	9.9495	
16203	96.9493	78.9488	12.7853	139.5266	165.6921	
18	96.9493	163.0158	11.9147	87.7965	48.7555	
3505	96.9493	201.4542	43.7494	-34.7538	33.5906	
24038	96.8976	512.3702	127.4492	214.5274	122.1253	
18296	96.8976	264.4690	9.2486	176.4902	78.1911	
2888	96.7942	572.6298	56.5113	985.9715	54.0493	
14960	96.7425	2827.0198	325.2308		212.4677	
21796	96.5874	546.7450	109.0500	1623.3914	445.4860	
10269	96.4840	3223.7554	534.9910	267.5819	90.7752	
20845	96.4323	756.6490	199.2139	1981.1927	399.6866	
8339	96.3806	67.1254	3.5227	283.6651	204.3095	
8729	96.2771	37.7988	23.4009	109.8235	26.8107	
4670	96.2254	651.6486	37.0112	-26.2680	25.5023	
16496	96.2254	1007.5318	80.5526	968.8950	197.5406	
19778	96.2254	162.7704	19.4915	662.3587	140.2810	
16584	96.1737	206.5866	43.5278	96.6441	28.4757	
7213	96.1220	982.3286	81.0719	99.5119	41.5816	
19458	96.1220	175.6176	45.8215	596.6911	156.4134	
13934	96.0703	-9.7620	18.9704	81.8809	28.5183	
2173	96.0703	6108.5984	663.8294	108.1365	52.0482	
11157	96.0186	1426.7052	70.8267	3420.8716	1129.3754	
23173	96.0186	2830.0816	416.7392	1973.4101	332.9831	
6808	96.0186	633.8266	119.9903	1561.9613	463.9543	
21927	95.9669	986.1244		355.8146	97.7043	
10919	95.9152	2262 2648	93.9318	636.1205	133.3608	
18507	95.8635	845.7300	491 2299	842.8495	664.3673	
19379	95.8635	483.4050	91.6336	509.8879	133.9074	
20046	95.8118	36.0804	16.0720	371.4526	67.5500	
		30.0604	13.2519	9.6159	8.6421	

Timepoint(s):		<u> </u>	Att	0-01-WO/2105485	
Grec id	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
11864		53.4336	6.5507	86.2261	22.5507
22171	331.331	459.3624	3.3321	481.9651	81.2899
4858	95.7601	26.0362	6.4666	-26.1668	33.6523

imepoint/s	ISOPROTERE	ENOL	Att	y. Ref. 44921-509	0-01-WO/210548
LGC ID		Mean Tox	SD Tox		
12978	98.7552			Mean Nontox	SD Nontox
15353	98.7552			76.0207	44.163
10071	98.7033			18.8333	
15191	98.5996	2781.0180		261.6078	96.512
18597	98.4959		387.0119	163.7317	512.074
21663	98.4440		190.0962	91.7173	49.738
21654	98.4440	1334.9931	249.2728	374.6519	167.296
923		611.2753	171.5647	201.7092	64.949
18349	98.4440	90.8740	16.6163	16.7889	18.427
15189	98.4440	478.1215	106.8624	173.0242	57.020
	98.4440	1742.6363	442.7734	328.3733	338.774
5297	98.3921	615.3920	146.7141	202.9419	86.020
355	98.3921	144.1484	66.8185	9.0417	
19085	98.3402	105.9926	7.1071	51.9125	25.8332
14213	98.3402	81.8985	39.5920	5.9781	13.531
15349	98.3402	33.7044	5.1757	5.5100	18.6993
606	98.1846	51.3164	25.3613	-42.5922	7.7175
9423	98.1328	553.7720	184.8660		30.7423
23871	98.0809	97.1849	16.2049	164.9800	70.6014
17908	98.0290	175.6236	70.8006	41.7192	22.3572
24235	97.7178	502.2883	120.4755	43.3557	32.3530
16168	97.6660	419.3260		200.2612	69.1510
23868	97.6141	878.2495	99.7763	174.7149	51.2477
4407	97.4585	149.4351	232.1880	212.7525	223.4270
21445	97.3548	101.0935	30.5043	76.4713	20.9009
16248	97.3548		31.3816	10.1848	21.8312
12580	97.2510	137.3399	55.4662	59.6988	28.2691
21063	97.0954	39.1018	3.7604	19.4473	9.3645
2555	96.9917	269.1979	68.9186	138.1918	40.8935
15580		102.6296	18.5182	45.7962	22.3728
21657	96.8880	20.8356	3.6311	57.5401	27.3956
857	96.5249	1417.1173	72.5551	952.3487	227.6092
12031	96.1100	28.9336	7.8593	10.3651	7.6321
	95.9025	122.3580	16.6208	79.3065	16.2251
13420	95.8506	741.9540	177.3292	447.9899	
21975	95.6950	379.2371	82.7804	179.8726	97.0308 77.7814
18654	94.9170	91.0856	22.2450	218.8543	
22670	94.9170	87.7800	10.8918	58.5102	64.7382
15372	94.8133	276.3340	31.1240	196.9995	22.1820
23166	94.5539	174.9606	35.0933	108.1004	35.3333
21772	94.5021	31.5186	6.3787		29.0997
17217	94.1390	220.3939	63.2378	53.9458	13.9213
20461	93.5166	39.6906	11.3937	406.5476	79.2552
1495	93.2054	58.7065	13.0068	86.3883	45.2957
20702	93.1017	62.6646	15.8674	97.8139	21.3675
6980	93.0498	73.5706		150.4033	64.8806
12364	92.7386	78.0485	20.6392	148.6863	42.9104
22406	92.5311		30.5955	150.6970	39.5405
15190	92.2977	32.1614	7.8468	71.1168	25.7014
1609	92.2977	1513.5051	492.4513	233.0620	318.7829
11114		2384.3983	748.6648	861.9603	250.1131
18695	92.2459	107.3391	45.4225	30.9844	37.0615
23872	92.2459	186.5778	60.9505	34.3160	37.8180
11258	92.1940	254.0449	68.2202	53.3226	76.4607
11200	92.1421	76.6668	51.8112	7.9910	23.7166

rimepoint(s GLGC ID	ISOPROTERI ): 3, 6 hrs		Atty. Ref. 44921-5090-01-WO/21054				
		Mean Tox	SD Tox	Mean Nontox	SD Nontox		
24431	92.0902		51.7590	75.3299			
357	92.0384		56.3783		74.67		
24219	91.9865		165.0733	293.2780	14.85		
8664	91.9346	449.4940	184.1137	121.8197	76.06		
79	91.9087		13.4528		232.34		
2629	91.7790	79.7505		46.8587	17.66		
23869	91.6234	191.3961		21.0142	16.11		
2628	91.6234	50.0411		41.5583	60.33		
13930	91.5716	341.2365		9.9134	14.53		
16081	91.4678	283.1665	71.6150	109.7446	63.80		
16173	91.4678	135.4999	115.5643	86.3178	64.810		
21653	91.4678	256.8784	47.5480	12.7211	22.29		
15558	91.2863	400.9904		115.5382	39.511		
24234	91.2604	178.7678		284.1459	67.055		
17301	91.2344	244.7880		76.5083	31.217		
1171	91.1826	12.3360	65.1023	503.6495	155.368		
19086	91.1566	182.9205	7.3422	42.4541	18.249		
3337	90.9751	32.8491	84.7158	74.4652	25.867		
15618	90.9492	170.6329	7.7769	56.5652	15.757		
5384	90.8973	221.5421	45.1415	99.3937	20.205		
25264	90.8973	227.0814	77.2111	41.6013	55.697		
21683	90.8454		69.5155	87.0662	38.034		
16080	90.7936	148.5981	40.5336	48.4630	35.207		
15708	90.6898	127.7414	44.5598	16.1566	40.045		
21682	90.6380	37.3911	38.2594	5.3283	17.907		
19481	90.6120	52.7226	24.3565	-9.6802	55.438		
20735	90.5861	60.8750	24.6242	130.6872	42.407		
13005	90.5861	206.9780	37.1741	101.6782	47.8880		
6478	90.5861	40.8021	15.7360	18.3284	7.085		
1146	90.5083	25.7568	8.7839	5.2883	15.542		
15299	90.4305	44.9031	8.1407	26.2567	11.3719		
244	90.3786	197.4190	65.7521	89.0845	56.6466		
4327		156.3640	46.9174	62.8042	43.9511		
1844	90.3786	167.6989	32.2599	91.1153	27.1878		
15301	90.3786	273.3641	60.0557	161.2621	33.1657		
21696	90.2749	275.3141	71.8896	99.3702	83.5499		
23715	90.1712	248.2800	45.9105	148.8757	35.6262		
11530	90.1712	50.0364	19.5135	9.8703	25.3169		
1742	90.1193	574.8966	215.2208	208.9971	171.5733		
18396	90.0674	92.4420	22.6140	32.5742			
	90.0156	120.3561	28.1293	42.0418	21.6654		
21709	89.8081	404.6953	99.5321	253.0117	30.9956		
18389	89.7562	2201.3679	666.7713	822.4031	57.5390		
19040	89.7562	479.3534	100.1299	253.0582	450.9286		
20981	89.6784	7.4018	4.3907	22.2741	74.9023		
11940	89.6006	45.3046	7.7585	25.0555	10.9001		
16871	89.4450	36.4405	7.8425	83.1332	8.4377		
11153	89.3932	810.0581	106.9252	466.5159	23.8242		
25770	89.3932	312.4753	89.7107	158.6471	161.7207		
15051	99.0664	443.4744	120.1727		58.7619		
14380	99.0145	109.7573	20.4326	118.1688	105.2816		
15212	98.9627	247.3969	36.9788	393.4073	117.0146		
11522	98.9527	578.4656		55.3243	36.9133		

TABLE 5Y: Timepoint(s GLGC ID	): 3, 6 hrs			Atty. Ref. 44921-5090-01-WO/21054			
		Mean Tox	SD Tox	Mean Nontox	SD Nontox		
10837	98.8071		78.4539				
3278	98.8071	657,2108	312.5556		36.85		
22197	98.7552	318.3303	41.7592		63.96		
9452	98.7552	2066,7979	515.2685	111.0003	47.292		
12979	98.6515	1450,3701	617.2876		195.987		
6632	98.5996	264,5670	28.3884	307.5710	166.267		
23005	98.5996	429,3003	118.3420	123.5062	41.064		
16631	98.5996	454.1945	144.2120	92.8878	61.399		
12999	98.5477	2114.0113	468.0488	63.0882	68.994		
13634	98.5477	1799.7813	262.5017	323.5830	261.273		
22311	98.5477	430.7144	129.7666	816.4888	202.096		
21632	98.5477	635.4675	93.9765	141.0606	46.354		
23038	98.5477	223.4274	94.5228	199.9939	94.638		
16053	98.4959	688.2729	332.0089	19.4000	121.866		
23165	98.4959	511.6118	163.8996	114.3908	65.961		
10020	98.4959	245.6274	41.4642	162.7842	66.525		
11873	98.3921	526.2920	199.8569	116.6828	99.394		
13633	98.3921	720.9066	85.3469	146.4113	112.825		
4725	98.3921	702.0448	322.4170	341.2228	109.875		
12581	98.2884	104.9441	11.7630	82.7935	80.903		
2459	98.2884	1557.5773	429.6716	46.5185	19.338 <sup>-</sup>		
22667	98.2365	195.3284	32.8641	118.6922	268.2199		
3823	98.1846	801.3471	113.8072	57.9737	39.4160		
22666	98.1846	237.1916	41.8806	367.7490	92.1859		
9583	98.0290	311.3110	95.8546	77.8696	37.2347		
8477	97.9772	1390.6749	243.1126	75.2475	55.2575		
20035	97.9253	475.5420	132.6227	591.4111	173.1700		
657	97.8734	486.1475	140.5853	167.5188	63.9564		
3014	97.8216	67.7219	140.3853	223.6214	55.7424		
21019	97.8216	90.2080	23.1470	250.0182	74.2719		
. 4285	97.8216	162.4419	16.7173	30.2218	21.6609		
2708	97.7697	1175.8810	20.6060	304.2127	62.7546		
22248	97.7178	884.1129	187.4086	654.7607	118.6857		
22596	97.6660	118.2271	234.6878	357.8314	137.9962		
23567	97.5104	182.7065	12.3468	69.8706	18.3731		
5442	97.4585	144.7093	33.4229	45.1516	63.5584		
22939	97.4066	-22.5254	59.1476	432.4571	111.2343		
13460	97.3548	163.2601	16.7130	77.9927	39.0291		
5461	97.1992	270.5833	30.5731	334.8609	66.5139		
22378	97.0954	125.3759	66.6813	117.8721	40.8380		
22711	97.0954	131.2524	37.6062	272.2137	61.3862		
3434		2080.6321	15.0016	230.5375	46.7545		
11325	96.7842	18.5315	375.1512	754.8197	380.5227		
14094	96.5249	62.1649	6.2871	67.2413	34.5907		
2519	96.4730	115.4741	6.0106	101.0184	19.5343		
7493	96.4212	180.9653	15.6764	66.6505	20.7364		
7451	96.4212	550.1054	38.9298	78.5313	34.8173		
4861	96.4212		54.2374	375.8753	61.5990		
22247	00.000	86.1575	14.1922	174.6200	46.5278		
3738	96.3174	414 7075	169.8130	585.7927	159.2645		
12233	96.3174		62.2:5C	214.5883	63.7076		
	20.0177	226.4356	57.4500	105.7821	47.8050		

imepoint(s):	3, 6 hrs			Ref. 44921-5090-	U 1-VVO/210548
SLGC ID		Mean Tox	SD Tox		ISD Nove
20448	98.7552				SD Nontox
12978	98.7552		148.1483		
15353	98.7552	81.3138		76.0207	44.163
10071	98.7033	821.1028		18.8333	
15191	98.5996	2781.0180	387.0119	261.6078	
20449	98.5477	998.4564		163.7317	512.074
18597	98.4959	499.5431	497.2317	98.8724	167.855
21663	98.4440	1334.9931	190.0962	91.7173	49.738
21654	98.4440	611.2753	249.2728	374.6519	167.296
923	98.4440	90.8740	171.5647	201.7092	64.949
18349	98.4440	478.1215	16.6163	16.7889	18.427
15189	98.4440	1742.6363	106.8624	173.0242	57.020
5297	98.3921	615.3920	442.7734	328.3733	338.774
355	98.3921	144.1484	146.7141	202.9419	86.020
19085	98.3402	105.9926	66.8185	9.0417	25.833
14213	98.3402		7.1071	51.9125	13.531
15349	98.3402	81.8985	39.5920	5.9781	18.699
606	98.1846	33.7044	5.1757	5.5100	7.717
9423	98.1328	51.3164	25.3613	-42.5922	30.742
23871	98.0809	553.7720	184.8660	164.9800	70.601
17908	98.0290	97.1849	16.2049	41.7192	22.357
17161		175.6236	70.8006	43.3557	32.353
15002	98.0290	899.1763	458.1172	200.9148	106.066
15002	97.9253	1147.2365	305.9131	202.0650	167.614
6477	97.8734	1127.1396	424.1492	88.1165	165.131
24235	97.7697 97.7178	28.2950	13.0796	4.5515	17.652
16168		502.2883	120.4755	200.2612	69.151
23868	97.6660	419.3260	99.7763	174.7149	51.247
17401	97.6141	878.2495	232.1880	212.7525	223.427
4407	97.4585	1283.2069	160.7080	602.9406	233.527
21445	97.4585	149.4351	30.5043	76.4713	20.900
16248	97.3548	101.0935	31.3816	10.1848	21.8312
12580	97.3548	137.3399	55.4662	59.6988	28.269
	97.2510	39.1018	3.7604	19.4473	9.364
11531	97.1992	1234.1090	315.0112	403.7401	287.920
21063	97.0954	269.1979	68.9186	138.1918	40.8935
2555	96.9917	102.6296	18.5182	45.7962	22.3728
15580	96.8880	20.8356	3.6311	57.5401	27.3956
574	96.7324	1198.1129	265.6557	601.0594	148.9908
21657	96.5249	1417.1173	72.5551	952.3487	227.6092
857	96.1100	28.9336	7.8593	10.3651	7.6321
12031	95.9025	122.3580	16.6208	79.3065	16.2251
13420	95.8506	741.9540	177.3292	447.9899	97.0308
21975	95.6950	379.2371	82.7804	179.8726	77.7814
18654	94.9170	91.0856	22.2450	218.8543	64.7382
22670	94.9170	87.7800	10.8918	58.5102	
15372	94.8133	276.3340	31.1240	196.9995	22.1820
23166	94.5539	174.9606	35.0933	108.1004	35.3333
21772	94.5021	31.5186	6.3787	53.9458	29.0997
17217	94.1390	220.3939	63.2378	406.5476	13.9213
29461	93.5166	39.6906	11.3937		79.2552
1495	93.2054	58.7065	13.0068	86.3883	45.2957
20702	93.1017	62.6646	15.8674	97.8139	21.3675

TABLE 5Z: Iso Timepoint(s):	3, 6 hrs		Atty. Ref. 44921-5090-01-WO/210548			
SLGC ID	LDA Score	Mean Tox		Mean Nontox		
6980		73.5706			SD Nontox	
12364	92.7386	78.0485		148.6863		
22406	92.5311	32.1614		150.6970		
20743	92.4274	105.6991		71.1168	25.70	
15190	92.2977	1513.5051	15.2831	155.1691	27.93	
1609	92.2977	2384.3983	492.4513	233.0620	318.78	
11114	92.2459	107.3391	748.6648	861.9603	250.11	
18695	92.2459	186.5778	45.4225	30.9844	37.06	
23872	92.1940	254.0449	60.9505	34.3160	37.81	
11258	92.1421	76.6668	68.2202	53.3226	76.46	
24431	92.0902	246.7884	51.8112	7.9910	23.71	
357	92.0384	131.7186	51.7590	75.3299	74.672	
24219	91.9865	700.8180	56.3783	24.7360	14.85	
8664	91.9346	449.4940	165.0733	293.2780	76.064	
79	91.9087	12.5920	184.1137	121.8197	232.348	
2629	91.7790	79.7505	13.4528	46.8587	17.662	
23869	91.6234	191.3961	28.9873	21.0142	16.118	
2628	91.6234	50.0411	43.7164	41.5583	60.332	
13930	91.5716	341.2365	22.4365	9.9134	14.536	
16081	91.4678	283.1665	123.7107	109.7446	63.807	
16173	91.4678	135.4999	71.6150	86.3178	64.810	
21653	91.4678	256.8784	115.5643	12.7211	22.291	
15558	91.2863	400.0004	47.5480	115.5382	39.511	
24234	91.2604	400.9904 178.7678	54.7628	284.1459	67.055	
17301	91.2344	244.7880	52.1777	76.5083	31.217	
1171	91.1826	12.3360	65.1023	503.6495	155.368	
19086	91.1566	182.9205	7.3422	42.4541	18.249	
3337	90.9751	32.8491	84.7158	74.4652	25.867	
15618	90.9492	170.6329	7.7769	56.5652	15.757	
5384	90.8973	221.5421	45.1415	99.3937	20.205	
25264	90.8973	227.0814	77.2111	41.6013	55.697	
21683	90.8454		69.5155	87.0662	38.0346	
16080	90.7936	148.5981	40.5336	48.4630	35.2076	
15708	90.6898	127.7414 37.3911	44.5598	16.1566	40.0453	
21682	90.6380		38.2594	5.3283	17.9073	
19481	90.6120	52.7226	24.3565	-9.6802	55.4380	
20735	90.5861	60.8750 206.9780	24.6242	130.6872	42.4070	
13005	90.5861	40.8021	37.1741	101.6782	47.8880	
6478	90.5861	25.7568	15.7360	18.3284	7.0857	
1146	90.5083	44.9031	8.7839	5.2883	15.5425	
17735	90.4824	2633.2529	8.1407	26.2567	11.3719	
15299	90.4305	197.4190	624.1825	1096.1175	562.1722	
244	90.3786	156.3640	65.7521	89.0845	56.6466	
4327	90.3786		46.9174	62.8042	43.9511	
1844	90.3786	167.6989 273.3641	32.2599	91.1153	27.1878	
15301	90.2749	275.3641	60.0557	161.2621	33.1657	
21696	90.1712		71.8896	99.3702	83.5499	
23715	90.1712	248.2800	45.9105	148.8757	35.6262	
15051	99.0664	50.0364	19.5135	9.8703	25.3169	
14380	99.0145	100 7572	120.1727	118.1688	105.2816	
15212	98.9627		20.4326	393.4073	117.0146	
11522	98.9627	247.3969	36.9788	55.3243	36.9133	
	00.3021	578.4656	132.9934	132.2183	69.5679	

imepoint(s): SLGC ID					-01-WO/21054	
			SD Tox		SD Nontox	
10837			78.4539	83.4558		
3278		657.2108	312.5556	98.5710		
22197		318.3303	41.7592	117.6359		
9452		2066.7979	515.2685	256.7530		
12979		1450.3701	617.2876			
6632		264.5670	28.3884	307.5710	166.26	
23005	98.5996	429.3003	118.3420	123.5062	41.06	
16631	98.5996	454.1945	144.2120	92.8878	61.39	
12999	98.5477	2114.0113	468.0488	63.0882	68.99	
13634	98.5477	1799.7813	262.5017	323.5830	261.27	
22311	98.5477	430.7144	129.7666	816.4888	202.09	
21632	98.5477	635.4675	93.9765	141.0606	46.35	
23038	98.5477	223.4274	94.5228	199.9939	94.63	
16053	98.4959	688.2729		19.4000	121.86	
23165	98.4959	511.6118	332.0089	114.3908	65.96	
10020	98.4959	245.6274	163.8996	162.7842	66.52	
11873	98.3921	526.2920	41.4642	116.6828	99.39	
13633	98.3921		199.8569	146.4113	112.82	
4725	98.3921	720.9066	85.3469	341.2228	109.87	
18830	98.3402	702.0448	322.4170	82.7935	80.90	
12581	98.2884	7951.0865	1512.4960	3660.0327	894.62	
2459	98.2884	104.9441	11.7630	46.5185	19.33	
22667		1557.5773	429.6716	118.6922	268.21	
3823	98.2365	195.3284	32.8641	57.9737	39.410	
22666	98.1846	801.3471	113.8072	367.7490	92.18	
9583	98.1846	237.1916	41.8806	77.8696	37.23	
8477	98.0290	311.3110	95.8546	75.2475	55.25	
15004	97.9772	1390.6749	243.1126	591.4111	173.170	
22432	97.9253	1643.2824	595.2255	326.5114	242.775	
	97.9253	247.4485	31.3929	123.2399	35.002	
20035	97.9253	475.5420	132.6227	167.5188		
657	97.8734	486.1475	140.5853	223.6214	63.956	
3014	97.8216	67.7219	23.1470	250.0182	55.742	
21019	97.8216	90.2080	16.7173	30.2218	74.271	
4285	97.8216	162.4419	20.6060	304.2127	21.660	
20086	97.7697	672.3814	66.6413	325.3166	62.754	
2708	97.7697	1175.8810	187.4086	654.7607	119.278	
21796	97.7178	588.2593	92.7064		118.685	
22248	97.7178	884.1129	234.6878	266.3687	88.326	
22596	97.6660	118.2271	12.3468	357.8314	137.996	
23567	97.5104	182.7065	33.4229	69.8706	18.373	
5442	97.4585	144.7093	59.1476	45.1516	63.558	
22939	97.4066	-22.5254	16.7130	432.4571	111.234	
13460	97.3548	163.2601	30.5731	77.9927	39.029	
5461	97.1992	270.5833	66 6040	334.8609	66.513	
22378	97.0954	125.3759	66.6813	117.8721	40.838	
22711	97.0954	131.2524	37.6062	272.2137	61.3862	
3434	97.0436	2080.6321	15.0016	230.5375	46.754	
11325	96.7842	18.5315	375.1512	754.8197	380.5227	
14094	96.5249	62.1649	6.2871	67.2413	34.5907	
4420	96.5249	250 2045	6.0106	101.0184	19.5343	
2519	96.4730	259.2045	27.0460	447.5475	93.3492	
7493	96.4212	115.4741	15.6764	66.6505	20.7364	
	00.72 12	180.9653	38.9298	78.5313	34.8173	

TABLE 5Z: Iso Timepoint(s):	3, 6 hrs_ 👉	T.	Atty. I	Ref. 44921-5090-	01-WO/2105485
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
7451			54.2374		
4861	96.4212	86.1575	14.1922		41.0000
22247		1014.8936			1 .0.0210
3738	96.3174	414.7075			100.2010
12233	96.3174				30.7070
	3010111	220.7000	37.4500	105.7821	47.8050

Timepoint(s	: MINOXIDIL ): 24, 360 hrs		Atty.	Ref. 44921-5090-0	1-WO/2105
GLGC ID	LDA Score	Mean Tox	SD Tox		٠. ٠.,
17159	97.9296			Mean Nontox	SD Nontox
13486	94.7205			1018.2949	243.6
19101	92.5983				24.20
4739	92.3395	86.8648		204.4361	48.12
18352	91.7184	1509.5612		57.5600	18.14
17257	91.4596	489.6277		1119.9762	225.62
20889	89.9068	409.02//	39.4658	363.6353	115.51
19077	89.8551	191.0543	22.3705	290.7158	82.00
653	89.8033	104.0118	22.2276	64.1095	30.69
22306	89.8033	58.0272	12.7224	113.7814	42.16
20519	89.6480	118.8083	6.6397	97.5426	27.78
2114	89.5445	247.3042	32.4829	184.0616	41.43
278		102.2935	19.1370	63.3928	27.23
24849	89.3375	28.2742	1.4531	21.2334	10.48
23481	89.1304	57.0278	15.2284	26.7227	
	88.6128	180.5617	37.1558	279.0484	18.96
15247	88.3540	594.1170	90.9858	1036.0101	69.06
4556	88.3023	57.4057	5.5534	73.5059	387.37
4447	88.2505	6.5295	4.3706	22.5996	14.24
21830	88.1988	22.2358	13.4090	6.4232	11.67
22845	87.9917	972.4108	249.9982	663.3576	13.26
14004	87.9917	6.1840	3.9783		133.73
1496	87.8882	38.5365	3.3711	20.6089	11.33
19279	87.7329	148.6213	8.3623	30.4905	10.167
24329	87.6294	177.1675	35.5945	175.1188	22.89
3446	87.6294	21.0733	5.0581	115.9628	50.313
22584	87.6294	27.7973	1.6250	35.2549	11.390
1324	87.2153	461.6210	49.8053	30.4191	13.565
16217	87.1118	3824.9220	882.7480	604.8895	117.967
15049	87.1118	4504.9502	852.5258	2319.0562	624.046
1323	87.1118	74.5447		3170.1238	567.333
18499	87.0600	149.7308	34.6738	184.6947	78.309
18317	86.8530	266.9008	36.8585	84.3176	23.557
24232	86.7495	107.0823	101.6113	637.2423	290.561
17136	86.6977	765.2605	23.2712	53.3905	21.713
15203	86.5424		188.8314	518.4444	370.799
15767	86.5424	209.2850	18.7806	175.4825	31.284
20619	86.5424	153.3083	19.9098	214.1710	51.918
24470	86.4907	8.4417	3.6252	22.0994	13.333
638	86.3872	5199.1175	1173.8016	3543.3523	655.670
20704	86.2836	220.1460	41.7079	154.1979	27.601
38		55.3490	10.3700	38.4184	13.407
1495	86.2836 86.2836	39.8378	5.5516	26.8456	15.667
8597		78.0432	7.0184	97.6129	21.6056
16220	86.1284	196.5925	21.7031	158.7965	41.788
3015	86.0248	3307.8400	955.9316	1861.1020	637.3267
15273	85.7660	3456.6195	319.6428	2832.5081	571.035
25802	85.7660	7.8428	8.3445	41.9616	33.9196
24676	85.7143	870.9612	173.0430	599.6281	
15050	85.6625	78.1665	66.5388	29.2018	153.6135
15052	85.6625	2988.2460	1447.5559	2738.9965	42.2911
6425	85.6625	133.3380	19.8127	171.6206	641.1183
24854 20243	85.6108		3057.9794	5883.6151	37.1599
ンロンオタモ	85.6108	102.1265	13.6846	10000.01011	2004.8095

ABLE SAA: MINOXIDIL  imepoint(s): 24, 360 hrs  LGC ID   LDA Score   Mean Tox   SD Tox   Mean Nontox   SD Nontox								
18066	85.6108			Mean Nontox	SD Nontox			
4748	85.5590	29.1457 10.3340	2.4528	21.0001	10.58			
23347	85.5072		6.7481	44.5435	44.79			
25743	85.4555	51.3743	12.1529	75.7981	18.37			
225	85.4555	10896.4638	3468.3621	6169.2740	2236.33			
13723	85.4037	118.1477	6.9233	100.7150	24.01			
18400		5941.5757	1135.6019	4146.5143	930.03			
15693	85.4037 85.3520	23.9422	3.9205	35.5996	11.72			
19053		41.9673	17.0293	11.3160	12.65			
18175	85.3520	7254.8842	1634.9432	4760.8397	1174.87			
7125	85.3520	1215.6852	370.8997	1104.2417	184.18			
	85.3002	6166.8172	1368.3779	4046.9460	1056.819			
16135	85.2484	10911.3320	3922.1706	5965.1645	2441.773			
2008	85.2484	27.9260	9.9940	62.6626	33.89			
20579	85.2484	297.5433	17.8361	330.2801	72.314			
25470	85.1967	48.7750	31.1751	113.5910				
15829	85.0932	9.4337	4.3052	51.1893	50.217			
492	85.0932	278.1547	97.2279	204.4257	73.598			
17160	85.0414	2458.4503	584.9161	1701.4877	142.375			
15688	85.0414	20.8720	10.3842	3.8851	418.373			
2006	85.0414	15.7493	11.3731		12.581			
1426	84.9896	138.3758	10.2143	48.6313	34.383			
14694	84.8861	8305.6658	1969.5601	164.7051	26.762			
1473	84.8344	55.8370	61.7688	5139.4218	1603.578			
20856	84.8344	894.7287	94.8152	87.6367	37.779			
574	84.7826	891.9672	157.5993	1096.4226	186.974			
457	84.7826	248.1988		604.1970	157.970			
8417	84.7826	6221.1195	59.0873	158.7303	42.870			
21715	84.7826	22.1428	1255.4826	4274.3303	1041.592			
19962	84.7826	226.9462	13.6070	16.2253	8.161			
17146	84.7826		21.9785	185.0458	47.117			
12349	84.7308	-18.3883 10182.5327	21.4537	25.1069	46.368			
14973	84.6791		2968.3730	6241.6225	2082.299			
20554	84.6791	-6.8377	19.9513	35.9551	37.245			
16476	84.6273	95.3840	10.5063	75.2273	36.995			
18761		8890.1327	2400.0048	5819.3897	1786.933			
1352	84.5756	280.9035	65.6858	183.3302	52.572			
15106	84.5756	29.7100	6.0583	42.8774	11.5999			
22567	84.4720	2774.0492	1085.5440	2609.7190	530.2224			
17039	84.4203	126.3540	15.3602	99.1372	25.0108			
16017	84.3685	289.4128	117.4056	481.3267	112.7896			
18956	84.3685	134.7493	10.8127	116.8148	30.173			
	84.3685	127.6873	13.5706	174.9933	58.0411			
1852	84.3168	3436.9930	678.2439	2513.5506	495.5841			
23895	84.2650	- 26.6828	4.2999	17.5019	8.6704			
25679	84.2650	1560.7147	84.3130	1414.3321	275.4721			
1502	84.2133	42.7670	3.5109	53.1598				
7602	84.1615	686.2697	64.4793	525.7856	20.5090			
15343	84.1615	116.0975	11.6612	141.1608	87.1102			
23585	84.1097	32.9085	23.8997		26.3964			
19006	94.7205	1785.7690	198.2123	26.0858	10.7947			
8815	94.2547	388.5740	27.2 <del>5</del> 50	1058.7331	328.0473			
11723	93.9441	55.8792	10.0073	259.0826	76.3901			
15365	93.8923	1108.1207	10.0073	4.4362	31.9769			

GC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	CD North
2088	92.9607				SD Nontox
22691	92.6501	1390.9820	238.5001	307.2277 919.3204	85.776
14869	92.1325	123.3242	6.6322		239.780
16984	92.1325	329.9662	62.9378	88.7640 602.8346	36.095
6168	92.0807	76.9700	5.1471		177.131
19004	91.8219	1833.6993	213.7395	53.9067 1107.2121	19.369
4177	91.7702	322.1253	33.4508	486.6640	448.308
20632	91.6149	91.8260	37.3026	192.7485	117.977
13427	91.2526	4.5580	12.9423	23.9666	55.438
2541	90.8903	67.8027	17.9265	24.7398	12.530
2534	90.8385	28.0445	4.0410	47.2322	26.413
9806	90.4762	10.4643	11.4493	34.3519	13.723
12298	90.3209	86.3223	32.0470		14.886
17013	90.2174	85.4747	9.4603	161.8749	46.419
13627	90.0104	75.7057	5.4585	122.4431	30.668
8039	89.8033	183.8938	14.1961	55.9724	31.314
9914	89.6998	-0.4020	34.7773	139.0876	49.822
8854	89.6480	67.5712	6.2645	72.2003	56.176
5421	89.5963	374.9627	38.3972	50.3999 283.4432	28.109
11791	89.5445	108.2222	7.7685		148.748
7842	89.5445	2.6935	8.9314	139.8817	32.949
12346	89.5445	472.4318	59.0587	25.5130 678.7885	14.743
2612	89.4410	36.9472	5.5990		440.234
13622	89.0787	375.5315	43.6054	57.8448 253.3860	17.553
5983	88.9752	311.8697	61.2478		94.445
18643	88.8716	239.7207	20.7273	585.0836 306.2247	201.781
22033	88.8716	132.9733	8.2770		60.999
5007	88.8716	572.3495	40.5614	174.4417	52.898
7011	88.7681	236.2587	24.5283	739.8550	164.160
12305	88.7164	184.9173	25.1616	327.1433	72.624
3904	88.5611	227.7152	28.3711	131.5672	39.8234
6649	88.5611	-10.8562	23.5637	135.5882 32.7590	94.2873
3836	88.5093	3826.9087	290.6592	2981.9296	148.9578
498	88.4576	888.2553	81.8895	700.3447	664.5439
17330	88.2505	91.7602	13.7975	59.3632	149.0531
7852	88.2505	106.6953	105.2722		23.0230
23027	88.1988	45.5408	2.7099	312.2733	70.4524
9305	88.0952	123.7258	5.2230	52.7099	36.7406
26114	87.9917	219.1497	24.9829	142.3025	30.6411
13928	87.9400	333.4505	72.3694	210.3639	119.0981
6455	87.8882	314.3333	78.4011	529.8971	149.5635
22942	87.8364	134.9742	30.7739	196.3007 193.5716	97.3929
22882	87.8364	100.1367	30.4959	165.3614	44.6292 46.6765

ABLE 5BB: M imepoint(s): 2	<u>4, 360 hrs</u>	,,,,		ef. 44921-5090-0	1-440/210548
FLGC ID	LDA Score	Mean Tox		Mean Nontox	ISD No.
17159	97.9296				SD Nontox
13486	94.7205	111.6373			
21239	94.3064	22.3625			
16426	93.7371	2794.4317			
20740	93.3230	658.5560			
21818	93.2195	67.1282		450.2627	144.344
19101	92.5983			35.9466	17.724
4739	92.3395	86.8648		204.4361	48.127
18352	91.7184			57.5600	18.140
17257	91.4596			1119.9762	225.624
25094	90.8903	180.9713		363.6353	115.517
22762	90.5797	16.6943		130.5678	45.941
15098	90.5797	40.3148		38.5006	16.728
20889	89.9068	40.3148		80.3784	48.073
19077	89.8551	191.0543		290.7158	82.005
653	89.8033	104.0118	22.2276	64.1095	30.695
22306		58.0272	12.7224	113.7814	42.1623
20519	89.8033	118.8083	6.6397	97.5426	27.7850
2114	89.6480	247.3042	32.4829	184.0616	41.4326
278	89.5445	102.2935	19.1370	63.3928	27.2316
	89.3375	28.2742	1.4531	21.2334	10.4896
4749	89.3375	118.0348	10.6809	199.1591	
24849	89.1304	57.0278	15.2284	26.7227	80.4388
24106	89.1304	16.5707	2.1016	27.3165	18.9685
15569	88.9752	515.0702	33.0112	450.4971	10.7777
23481	88.6128	180.5617	37.1558	279.0484	188.3790
15247	88.3540	594.1170	90.9858	1036.0101	69.0602
4556	88.3023	57.4057	5.5534		387.3794
4447	88.2505	6.5295	4.3706	73.5059	14.2452
21830	88.1988	22.2358	13.4090	22.5996	11.6781
22845	87.9917	972.4108	249.9982	6.4232	13.2608
14004	87.9917	6.1840	3.9783	663.3576	133.7391
18500	87.8882	417.7607	156.7008	20.6089	11.3367
2005	87.8882	15.2705		261.4327	60.1646
1496	87.8882	38.5365	9.9215	40.6188	18.0238
19279	87.7329	148.6213	3.3711	30.4905	10.1674
24329	87.6294	177.1675	8.3623	175.1188	22.8916
3446	87.6294		35.5945	115.9628	50.3133
22584	87.6294	21.0733	5.0581	35.2549	11.3903
1514	87.3706	27.7973	1.6250	30.4191	13.5657
1324	87.2153	350.3045	76.6199	236.9005	131.7093
16217	87.1118	461.6210	49.8053	604.8895	117.9678
15049	87.1118	3824.9220	882.7480	2319.0562	624.0469
22773		4504.9502	852.5258	3170.1238	567.3331
1323	87.1118	770.9792	186.8368	456.0336	110.1548
16130	87.1118	74.5447	34.6738	184.6947	78.3095
18499	87.0600	11743.3033	4153.6583	5911.3587	2296.0001
	87.0600	149.7308	36.8585	84.3176	23.5573
25319	86.9565	15949.7140	5786.8404	8021.2090	3356.7757
18317	86.8530	266.9008	101.6113	637.2423	
24232	86.7495	107.0823	23.2712	53.3905	290.5617
17136	86.6977	795.2 <del>88</del> 5	:88.8314	518.4444	21.7130
15203	86.5424	209.2850	18.7806	175.4825	370.7999
15767	86.5424	153.3083		170.4020	31.2844

C ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	en Na
20619	86.5424	8.4417			SD Nontox
24470	86.4907				
8641	86.4907				
25050	86.3872				
638	86.3872				1867.20
20704	86.2836			154.1979	27.60
38	86.2836			38.4184	13.40
1495	86.2836			26.8456	15.66
14983	86.1801		5866.9293	97.6129	21.60
17908	86.1801	14.8280	7.8844	7271.2874	3760.11
8597	86.1284		21.7031	44.6283	34.91
16220	86.0248		955.9316	158.7965	41.78
20848	86.0248	1885.2807	179.2060	1861.1020	637.32
18644	85.9213	6525.7058	2192.4313	1611.7709	278.30
600	85.9213	263.1263	18.4761	3783.2014	1348.42
3015	85.7660	3456.6195	319.6428	327.9509	63.14
15273	85.7660	7.8428	8.3445	2832.5081	571.03
16312	85.7660	36.0062	8.4127	41.9616	33.91
15886	85.7660	489.1110	29.4380	68.2350	37.35
21583	85.7143	649.1815	148.8583	405.7301	96.63
25802	85.7143	870.9612	173.0430	367.9905	122.349
24676	85.6625	78.1665	66.5388	599.6281	153.613
15052	85.6625	2988.2460	1447.5559	29.2018	42.29
6425	85.6625	133.3380	19.8127	2738.9965	641.118
19421	85.6108	10187.8595	2889.2061	171.6206	37.159
24854	85.6108	9986.6790	3057.9794	5515.1032	2050.075
20243	85.6108	102.1265	13.6846	5883.6151	2004.809
18066	85.6108	29.1457	2.4528	145.6152	39.49
4748	85.5590	10.3340	6.7481	24.3851	10.583
15185	85.5072	1365.5805	220.1448	44.5435	44.790
23347	85.5072	51.3743	12.1529	930.1042	185.448
25743	85.4555	10896.4638	3468.3621	75.7981	18.370
225	85.4555	118.1477		6169.2740	2236.334
25439	85.4037	9451.4727	6.9233 3142.0210	100.7150	24.014
13723	85.4037	5941.5757	1135.6019	5039.2187	2135.409
18400	85.4037	23.9422		4146.5143	930.037
15693	85.3520	41.9673	3.9205 17.0293	35.5996	11.721
19053	85.3520	7254.8842	1634.9432	11.3160	12.659
18175	85.3520	1215.6852	370.8997	4760.8397	1174.879
7125	85.3002	6166.8172	1368.3779	1104.2417	184.183
16135	85.2484	10911.3320	3922.1706	4046.9460	1056.819
2008	85.2484	27.9260	9.9940	5965.1645	2441.773
20579	85.2484	297.5433	17.8361	62.6626	33.895
16001	85.1967	15974.5118	5460.2030	330.2801	72.314
25470	85.1967	48.7750		8722.9676	3508.973
15829	85.0932	9.4337	31.1751	113.5910	50.217
21152	85.0932	13313.3515	4.3052	51.1893	73.598
25051	85.0932	10025.3403	3985.4397	7030.1502	2975.029
4330	99.6894	1252.8993	2691.1454	5378.7115	1991.535
14668	96.0145	112.8827	159.2015	451.2431	125.827
2757	95.5487	1366.7942	12.5993	59.0254	21.3859
19006	94.7205	1785.7690	213.6854	812.0674	245.092°
	200	1700.7090	198.2123	1058.7331	328.047

4, Souries	4 1,1		011 1 192 1 000020	Atty. Ref. 44921-5090-01-WO/21054			
LDA Score							
				SD Nontox			
93.9441				76.39			
				31 97			
93.8923		10071	1030.5675	215.30			
92,9607			2495.9422	667.42			
			307.2277	85.77			
				379.88			
			55.6612	29.25			
			919.3204	239.78			
				172.16			
		6.9909		27.74			
92 1325		6.6322	88.7640	36.09			
		62.9378	602.8346	177.13			
91 9772		5.1471		19.369			
91.8712		19.7930		53.298			
91 7703	1833.6993	213.7395	1107.2121	448.308			
	322.1253	33.4508		117.977			
	91.8260		192,7485	55.438			
91.3043			232.3437	95.291			
	4.5580	12.9423		12.530			
		17.9265		26.413			
	28.0445	4.0410		13.723			
90.6832	222.7068	17.6865	161.6796				
		11.4493		56.240			
		31.3499	429 4605	14.886			
	86.3223	32.0470		123.960			
		17.4882		46.419			
		9.4603	122 4431	75.755			
	75.7057	5.4585	55 9724	30.668			
89.8033		14.1961	139 0876	31.314			
89.6998		34.7773		49.8228			
89.6480	67.5712			56.1763			
	374.9627			28.1094			
	104.6767		154 3022	148.7481			
	712.2452			40.2828			
89.5445	108.2222			118.9825			
	2.6935			32.9493			
	472.4318		679 7905	14.7431			
	36.9472		57 9440	440.2343			
			252 2960	17.5537			
	311.8697	61.2478	595,0000	94.4454			
	239.7207		306.0036	201.7810			
88.8716				60.9991			
	572.3495			52.8980			
		24 5283		164.1606			
88.7164	184.9173			72.6244			
88.5611			131.56/2	39.8234			
88.5611				94.2873			
88.5093	3826.9087			148.9578			
	888.2553			664.5439			
88.2505				149.0531			
88.2505	106,6953			23.0230			
88.1988	156.8232	100.2127	312 2722	70.4524			
	94.2547 93.9441 93.8923 93.8923 92.9607 92.9089 92.8054 92.6501 92.6501 92.3913 92.1325 92.1325 92.0807 91.9772 91.8219 91.7702 91.6149 91.3043 91.2526 90.8903 90.8385 90.6832 90.4762 90.3727 90.3209 90.2174 90.2174 90.2174 90.2174 90.2174 90.2174 90.2174 90.2174 90.563 89.5963	Date	SECTION   SECTION   SPACE   SECTION   SECTIO	DA Score   Mean Tox   SD Tox   Mean Nontox   94.2547   388.5743   27.2550   259.0826   93.9441   55.8792   10.0073   4.4362   93.8923   1108.1207   492.5541   1030.5675   93.8923   3436.3307   405.7014   2495.9422   92.9607   485.9728   85.8473   307.2277   92.9089   2041.7307   65.2682   1674.6607   92.8054   36.3220   2.5840   55.6612   92.6501   1390.9620   238.5001   919.3204   92.6501   298.9320   9.0540   234.2646   92.3913   157.3257   6.9909   129.3154   92.1325   123.3242   6.6322   88.7640   92.1325   329.9662   62.9378   602.8346   92.0807   76.9700   5.1471   53.9067   91.9772   100.7265   19.7930   178.9038   91.8219   1833.6993   213.7395   1107.2121   91.7702   322.1253   33.4508   486.6400   91.3043   131.6897   19.9910   232.3437   91.2526   4.5880   12.9423   23.96666   90.8385   28.0445   4.0410   47.2322   90.8385   28.0445   4.0410   47.2322   90.8385   28.0445   4.0410   47.2322   90.8385   28.0445   4.0410   47.2322   90.8385   28.0445   4.0410   47.2322   90.8323   183.8938   14.1961   139.0876   90.2174   167.0213   17.4862   249.0241   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   90.2174   85.4747   9.4603   122.4431   89.5963   104.6767   14.1076   154.3923   89.5963   104.6767   14.1076   154.3923   89.5963   104.6767   14.1076   154.3923   89.5963   104.6767   14.1076   154.3923   89.5963   104.6767   14.1076   154.3923   89.5963   104.6767   14.1076   154.3			

TABLE 5BB: MinoxidilCore Tox Markers Atty. Ref. 44921-5090-01-WO/2105								
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox			
23027		45.5408						
23596		216.1497	32.2812	306.1806				
9305	- TO:0002		5.2230	142.3025				
20038	88.0952	135.2602	21.1150	199.3672	00.0111			
26114	87.9917	219.1497	24.9829	210.3639				
13928			72.3694	529.8971	149.5635			
6455	87.8882	314.3333		196.3007	97.3929			
18826	87.8882	683.4078	108.4593	1028.9475	264.7740			
22942	87.8364	134.9742	30.7739	193.5716	44.6292			
22882	87.8364	100.1367	30.4959	165.3614	46.6765			

GC ID	LDA Score ×	Mean Tox	Atty. Ref. 44921-5090-01-WO/210  SD Tox   Mean Nontox   SD Nontox			
20863	99.6904			Mean Nontox	SD Nontox	
17431	99.1228		1.2093			
21951	98.6584		1.4949			
17211	98.0392		0.1386	11.0014	18.0	
17648	97.9876	167.4683	23.7082	2036.3654		
17808	97.9360	1712.9783	0.6089	178.3401	43.2	
14983	97.9360	9490.9897	24.2555	1271.1624	255.7	
19411	97.8844		246.4261	7314.6962	3829.3	
20357	97.7812	100.8437	0.4210	112.6130	36.6	
10660	97.6780	41.3160	1.5967	92.4611	37.0	
20844	97.4200	71.1927	0.3765	68.2986	17.8	
17298	97.4200	2095.0633	27.4653	1583.7326	367.3	
2811	97.4200	197.8003	1.1728	202.4156	46.4	
16924	97.2136	54.3710	1.4083	86.9006	26.2	
23357		325.3807	6.4975	225.0529	107.43	
17991	97.1620	127.7170	1.0540	144.3015	32.4	
21801	97.0072	13.6307	0.6479	26.1271	9.25	
5049	97.0072	191.3690	1.7931	160.2509	36.77	
21087	96.9556	453.6563	28.9136	737.2678	170.47	
20746	96.8524	20.9507	0.6866	27.2381	320.91	
18221	96.8524	575.6373	6.1367	491.5957	121.82	
	96.5944	137.9597	2.3388	189.7786	52.65	
17757	96.5428	147.7873	1.3945	128.8930	28.27	
14924	96.4396	51.8627	1.3141	38.0575		
25643	96.1300	105.8687	1.0779	127.2940	24.11	
13489	95.9752	6.2677	1.7932	21.3974	27.85	
20386	95.7172	265.7490	2.9274	333.1644	9.14	
19768	95.7172	674.4197	8.5199	796.3149	84.50	
15996	95.6140	105.4843	2.2465	154.0898	122.85	
2812	95.6140	63.1260	1.6503	89.8743	79.17	
194	95.5624	24.1963	0.4803	19.9540	24.91	
2696	95.5624	1762.8073	31.4524	1422.2921	14.38	
16070	95.4592	50.8690	1.5166	71.7919	365.68	
20235	95.4592	37.5317	1.8408		28.58	
2632	95.4076	167.9587	1.6753	47.0293	26.55	
13647	95.3560	1105.3833	354.4977	186.7841	29.58	
571	95.3560	79.6580	3.0611	561.0303	204.23	
16001	95.3560	11808.5667	498.3945	97.1701	46.033	
15772	95.3044	20.7357	0.4255	8758.3158	3566.987	
16507	95.2012	102.8060	2.9377	25.8650	10.509	
15384	95.0464	26.9193	2.2940	144.1605	46.303	
15202	94.9948	1630.9773		48.4330	18.736	
19694	94.8400	35.2940	97.0261	1017.4003	358.399	
18076	94.7884	0.4443	1.0696	39.4846	18.536	
15450	94.7884	14.0293	1.5758	32.3208	28.913	
23343	94.7884	22.5627	0.5515	20.3809	6.577	
24644	94.6852	48.7800	0.8490	30.7679	10.133	
16292	94.5820		35.4267	59.7429	17.054	
14966	94.5820	55.0530	4.1845	23.2692	28.501	
25547	94.5304	92.8293	8.8838	39.4153	46.011	
17875	94.4788	260.6713	11.4421	355.9494	129.429	
20945	94.4788	20,1588	1.4421	2.7236	25.529	
15380		2040.6570	88.0696	1595.1554	294.262	
.0000;	94.4272	1863.6317	378.2755	935.9807	366.647	

imepoint(s	: NOREPINE ): 24 hrs	tty. Ref. 44921-50	Ref. 44921-5090-01-WO/210548		
LGC ID	LDA Score	Mean Tox	SD Tox	**	
17729	94.3756			Mean Nontox	SD Nontox
5050	94.3756		120.0020		
1299	94.3756		10.0703		120 79
20994	94.3756	138.7977			73.05
11350	94.3240				30.776
24609	94.2724		1.8216		29.990
20975	94.2724		0.8361	37.0927	240.428
16139	94.2208		6.9311	148.5012	
25110	94.2208		1.4153	140.0184	
19321	94.1692		2.2815	84.1086	16.126
25137	94.1692		2.7681	249.6174	41.825
1977	94.0144	25.3893	0.8747	34.1161	11.257
5837	94.0144	318.8380	83.1405	552.5388	109.770
13090		20.2693	20.7539	108.6565	64.804
19888	93.9628	75.7560	2.9234	99.2587	
18365	93.9628	183.8520	7.2264	133.6778	42.808
15911	93.9112	88.5537	2.3153	112.8918	51.278
	93.9112	134.4520	7.6642	194.2536	77.157
4615	93.8596	. 884.0333	50.4101	586.9161	44.994
4035	93.8596	79.2893	2.2117	89.5571	207.190
21989	93.8080	87.8107	1.1828		32.100
1283	93.7564	90.1383	2.9178	98.5063 110.1922	18.7718
25262	93.7564	44.5400	1.0002		40.4636
17653	93.7564	24.3393	0.6370	42.3342	14.5553
22499	93.7564	32.1947	2.0163	26.8303	11.6319
16715	93.7049	21.5823	1.3680	20.9150	12.1488
15761	93.6533	12.5080	2.4564	15.6291	12.6757
16382	93.6533	81.5550	2.0418	32.0276	15.4752
19152	93.6533	78.5820	1.4082	97.3052	31.9369
23083	93.6017	51.3330	1.3946	90.5775	21.3603
23486	93.5501	290.4820		55.2908	16.9676
12360	93.4985	35.1090	8.6006	378.9140	72.1118
20728	93.4985	699.3180	3.2411	60.0728	25.8807
21086	93.3953	60.6500	33.9924	915.6553	202.6830
20840	93.3437	101.9150	3.0185	87.2985	25.8805
16099	93.2921	512.4647	2.6021	91.4824	39.3794
15683	93.2405	79.7163	14.8688	429.8306	62.4877
:3400	93.1889		2.9852	102.8190	42.0203
25103	93.1373	483.1180	51.1795	316.1201	193.0789
17649	93.1373	87.7253	2.0728	65.0932	41.5711
23825	93.1373	192.8347	9.2057	262.4957	83.2930
9620	93.0857	57.1467	1.4480	63.5002	19.0013
9952	93.0857	1102.1280	83.6335	797.7883	183.0347
1097	93.0857	415.3687	15.3125	545.4961	105.7077
5014	93.0341	264.3353	8.4195	303.0990	100.2771
14504		23.0340	1.6781	43.0242	18.7763
20554	93.0341 92.9825	388.5153	24.7725	528.3181	118.3967
16361		64.9137	3.4897	75.3841	36.9748
17157	92.9825	28.3843	2.5207	44.7460	11.8878
22028	92.9825	107.4930	5.5723	80.0165	
12787	99.5872	13375.5767	47.8547	9974.9350	26.0867
	99.3808	37.6450	0.1778	53.1175	3731.3312
17662	99.0712	118.4780	2.1611	176.1766	15.6581
9466	98.9164	175.5210	1.9121	31.3618	35.6440

LGC ID	): 24 hrs		Atty. Ref. 44921-5090-01-WO/210548			
		Mean Tox	SD Tox	Mean Nontox	SD Nontox	
2360	98.8648		0.5882	219.7876		
16087	98.8132	67.8230	0.4857	100.7151	10.002	
7992	98.6584	127.6070	0.5441	139.5139	01:100	
16203	98.6068	85.3683	3.5578	139.3817		
5371	98.6068	23.7507	0.4097	10.4518	48.812	
8285	98.4520	90.8623	0.4857	95.7843		
12796	98.2972	38.0497	0.3103	41.2723		
24290	98.2972	90.5837	2.6147	361.6428	27.330	
16	98.1940	1822.0580	42.5386	1233.0724	374.602	
9114	98.1424	-8.5253	1.4263	31.4281	320.494	
11500	97.9360	671.5923	15.7799	465.7576	25.972	
21805	97.8844	480.5100	7.3892	343.1120	119.395	
6136	97.8328	47.2520	0.9249	66.0209	76.113	
21468	97.7812	-83.5257	5.4755		16.097	
15969	97.6780	280.0903	1.1936	44.3069	81.337	
19371	97.5748	65.2587	0.7805	311.6277	53.208	
26148	97.5748	44.5913	0.4646	89.8295	32.098	
5891	97.5232	110.9577	3.0678	43.9464	31.926	
23097	97.5232	89.0547	1.0120	40.5915	59.694	
15246	97.4716	46.4467	0.4743	70.6426	24.013	
13375	97.4716	4.4203	0.9991	53.2756	15.3668	
4911	97.4716	23.6933	0.9991	35.7215	22.1446	
16438	97.4716	635.3450		28.3943	14.1208	
2095	97.4716	93.3360	11.7897	472.8945	130.7109	
10614	97.4716	316.9750	1.4555	124.5051	25.6095	
9310	97.3684	91.8597	10.2247	136.9156	110.6099	
18212	97.3684	41.2213	1.0511	121.8552	36.8422	
12654	97.3684	112.8583	5.1671	-19.9520	34.9405	
22493	97.3684	256.6973	10.6705	234.9660	90.1942	
10302	97.3684	27.9787	1.8373	213.1873	56.4399	
6387	97.3168	70.9853	0.5209	17.3983	19.9656	
17642	97.2136	21.3120	0.3674	75.6112	15.3600	
22682	97.2136	23.4507	0.7327	43.6575	20.4405	
14202	97.1620	77.3710	0.9202	27.2053	31.3254	
21456	97.1620		1.1937	96.9214	35.6696	
19016	97.1104	22.3423	0.8300	7.7116	22.1473	
15091	97.0588	395.3907	7.3295	277.0878	74.8662	
20087	97.0072	99.1530	1.7515	138.2585	37.7845	
6712	96.9556	67.3520	0.6694	66.8587	27.1307	
2476	96.9040	169.7277	1.8176	189.1622	57.1238	
22707	96.8008	53.3413	0.8480	55.5428	32.4163	
7171	96.8008	17.7820	1.2756	42.3511	26.8561	
23703	96.6976	94.3337	1.2532	83.6124	30.5140	
24212	96.6976	31.0490	0.3480	29.0504	14.2729	
149	96.6976	2582.6843	21.4587	2283.2783	408.2796	
8423	96.6976	66.2783	0.8071	76.7152	15.8431	
14625		227.7503	3.3440	366.9388	292.2468	
9408	96.6976	68.5233	0.9441	81.2621	23.5113	
21825	96.5944	59.6917	1.7766	39.0365	17.3643	
21427	96.5944	56.4700	1.5143	88.3463	35.4890	
12828	96.4912	78.2120	i.3783	103.8133	29.5468	
20757	96.4396	57.7353	0.9357	66.8836	23.7075	
20/5/	96.3364	2414.1663	17.0973	2271.8254	32.7675 422.0171	

GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
24117	96.3364	26.6910	2.0888		
2675	96.3364				17.000
12778	96.2848			183.5233	
21500	96.2848		54.4652	89.4782	
16689	96.2332	104.0237	1.2517	108.6236	89.724
22595	96.2332	166.8360	2.7171	194.4342	
21264	96.2332	122.8987	1.7320	103.6940	42.3266
13741	96.1816	26.0263	0.3138	32.8458	20.7544
20327	96.1300	122.6457	1.3007	117.4239	17.8267
4189	96.0784	343.5817	2.9074	392.8493	39.8879
8959	96.0784	82.2207	1.8721	58.2600	91.935
7036	96.0784	90.0790	2.0404	113.9122	21.4847
4732	96.0784	165.0377	1.5663	187.3527	21.4538
8265	96.0784	118.6537	1.7219	90.1576	37.0863
5454	96.0784	32.1143	2.3840	14.5283	33.6246
15393	96.0268	270.5937	15.8566	187.4393	17.3022 42.2588
2208	96.0268	162.0793	6.7166	223.0357	44.7220
10685	96.0268	23.6977	0.5614	36.1425	
15085	95.9752	885.2107	4.7521	972.5390	15.1425 174.5670

epoint(s): 2	orepinephrine 24 hrs	•		Atty. Ref. 44921-509	0-01-11054
3C ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
20863		57,5080	1.2093		
17431	99.1228	474,9520	1.4949		
21951	98.6584	69.3167	0.1386		
17211	98.0392	2705.5817	23.7082	77.8674	
17648	97.9876	167.4683	0.6089	2036.3654	574.61
17808	97.9360	1712.9783	24.2555	178.3401	43.245
14983	97.9360	9490.9897	246.4261	1271.1624	255.719
19411	97.8844	100.8437		7314.6962	3829.344
20357	97.7812	41.3160	0.4210 1.5967	112.6130	36.626
10660	97.6780	71.1927	0.3765	92.4611	37.076
20844	97.4200	2095.0633	27.4653	68.2986	17.821
17298	97.4200	197.8003		1583.7326	367.353
2811	97.4200	54.3710	1.1728	202.4156	46.417
16924	97.2136	325.3807	1.4083	86.9006	26.212
23357	97.1620	127.7170	6.4975	225.0529	107.439
17991	97.0072	13.6307	1.0540	144.3015	32.450
21801	97.0072	191.3690	0.6479	26.1271	9.257
5049	96.9556	453.6563	1.7931	160.2509	36.770
21087	96.8524	20.9507	28.9136	737.2678	170.471:
20746	96.8524	575.6373	0.6866	27.2381	320.915
18221	96.5944	137.9597	6.1367	491.5957	121.8270
17757	96.5428		2.3388	189.7786	52.6548
14924	96.4396	147.7873	1.3945	128.8930	28.2779
25643	96.1300	51.8627	1.3141	38.0575	24.1160
13489	95.9752	105.8687	1.0779	127.2940	27.8507
17100	95.9236	6.2677	1.7932	21.3974	9.1426
20386	95.7172	1933.0853	99.4724	1310.1293	296.4873
19768	95.7172	265.7490	2.9274	333.1644	84.5056
15996	95.6140	674.4197	8.5199	796.3149	122.8559
2812	95.6140	105.4843	2.2465	154.0898	79.1755
194	95.5624	63.1260	1.6503	89.8743	24.9196
2696	95.5624	24.1963	0.4803	19.9540	14.3888
16070	95.4592	1762.8073	31.4524	1422.2921	365.6896
20235	95.4592	50.8690	1.5166	71.7919	28.5871
2632	95.4076	37.5317	1.8408	47.0293	26.5541
13647	95.3560	167.9587	1.6753	186.7841	29.5856
571	95.3560	1105.3833	354.4977	561.0303	204.2384
16001	95.3560	79.6580	3.0611	97.1701	46.0338
15772	95.3044	11808.5667	498.3945	8758.3158	3566.9879
16507	95.2012	20.7357	0.4255	25.8650	10.5094
15384	95.0464	102.8060	2.9377	144.1605	46.3039
15202	94.9948	26.9193	2.2940	48.4330	18.7361
19694	94.8400	1630.9773	97.0261	1017.4003	358.3999
18076		35.2940	1.0696	39.4846	18.5360
15450	94.7884	0.4443	1.5758	32.3208	28.9133
23343	94.7884	14.0293	0.5515	20.3809	6.5776
24644	94.7884	22.5627	0.8490	30.7679	10.1335
16292	94.6852	48.7800	35.4267	59.7429	17.0549
14966	94.5820	55.0530	4.1845	23.2692	28.5015
25547	94.5820	92.8293	8.8838	39.4153	46.0119
17875	94.5304	260.6713	11.4421	355.9494	129.4296
20945	94.4788	20.1533	1.4421	2.7236	25.5290
20340	94.4788	2040.6570	88.0696	1595.1554	294.2624

C ID	4 hrs LDA Score	Mean Tox	ISD TAV	Maca	
15380	94.4272			Mean Nontox	SD Nonto
17729	94.3756			935.9807	
5050	94.3756		125.5025		
1299	94.3756		15.9769	516.2596	
20994	94.3756			115.5967	73.0
11350	94.3240		2.4628	119.6022	30.
24609	94.2724		1.8216	63.4682	29.9
20975	94.2724		0.8361	37.0927	240.4
16139		97.1543	6.9311	148.5012	38.4
25110	94.2208	131.1017	1.4153	140.0184	32.8
19321	94.2208	66.0483	2.2815	84.1086	16.1
	94.1692	221.5020	2.7681	249.6174	41.8
25137	94.1692	25.3893	0.8747	34.1161	11.2
1977	94.0144	318.8380	83.1405	552.5388	109.7
5837	94.0144	20.2693	20.7539	108.6565	
13090	93.9628	75.7560	2.9234	99.2587	64.8
19888	93.9628	183.8520	7.2264	133.6778	42.8
18365	93.9112	88.5537	2.3153	112.8918	51.2
15911	93.9112	134.4520	7.6642	194.2536	77.1
4615	93.8596	884.0333	50.4101		44.9
4035	93.8596	79.2893	2.2117	586.9161	207.1
21989	93.8080	87.8107	1.1828	89.5571	32.1
1283	93.7564	90.1383	2.9178	98.5063	18.7
25262	93.7564	44.5400		110.1922	40.4
17653	93.7564	24.3393	1.0002	42.3342	14.5
22499	93.7564	32.1947	0.6370	26.8303	11.6
16715	93.7049	21.5823	2.0163	20.9150	12.1
15761	93.6533	12.5080	1.3680	15.6291	12.6
16382	93.6533		2.4564	32.0276	15.4
19152	93.6533	81.5550	2.0418	97.3052	31.9
23083	93.6017	78.5820	1.4082	90.5775	21.3
23486	93.5501	51.3330	1.3946	55.2908	16.9
12360		290.4820	8.6006	378.9140	72.1
20728	93.4985	35.1090	3.2411	60.0728	25.88
21086	93.4985	699.3180	33.9924	915.6553	202.68
20840	93.3953	60.6500	3.0185	87.2985	25.88
16099	93.3437	101.9150	2.6021	91.4824	39.37
	93.2921	512.4647	14.8688	429.8306	62.48
15683	93.2405	79.7163	2.9852	102.8190	42.02
16400	93.1889	483.1180	51.1795	316.1201	193.07
25103	93.1373	87.7253	2.0728	65.0932	41.57
17649	93.1373	192.8347	9.2057	262.4957	83.29
23825	93.1373	57.1467	1.4480	63.5002	
9620	93.0857	1102.1280	83.6335	797.7883	19.00
9952	93.0857	415.3687	15.3125	545.4961	183.03
1097	93.0857	264.3353	8.4195	303.0990	105.70
5014	93.0341	23.0340	1.6781		100.27
14504	93.0341	388.5153	24.7725	43.0242	18.77
20554	92.9825	64.9137	3.4897	528.3181	118.39
16361	92.9825	28.3843		75.3841	36.97
22028	99.5872	13375.5767	2.5207	44.7460	11.88
12797	99.3808	37.6450	47.8547	9974.9350	3731.33
17662	99.0712	118.4780	0.1778	53.1175	15.65
9466	98.9164		2.1611	176.1766	35.64
	00.0104	175.5210	1.9121	31.3618	134.62

C ID	LDA Score	Mean Tox	SD Tox	Man News	
2360	98.8648			Mean Nontox	SD Nontox
16087	98.8132	67.8230			
7992	98.6584				
16203	98.6068	1-110010		. 40.0100	42.586
5371	98.6068				48.812
8285	98.4520			10.4518	9.488
12796	98.2972	90.8623		95.7843	28.657
24290	98.2972	38.0497		41.2723	27.330
16	98.1940	90.5837 1822.0580	2.6147	361.6428	374.602
9114	98.1424			1233.0724	320.494
11500	97.9360	-8.5253	1.4263	31.4281	25.972
21805	97.8844	671.5923	15.7799	465.7576	119.395
6136	97.8328	480.5100	7.3892	343.1120	76.113
21468	97.7812	47.2520	0.9249	66.0209	16.097
15969	97.6780	-83.5257	5.4755	44.3069	81.337
19371		280.0903	1.1936	311.6277	53.208
26148	97.5748	65.2587	0.7805	89.8295	32.098
5891	97.5748	44.5913	0.4646	43.9464	31.926
23097	97.5232	110.9577	3.0678	40.5915	59.694
15246	97.5232	89.0547	1.0120	70.6426	24.013
	97.4716	46.4467	0.4743	53.2756	15.366
13375	97.4716	4.4203	0.9991	35.7215	22.144
4911	97.4716	23.6933	0.2376	28.3943	14.120
16438	97.4716	635.3450	11.7897	472.8945	130.710
2095	97.4716	93.3360	1.4555	124.5051	25.609
10614	97.4716	316.9750	10.2247	136.9156	110.609
9310	97.3684	91.8597	1.0511	121.8552	36.842
18212	97.3684	41.2213	5.1671	-19.9520	34.940
12654	97.3684	112.8583	10.6705	234.9660	90.194
22493	97.3684	256.6973	1.8373	213.1873	56.439
10302	97.3684	27.9787	0.5209	17.3983	19.965
6387	97.3168	70.9853	0.3674	75.6112	15.360
17642	97.2136	21.3120	0.7327	43.6575	20.440
22682	97.2136	23.4507	0.9202	27.2053	31.325
14202	97.1620	77.3710	1.1937	96.9214	35.6696
21456	97.1620	22.3423	0.8300	7.7116	22.1473
19016	97.1104	395.3907	7.3295	277.0878	
15091	97.0588	99.1530	1.7515	138.2585	74.8662 37.7845
20087	97.0072	67.3520	0.6694	66.8587	27.1307
6712	96.9556	169.7277	1.8176	189.1622	57.1238
2476	96.9040	53.3413	0.8480	55.5428	
22707	96.8008	17.7820	1.2756	42.3511	32.4163
7171	96.8008	94.3337	1.2532	83.6124	26.8561
23703	96.6976	31.0490	0.3480	29.0504	30.5140
24212	96.6976	2582.6843	21.4587	2283.2783	14.2729
149	96.6976	66.2783	0.8071	76.7152	408.2796
8423	96.6976	227.7503	3.3440	366.9388	15.8431
14625	96.6976	68.5233	0.9441		292.2468
9408	96.5944	59.6917	1.7766	81.2621	23.5113
21825	96.5944	56.4700	1.5143	39.0365	17.3643
21427	96.4912	79.2123	1.3783	88.3463	35.4890
12828	96.4396	57.7353	0.9357	103.8133	29.5468
20757	96.3364	2414.1663	17.0973	66.8836 2271.8254	32.7675 422.0171

TABLE 5DD: N Timepoint(s): 2	24 hrs	Core Tox		Atty. Ref. 44921-509	0-01-WO/2105485
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
24117	96.3364	26.6910			
2675		1148.9510			
12778	96.2848	152.6843	2.5320		
21500	96.2848		54.4652		
16689	96.2332	104.0237	1.2517	108.6236	
22595	96.2332	166.8360		194.4342	
21264	96.2332	122.8987	1.7320		42.3266
13741	96.1816	26.0263	0.3138	103.6940	20.7544
11516	96.1300	81.2373		32.8458	17.8267
20327	96.1300	122.6457	2.7040	119.3780	33.2341
4189	96.0784		1.3007	117.4239	39.8879
8959	96.0784	343.5817	2.9074	392.8493	91.9355
7036		82.2207	1.8721	58.2600	21.4847
4732	96.0784	90.0790	2.0404	113.9122	21.4538
8265	96.0784	165.0377	1.5663	187.3527	37.0863
	96.0784	118.6537	1.7219	90.1576	33.6246
5454	96.0784	32.1143	2.3840	14.5283	17.3022
15393	96.0268	270.5937	15.8566	187.4393	42.2588
2208	96.0268	162.0793	6.7166	223.0357	44.7220
10685	96.0268	23.6977	0.5614	36.1425	15.1425
15085	95.9752	885.2107	4.7521	972.5390	174.5670

imepoint(s	). 3, 6 ms	, <i>;</i>		Ref: 44921-5090-0	
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
6892	99.4813	263.3163		66.7882	
6891	99.4295		119,4903	250.4163	
8664	99.2739	1607.5828	418.0726	112.2090	
17734	98.7033	3990.9268		1027.2344	
16518	98.6515	1977.6365	445.9983		
· 17736	98.4440	2529.2289	492.7151	763.7900	
21663	98.3921	1440.2189	312.1577	608.7162	319.51
363	98.2365	112.7505	30.0230	373.7786	161.12
1892	98.1328	2802.2854	341.4428	44.4177	19.38
357	98.0809	73.5020		1202.3530	371.20
354	98.0809	553.4614	15.4920	25.2192	17.80
17765	98.0809	2316.9869	186.9081	160.6835	74.36
17401	97.8734	1692.6079	210.1469	1388.9983	275.77
17735	97.8216	4082.1361	353.9725	599.5431	218.58
385	95.6950		1121.4657	1084.0936	505.11
20204	95.4876	-0.6526	7.8050	46.1192	22.57
16026	95.2801	9.0690	9.4593	42.6701	13.71
11865		78.3944	13.6112	159.1730	46.78
23058	93.9315	26.5984	8.8112	64.6395	19.33
8663	93.6722	146.0564	35.0956	283.2263	71.99
1475	93.2832	727.9441	520.6358	-55.1429	146.53
18059	92.7645	1938.9946	1033.7095	94.4565	217.46
	92.4533	273.4070	133.1863	27.2551	31.38
20448	92.4015	736.0876	490.7340	74.8256	
11258	92.2977	110.7936	89.7714	7.7077	108.998
20449	92.2459	1033.4939	521.5685	98.5816	21.787
2629	92.0902	90.5585	40.0410	20.9245	165.714
923	92.0384	103.1869	40.4358	16.6868	15.580
17908	92.0384	202.9623	78.7039	43.1288	17.699
18259	91.9865	238.4859	97.3566	93.3552	31.173
355	91.9346	87.8504	34.0407		46.007
15461	91.9346	444.1755	193.8804	9.5089	28.128
18597	91.8309	263.7544	75.1004	106.2839	54.278
353	91.8309	435.7853	161.9288	93.6741	61.867
223	91.7790	144.8780	67.7257	114.4376	63.191
244	91.6753	303.9644	134.5401	12.5453	23.909
15191	91.4160	1323.7188	675.7651	61.5793	37.472
23868	91.3122	894.6342		175.8255	552.785
11530	91.1566	999.6595	436.2035	212.6165	220.782
5167	91.0788	73.3379	378.7252	205.4721	156.964
19085	91.0529	92.1740	26.1360	25.7047	27.923
15510	91.0270		18.5335	52.0272	13.848
22868	90.9232	196.0304	36.3396	281.5123	54.259
3799	90.6380	14.9119	4.4812	28.6827	8.860
1742	90.6380	750.1286	157.2905	379.7988	110.5080
79	90.6120	104.5040	42.1347	32.4741	21.142
21662	90.4305	18.4890	9.5247	46.8097	17.767
18582		37.9036	11.1011	3.7015	11.5339
16173	90.2490	168.8623	27.1634	251.9951	55.6036
5496	90.2230	67.9840	34.6720	13.2814	26.1690
20728	90.1971	45.9714	10.2833	68.5173	13.6940
	90.1452	606.7142	125 9443	917.5459	201.3214
17764	90.0156	3163.5308	519.9248	1938.2249	
11940	89.9637	45.6983	7.5672	25.0523	384.4218

nepoint(s	): 3, 6 hrs 🖖	<u>.                                    </u>	Atty. Ref. 44921-5090-01-WO/21054				
GC ID	LDA Score		SD Tox	Mean Nontox	SD Nontox		
857	89.9118				7.613		
10071	89.8081			263.9332	106.177		
22499				20.7009	11.839		
15617	89.5488			15.0018	8.247		
15618	89.2894		29,2866		20.997		
18715	89.2376			151.0548	40.582		
21400	89.0560	61.2115	13.3773		32.154		
19040	89.0301	452.5429	120.7826	253.2807	75.312		
21445	88.9782	60.1424		10.5246	22.967		
19481	88.7967	68.2556	21.4951	130.6260	42.514		
15189	88.5114	757.2838		336.5505			
18389	88.2521	1826.1269	641.7089	825.5171	361.656		
21239	88.2521	243.9681	83.0284	118.3888	459.339		
16499	88.0965	-1.1534	33.3176	57.7244	62.391		
23166	88.0446	170.4068	42.1077	108.1382	33.357		
753	87.9149	68.1009	5.2162		29.116		
25039	87.6037	286.6995	44.2026	57.5494	20.530		
16122	87.5778	119.7388	37.9603	404.9923	94.388		
5034	87.5778	1164.1774	132.1500	64.7526	28.171		
14997	87.5000	555.6661	54.0072	884.7553	148.413		
1377	87.5000	38.9810	5.4946	746.1537	155.871		
1521	87.4222	128.7296		57.5690	19.588		
602	87.3185	139.4460	49.7904	68.1875	34.194		
8662	86.9813	257.6134	48.7242	229.9013	48.244		
8661	86.9813	250.8268	185.2497	34.8090	75.281		
22351	86.7998	65.9775	154.0243	10.2067	65.050		
1527	86.7220	8.1863	18.6803	41.1423	15.189		
12364	86.6961	74.7339	6.8239	25.1339	12.302		
18295	86.6961	83.1748	33.5477	150.7245	39.471		
20983	86.4108		64.3321	173.4615	51.168		
18654	86.3330	345.9545	55.2211	479.1295	109.697		
764	86.3330	89.2891	44.9318	218.8692	64.622		
6349	86.2033	50.5666	18.4217	101.3529	27.530		
1271	86.1255	116.8153	14.3162	151.7734	33.002		
12978		52.7259	9.5378	80.4345	15.650		
22625	86.0996	308.5996	230.1202	76.3885	43.732		
23336	86.0477	188.2085	98.2440	65.0820	29.2058		
11422	85.9959	66.5710	8.7131	93.1635	24.984		
4448	85.9699	53.8790	22.4691	113.2816	31.5290		
24431	85.8662	17.4248	5.1796	35.2285	10.6554		
17257	85.7884	425.6855	273.1575	73.8453	65.3863		
17137	85.7884	242.1913	50.2257	365.4273	115.4767		
5676	85.7624	367.5156	191.1552	857.4529	258.2968		
21069	85.7365	25.5498	28.0838	76.9172	45.5600		
	85.6846	36.6796	3.9627	49.5086	14.2318		
15460	85.6328	436.1656	264.6770	100.3814	63.7207		
19058	85.6328	19.0441	2.7660	24.9122	12.4186		
14213	85.5809	75.0461	41.6040	6.0349	18.8872		
20795	85.5290	361.8271	199.9596	110.7948	57.7895		
8665	99.1183	3826.7229	1669.2221	413.1920	335.0125		
8759	98.4440	339.5654	116.1490	35.3245			
23732	98.3921	1134.9133	214.4420	329.8413	57.8247 145.8289		
15212	98.2884	254.2340	76.3460		140.0289		

LGC ID	): 3, 6 hrs	Maar Ta	Atty. Ref. 44921-5090-01-WO/2105			
3808	98.1328		SD Tox	Mean Nontox	SD Nontox	
23314				556.3567	199.87	
3139	98.0290				192.534	
9604	97.9772	3317.1991		1711.6874	340.08	
16053	97.9772	2744.8634		384.8144	345.904	
15171	97.9253	333.2519		117.3370	86.254	
2331	97.7697	2108.9989		1029.9120		
16124	97.7697	1845.3030		379.6211	333.852	
14712		619.0150		228.5083	87.750	
22378	97.5104	324.5103		155.8050	42.383	
21632	97.2510	134.3710		272.1390	61.594	
	97.1473	516.5784	118.5630	200.9806	98.286	
3434	97.0436	2236.3513	500.5160	753.5275	374.654	
23304	96.9398	214.1941	40.7498	123.0396		
12664	96.1618	37.5723	14.3677	112.9597	36.311	
2861	96.1618	83.9905	15.7656	46.8376	33.658	
13460	95.5394	185.8708	40.8718	334.6733	15.681	
21514	95.3320	108.6159	26.3403	57.8617	66.924	
3290	95.2282	259.4525	54.3802	444.5074	20.483	
6102	95.0207	68.4524	17.6339		79.649	
3511	94.9689	224.9530	44.7671	36.5686	14.904	
4790	94.9170	-39.7215	33.4762	91.6020	52.832	
12946	94.8651	135.0391	20.0304	151.9333	96.736	
3207	94.7614	45.5745	48.5801	218.9686	41.976	
8938	94.6058	9.0184	10.2678	242.4891	97.519	
8917	94.3465	85.9886	24.2129	71.8879	34.749	
12662	93.8797	24.1668	17.5314	168.4718	38.958	
14494	93.8278	146.9951		85.9064	31.095	
4873	93.6722	223.9209	34.1009	226.4663	37.3047	
5442	93.5166	224.1333	72.9117	447.2041	116.5943	
18350	93.3091	241.2716	69.1508	431.7980	112.6526	
16599	93.2054	335.5149	40.0402	140.0376	60.8767	
14088	93.0498	14.6839	61.8090	591.6306	143.1488	
16596	92.9979	158.2274	16.9187	81.9165	37.8533	
22929	92.9979	278.7673	46.7335	315.6517	82.3981	
2729	92.8423		75.8229	735.8519	314.8335	
15051	92.5311	230.7750	70.2194	481.2179	151.9874	
6054	92.4533	208.6471	41.5312	120.1176	109.4713	
7913	92.3496	691.3863	298.0596	51.1399	82.1514	
11238	92.2199	159.3261	65.7056	52.0903	38.6015	
8820	92.1162	12.9080	5.0509	41.7424	22.5899	
24022	92.0643	191.3825	68.6766	400.2327	122.6294	
9452	92.0384	56.1263	13.4650	102.0367	26.9371	
2459		1134.7661	463.3626	264.4877	243.9946	
4188	91.9865	1774.2951	789.0601	116.8937	251.3637	
13291	91.9606	0.5915	9.1017	33.1719	22.3639	
4725	91.9346	500.4205	228.8126	170.4361	55.9152	
11326	91.9346	500.0794	221.4606	84.4696	93.1704	
8012	91.9087	82.5878	44.3182	192.7032	58.3028	
	91.9087	50.4938	7.5181	29.4405	13.8090	
7700	91.7790	130.7185	44.6686	39.2479	24.6893	
5775	91.7790	286.7219	134.6842	25.8344		
13365	91.7531	27.3019	13.9094	80.7765	40.0816	
17783	91.7272	686.6200	210.1304	234.4352	43.8288	

TABLE 5EE Timepoint(s	Ref. 4492/1-5090-0	1-WO/2105485			
GLGC ID	LDA Score		SD Tox	Mean Nontox	SD Nontox
17402			84.0620		
10710		0 1:020	13.7797		
8290		22:200	13.4745		
10837	91.5716			84.1778	
22443 5675	0.101.10		. 5.5551		
11721	01.0101	406.3161	126.2639		
22666	91.4419				30.2750
12233	91.4160 91.4160		80.8618		36.8367
12200	91.4160	267.2036	65.8534	105.4438	46.7134

BLE 5FF: Norepinephrine—Core Tox nepoint(s): 3, 6 hrs GC ID ILDA Score Moon Tox			Atty. Ref. 44921-5090-01-WO/21054			
	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox	
6892			66,1789			
6891	99.4295		119,4903			
8664	99.2739	1607.5828	418.0726			
17734	98.7033	3990.9268	581.3210	1027.2344	188.20	
16518	98.6515	1977.6365	445.9983	763.7900	428.84	
17736	98.4440	2529.2289	492.7151	608.7162	253.82	
21663	98.3921	1440.2189		373.7786	319.51	
363	98.2365	112.7505		44.4177	161.12	
1892	98.1328	2802.2854	341.4428	1202.3530	19.38	
357	98.0809	73.5020	15.4920	25.2192	371.20	
354	98.0809	553.4614	186.9081	160.6835	17.80	
17765	98.0809	2316.9869	210.1469	1388.9983	74.36	
17401	97.8734	1692.6079	353.9725	599.5431	275.77	
17735	97.8216	4082.1361	1121.4657	1084.0936	218.58	
385	95.6950	-0.6526	7.8050	46.1192	505.11	
20204	95.4876	9.0690	9.4593	40.1192	22.57	
16026	95.2801	78.3944	13.6112	42.6701	13.71	
11865	93.9315	26.5984	8.8112	159.1730	46.78	
23058	93.6722	146.0564	35.0956	64.6395	19.33	
8663	93.2832	727.9441	520.6358	283.2263	71.998	
1475	92.7645	1938.9946	1033.7095	-55.1429	146.532	
18059	92.4533	273.4070	133.1863	94.4565	217.463	
20448	92.4015	736.0876	490.7340	27.2551	31.386	
11258	92.2977	110.7936	89.7714	74.8256	108.998	
20449	92.2459	1033.4939	521.5685	7.7077	21.787	
2629	92.0902	90.5585	40.0410	98.5816	165.714	
923	92.0384	103.1869	40.4358	20.9245	15.580	
17908	92.0384	202.9623	78.7039	16.6868	17.699	
18259	91.9865	238.4859	97.3566	43.1288	31.173	
355	91.9346	87.8504	34.0407	93.3552	46.007	
15461	91.9346	444.1755	193.8804	9.5089	28.128	
18597	91.8309	263.7544	75.1004	106.2839	54.278	
353	91.8309	435.7853	161.9288	93.6741	61.867	
223	91.7790	144.8780	67.7257	114.4376	63.191	
244	91.6753	303.9644	134.5401	12.5453	23.909	
11531	91.4160	1886.5684	868.1506	61.5793	37.472	
15191	91.4160	1323.7188	675.7651	398.3255	256.073	
23868	91.3122	894.6340	436.2035	175.8255	552.785	
11530	91.1566	999.6595	378.7252	212.6165	220.782	
5167	91.0788	73.3379	26.1360	205.4721	156.964	
19085	91.0529	92.1740	18.5335	25.7047	27.923	
15510	91.0270	196.0304	36.3396	52.0272	13.848	
22868	90.9232	14.9119	4.4812	281.5123	54.259	
3799	90.6380	750.1286	157.2905	28.6827	8.860	
1742	90.6380	104.5040		379.7988	110.508	
79	90.6120	18.4890	42.1347	32.4741	21.1420	
21662	90.4305	37.9036	9.5247	46.8097	17.767	
18582	90.2490	168.8623	11.1011	3.7015	11.5339	
16173	90.2230	67.9840	27.1634	251.9951	55.6036	
5496	90.1971	45.97 (4)	34.5720	13.2814	26.1690	
20728	90.1452	606.7143	10.2633	68.5173	13.6940	
17764	90.0156	3163.5308	125.8443	917.5459	201.3214	
	33.3100		519.9248	1938.2249	384.4218	

ABLE 5FF: No imepoint(s): 3, BLGC ID	6 hrs		Atty. Ref: 44921-5090-01-WO/2105485			
	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox	
11940	89.9637	45.6983				
857	89.9118		7.9906	-0.0020		
10071	89.8081	540.8850	117.5623		7.613	
22499	89.6006	50.9446	12.0167	20.7009	106.177	
15617	89.5488	35.0314	14.6256	15.0018	11.839	
15618	89.2894	146.0054	29.2866	99.5980	8.247	
18715	89.2376	256.8166	57.9299	151.0548	20.997	
21400	89.0560	61.2115	13.3773	101.0548	40.582	
19040	89.0301	452.5429	120.7826	106.3284	32.154	
21445	88.9782	60.1424	23.7036	253.2807	75.312	
19481	88.7967	68.2556	21.4951	10.5246	22.967	
15189	88.5114	757.2838	239.9481	130.6260	42.514	
18389	88.2521	1826.1269	641.7089	336.5505	361.656	
21239	88.2521	243.9681	83.0284	825.5171	459.339	
16499	88.0965	-1.1534	33.3176	118.3888	62.3919	
23166	88.0446	170.4068	42.1077	57.7244	33.357°	
753	87.9149	68.1009	5.2162	108.1382	29.1160	
25039	87.6037	286.6995	44.2026	57.5494	20.5305	
16122	87.5778	119.7388		404.9923	94.3883	
5034	87.5778	1164.1774	37.9603	64.7526	28.1717	
14997	87.5000	555.6661	132.1500	884.7553	148.4135	
1377	87.5000	38.9810	54.0072	746.1537	155.8718	
1521	87.4222	128.7296	5.4946	57.5690	19.5886	
602	87.3185	139.4460	49.7904	68.1875	34.1946	
8662	86.9813	257.6134	48.7242	229.9013	48.2442	
8661	86.9813	250.8268	185.2497	-34.8090	75.2818	
22351	86.7998	65.9775	154.0243	10.2067	65.0503	
1527	86.7220		18.6803	41.1423	15.1897	
12364	86.6961	8.1863 74.7339	6.8239	25.1339	12.3022	
18295	86.6961		33.5477	150.7245	39.4713	
20983	86.4108	83.1748	64.3321	173.4615	51.1680	
18654	86.3330	345.9545	55.2211	479.1295	109.6979	
764	86.3330	89.2891	44.9318	218.8692	64.6229	
6349	86.2033	50.5666	18.4217	101.3529	27.5301	
1271	86.1255	116.8153	14.3162	151.7734	33.0023	
12978	86.0996	52.7259	9.5378	80.4345	15.6506	
22625	86.0477	308.5996	230.1202	76.3885	43.7321	
23336	85.9959	188.2085	98.2440	65.0820	29.2058	
11422	85.9699	66.5710	8.7131	93.1635	24.9841	
4448		53.8790	22.4691	113.2816	31.5290	
24431	85.8662	17.4248	5.1796	35.2285	10.6554	
17257	85.7884	425.6855	273.1575	73.8453	65.3863	
17137	85.7884	242.1913	50.2257	365.4273	115.4767	
5676	85.7624 85.7365	367.5156	191.1552	857.4529	258.2968	
21069	85.6846	25.5498	28.0838	76.9172	45.5600	
15460		36.6796	3.9627	49.5086	14.2318	
19058	85.6328	436.1656	264.6770	100.3814	63.7207	
14213	85.6328	19.0441	2.7660	24.9122	12.4186	
	85.5809	75.0461	41.6040	6.0349	18.8872	
8665	99.1183	3826.7229	1669.2221	413.1920	335.0125	
8759	98.4440	339.5654	118.1490	35.3245	57.8247	
23732	98.3921	1134.9133	214.4420	329.8413	145 9390	
15212	98.2884	254.2340	76.3460	55.2676	145.8289 36.1656	

BLE 5FF: No nepoint(s): 3	6 hrs		Atty. Ref. 44921-5090-01-WO/210548			
GC ID	LDA Score	Mean Tox	SD Tox:		SD Nontox	
3808		1556.4444				
23314		1320.4768	670.9375			
3139	98.0290	3317.1991	585.8836			
9604	97.9772	2744.8634	1014.6649			
16053	97.9772	333.2519	75.7808		345.904	
15171	97.9253	2108.9989	591.0550		86.254	
2331	97.7697	1845.3030	533.8146		260.360	
16124	97.7697	619.0150	169.0273	379.6211	333.852	
14712	97.5104	324.5103		228.5083	87.750	
22378	97.2510	134.3710	65.6300 28.4687	155.8050	42.383	
21632	97.1473	516.5784		272.1390	61.594	
3434	97.0436	2236.3513	118.5630	200.9806	98.286	
23304	96.9398	214.1941	500.5160	753.5275	374.654	
12664	96.1618		40.7498	123.0396	36.311	
2861	96.1618	37.5723	14.3677	112.9597	33.658	
13460	95.5394	83.9905	15.7656	46.8376	15.681	
21514	95.3320	185.8708	40.8718	334.6733	66.924	
3290		108.6159	26.3403	57.8617	20.483	
6102	95.2282	259.4525	54.3802	444.5074	79.649	
3511	95.0207	68.4524	17.6339	36.5686	14.904	
4790	94.9689	224.9530	44.7671	91.6020	52.832	
12946	94.9170	-39.7215	33.4762	151.9333	96.736	
	94.8651	135.0391	20.0304	218.9686	41.976	
3207	94.7614	45.5745	48.5801	242.4891	97.519	
8938	94.6058	9.0184	10.2678	71.8879	34.749	
8917	94.3465	85.9886	24.2129	168.4718	38.958	
12662	93.8797	24.1668	17.5314	85.9064		
14494	93.8278	146.9951	34.1009	226.4663	31.0954	
4873	93.6722	223.9209	72.9117	447.2041	37.3047	
5442	93.5166	224.1333	69.1508	431.7980	116.5943	
18350	93.3091	241.2716	40.0402	140.0376	112.6526	
16599	93.2054	335.5149	61.8090	591.6306	60.8767	
14088	93.0498	14.6839	16.9187	81.9165	143.1488	
16596	92.9979	158.2274	46.7335		37.8533	
22929	92.9979	278.7673	75.8229	315.6517	82.3981	
2729	92.8423	230.7750	70.2194	735.8519	314.8335	
15051	92.5311	208.6471	41.5312	481.2179	151.9874	
6054	92.4533	691.38€3	298.0596	120.1176	109.4713	
7913	92.3496	159.3261	65.7056	51.1399	82.1514	
11238	92.2199	12.9080	5.0509	52.0903	38.6015	
8820	92.1162	191.3825	68.6766	41.7424	22.5899	
24022	92.0643	56.1263		400.2327	122.6294	
9452	92.0384	1134.7661	13.4650	102.0367	26.9371	
2459	91.9865	1774.2951	463.3626	264.4877	243.9946	
4188	91.9606	0.5915	789.0601	116.8937	251.3637	
13291	91.9346		9.1017	33.1719	22.3639	
4725	91.9346	500.4205	228.8126	170.4361	55.9152	
11326	91.9087	500.0794	221.4606	84.4696	93.1704	
8012	91.9087	82.5878	44.3182	192.7032	58.3028	
7700	91.7790	50.4938	7.5181	29.4405	13.8090	
5775	91.7790 91.7790	130.7185	44.6686	39.2479	24.6893	
13365		286.7219	134.6842	25.8344	40.0816	
17783	91.7531	27.3019	13.9094	80.7765	43.8288	
11103	91.7272	686.6200	210.1304	234.4352	89.0104	

TABLE 5FF: No Timepoint(s): 3	repinephrine- , 6 hrs	Core Tox	Atty. R	ef. 44921-5090-0	1-WO/2105485
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
17402		361.7129	84.0620	120.8395	
10710	0.10.01	64.5291	13.7797	100.4503	
8290	- ::0010		13.4745		
10837	91.5716		71.4687	84.1778	
22443	31.07.10		78.8654	32.8697	23.8497
5675		406.3161	126.2639	157.5955	
11721	91.4419	U 1.UA-T-T	10.5013	77.0222	30.2750
22666			80.8618	77.8863	
12233	91.4160	267.2036	65.8534	105.4438	46.7134

GC ID	: 3 hrs LDA Score	Mean Tox		Tax .	<u> </u>
22871		51.0920			SD Nontox
8385	100.0000				16.83°
353	100.0000				52.940
22630	100.0000			1,0.00,7	69.706
21120	99.9485			42.9443	16.604
1238	99.9485	168.2730		153.2225	44.336
16499	99.9485	181.9290	0.1174	95.7088	41.265
1693	99.9485	-2.6195	0.7573	57.3633	33.686
11113		-10.6570	0.0764	49.9027	32.934
17145	99.9485	36.4690	0.0071	36.2673	19.670
20746	99.8969	92.9605	0.1025	172.2985	46.149
17154	99.8969	318.6620	0.6661	492.2122	121.599
	99.8969	642.6685	0.1280	863.0957	213.592
15638	99.8969	521.2955	0.4179	929.6362	307.519
17218	99.8969	441.5540	0.2800	363.4876	95.735
1970	99.8969	172.2320	0.1131	123.1975	40.774
3455	99.8969	163.8175	0.0658	139.2460	
25638	99.8454	28.0365	0.0530	17.3435	43.341
20740	99.8454	269.2450	1.1003	451.9244	8.934
20731	99.8454	34.5160	0.0170	28.2257	144.815
1852	99.8454	2247.2410	0.4765	2519.8118	9.817
322	99.8454	31.1435	0.0191		502.053
21062	99.8454	136.3905	0.1068	19.1650	11.459
21400	99.8454	51.6450	0.2305	69.9867	37.854
1625	99.8454	35.0385	0.1676	106.0690	32.239
17894	99.8454	146.7080	0.0735	13.3271	12.235
22763	99.7938	78.9745	0.8167	168.1589	37.273
21498	99.7938	12.4685	0.0205	40.9825	12.954
10819	99.7938	1241.1000	0.5813	31.5048	18.760
25593	99.7938	237.3455	1.0317	1735.3772	412.156
21682	99.7938	30.0825	0.7248	135.8000	39.485
17202	99.7938	49.2500		-9.2475	55.563
5283	99.7938	117.2625	0.0325	36.4196	10.921
1463	99.7423	263.6415	1.1830	67.2504	18.069
17181	99.7423	317.0000	0.3175	364.7819	135.6430
18430	99.7423		1.9106	191.7197	62.6368
436	99.7423	314.4045	0.6300	208.5937	71.2632
18694	99.7423	24.2485	0.2949	58.5359	17.3593
16401	99.7423	31.5855	0.5424	-7.0364	26.3577
19658	99.7423	645.7720	0.9390	1039.6784	520.0369
2697	99.7423	45.0500	0.9518	12.5121	15.5439
4422	99.6907	1502.2910	2.2868	2254.4653	411.6071
1952	99.6907	19.8810	0.0127	25.0508	6.7236
22661		39.0605	0.0559	21.2590	10.8957
17626	99.6907	2011.6865	1.8066	2453.7766	431.6276
20242	99.6907	639.4775	0.1181	733.3278	139.0769
8384	99.6907	25.9245	0.0898	2.8847	14.0621
17661	99.6907	208.5360	0.4695	96.5039	53.1497
	99.6907	191.8995	0.0827	190.0693	49.9046
4809	99.6907	101.6030	0.0467	79.9599	21.4435
16219	99.6907	609.0060	0.8499	786.7393	259.2468
14754	99.6907	159.2985	0.1549	129.1452	24.2971
15683	99.6392	190.3800	1.1116	102.5670	
21807	99.6392	23.4740	0.0679	6.9674	41.8290 13.5151

20849 99.6392 1044.1320 1.9474 794.4856 153.21 9082 99.6392 32.6350 0.0184 37.6016 10.22 17936 99.6392 13.9605 0.0158 25.933 10.73 16581 99.6392 177.3230 2.2062 100.6605 84.94 18899 99.6392 61.9780 0.0523 45.2072 17.15 18065 99.6392 161.9780 0.0523 45.2072 17.15 18365 99.6392 114.2270 4.8437 52.4727 17.13 17991 99.5876 31.0076 0.0983 26.0638 9.26 25278 99.5876 17.9070 0.0311 20.2940 11.97 25264 99.5876 17.9070 0.0311 20.2940 11.97 25264 99.5876 31.33.105 2.0584 77.0038 20.41 25264 99.5876 17.367.00 0.5218 88.3147 40.356 15888 99.5361 673.6840 0.6109 790.2653 146.76 18274 99.5361 37.8110 0.3861 191.4369 42.91 18274 99.5361 37.8110 0.3861 191.4369 42.91 1918 99.4845 20.1245 0.1336 3.2394 14.25 16649 99.4845 20.1245 0.1336 3.2394 14.25 16649 99.4845 211.1840 5.8548 349.3276 65.42 17075 99.4845 211.1840 5.8548 349.3276 65.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17075 99.4845 211.1840 5.8548 349.3276 55.42 17076 99.4845 211.1840 5.8548 349.3276 55.42 17077 99.4330 162.1815 0.1167 145.3141 35.44 8661 99.4330 78.6675 0.2792 44.8844 21.656 18089 99.4330 162.1815 0.1167 145.3141 35.44 18482 99.4330 78.6675 0.2792 44.8844 21.656 24327 99.4330 180.8330 0.1343 62.5162 18.626 17988 99.4330 180.8330 0.1343 62.5162 18.626 17988 99.4330 180.8330 0.1343 62.5162 18.626 17988 99.3314 99.0705 0.1407 68.1044 24.931 1016 99.3314 99.0705 0.1407 68.1044 24.931 1016 99.3314 99.0705 0.1407 68.1044 24.931 1016 99.3314 99.0705 0.1407 68.1044 24.931 1016 99.3314 99.0705 0.1407 68.1040 99.3306 88.366 10	Timepoint(s)		Ą	Atty. I	Ref. 44921-5090-0	01-WO/2105485
20849 99.6392 1044.1320 1.9474 794.4656 153.21 9082 99.6392 32.6350 0.0184 37.6016 10.22 17936 99.6392 13.9605 0.0474 25.6337 13.98 16581 99.6392 13.9605 0.0474 25.6337 13.98 15301 99.6392 177.3230 2.2062 100.6605 84.94 18899 99.6392 60.6635 0.0403 46.7844 12.22 16006 99.6392 61.9780 0.0523 45.2072 17.15 18365 99.6392 115.6865 0.1011 112.7902 77.12 531 99.6392 114.2270 4.8437 52.4727 17.13 17991 99.5876 38.0675 0.0983 26.0638 9.26 25278 99.5876 17.9070 0.0311 20.2940 11.97 25647 99.5876 361.9505 0.6894 247.9105 131.644 23194 99.5876 361.9505 0.6894 247.9105 131.644 23194 99.5876 41.5630 0.5218 88.3147 40.35 15888 99.5361 673.6840 0.6109 790.2653 146.76 21002 99.5361 137.8110 0.3661 191.4369 42.91 14874 99.5361 348.0135 4.7751 558.8275 137.48 16849 99.4845 20.1245 0.1336 3.2394 14.25 16849 99.4845 211.1840 5.8548 349.3276 65.42 17075 99.4845 48.4830 3.9301 84.79 25538 99.4330 88.7140 1.0974 52.1067 20.03 25411 99.4330 7.6315 0.0219 25.9159 66.42 17075 99.4845 48.8030 3.9301 84.739 24.77 25539 99.4330 88.7140 1.0974 52.1067 20.03 25411 99.4330 7.6315 0.0219 2.89355 102.79 25541 99.4330 162.1815 0.1167 145.3141 35.446 26625 99.4845 48.8030 3.9301 84.739 24.77 25538 99.4330 18.7140 1.0974 52.1067 20.03 25411 99.4330 7.6315 0.0219 2.89355 122.79 25538 99.4330 141.6685 0.3387 194.3194 41.56 25639 99.4330 174.6685 0.3387 194.3194 41.56 25639 99.4330 174.905 2.1722 44.8844 21.65 25639 99.4330 174.905 2.1722 44.8844 21.65 24227 99.4330 99.6675 0.2722 44.8844 21.65 24227 99.4330 99.6675 0.2722 44.8844 21.65 24237 99.4330 99.6675 0.2722 44.8844 21.65 24242 99.4330 99.6675 0.2792 95.9159 66.42 24249 99.4330 99.6675 0.2792 95.9159 66.42 24249 99.4330 99.6675 0.2792 95.9109 28.8036 122.79 24330 99.4330 174.905 2.1729 98.1004 41.76 24248 99.4330 99.6675 0.2792 44.8844 21.656 24248 99.4330 99.6675 0.2792 44.8844 21.656 24248 99.4330 99.6675 0.2792 44.8844 21.656 24248 99.4330 99.66575 0.4569 66.2579 98.6226 24268 99.3814 99.6500 0.6675 0.4569 66.2579 98.6226 24269 99.3814 99.6505 0.6683 29.9608 8.836 2662 99.3814 99.6505 0.668	GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
9082 99.6392 32.6350 0.0184 37.6016 10.22 17936 99.6392 13.9605 0.0474 25.6337 13.98 15301 99.6392 177.3230 2.2062 100.6605 84.94 15301 99.6392 177.3230 2.2062 100.6605 84.94 16006 99.6392 60.6635 0.0403 46.7844 12.22 16006 99.6392 61.9780 0.0523 45.2072 17.15 18365 99.6392 125.6865 0.1011 112.7902 77.12 17931 99.6392 114.2270 4.8437 52.4727 17.13 17991 99.5876 38.0675 0.0983 26.0638 9.26 25278 99.5876 17.9070 0.0311 20.2940 11.97 25647 99.5876 31.33.3105 2.0584 77.0038 20.411 25264 99.5876 41.5630 0.5218 88.3147 40.355 15888 99.5361 673.6840 0.6109 790.2653 146.76 18274 99.5361 37.6110 0.3861 191.4369 42.91 18274 99.5361 37.6110 0.3861 191.4369 42.91 1818 99.4845 20.1245 0.1336 3.2394 14.25 16649 99.4845 20.1245 0.1336 3.2394 14.25 16649 99.4845 211.1840 5.8548 349.3276 65.42 17075 99.4845 211.1840 5.8548 349.3276 65.42 17075 99.4845 211.1840 5.8548 349.3276 65.42 15641 99.4330 76.6315 0.0219 22.8935 102.79 3910 99.4330 162.1815 0.0119 22.8935 102.79 3910 99.4330 162.1815 0.0119 22.8935 102.79 3910 99.4330 162.1815 0.0119 22.8935 102.79 11935 99.4330 18.740 1.0974 52.1067 20.03 2441 99.4330 78.6675 0.2722 44.8844 21.655 11985 99.4330 18.740 1.0974 52.1067 20.03 25539 99.4330 18.740 1.0974 52.1067 20.03 25411 99.4330 78.6675 0.2722 44.8844 21.655 11985 99.4330 18.7490 5.3891 19.3194 41.55 11985 99.4330 18.7490 5.2722 44.8844 21.655 11985 99.4330 18.7490 0.2722 44.8844 21.655 11985 99.4330 18.7490 0.3722 44.8844 21.655 11985 99.4330 18.7490 0.3722 44.8844 21.655 11985 99.4330 18.7890 0.0000 1.739 126.6171 28.88 17083 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3314 99.0705 0.1407 68.1044 24.931 11016 99.3314 99.0705 0.1407 68.1044 24.931 11935 99.3394 99.3814 90.0					794.4656	
17956   99.6392   28.5700   0.0156   28.9933   10.73   16581   99.6392   177.3230   2.2062   100.6605   84.94   15301   99.6392   60.6635   0.0403   46.7844   12.22   16006   99.6392   60.6635   0.0403   46.7844   12.22   16006   99.6392   61.9780   0.0523   45.2072   17.155   18365   99.6392   125.6865   0.1011   112.7902   77.172   17991   99.5876   38.0675   0.0983   26.0638   9.265   25278   99.5876   17.9070   0.0311   20.2940   11.97   25647   99.5876   361.9505   0.6894   247.9105   131.644   25264   99.5876   313.3105   2.0584   77.0038   20.4163   22.2528   99.5876   41.5630   0.5218   88.3147   40.355   15888   99.5381   673.6840   0.6109   790.2653   146.765   146.765   149.5888   99.5361   137.8110   0.3861   191.4369   42.911   1918   99.4845   20.1245   0.1336   3.2394   42.55   16649   99.4845   20.1245   0.1336   3.2394   42.55   16649   99.4845   20.1245   0.1336   3.2394   42.55   16649   99.4845   216.8705   0.2199   259.9159   56.447   17075   99.4845   211.1840   5.8548   349.3276   65.422   56.525   99.4845   48.830   3.9301   8.4739   24.777   25411   99.4330   7.6315   0.0219   22.8935   102.79   3910   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   88.7140   1.0974   52.1067   20.033   12588   99.4330   162.1815   0.1167   145.3141   35.4488   99.4330   36.2615   566.5361   10.8047   59.915   16482   99.4330   362.6415   566.5361   10.8047   59.915   10.6565   20.3131   41.765   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050   41.6050						
15301   99.6392   177.3230   2.2062   100.6605   84.94   177.3230   2.2062   100.6605   84.94   18899   99.6392   60.6635   0.0403   46.7844   12.22   16006   99.6392   61.9780   0.0523   45.2072   17.155   18365   99.6392   114.270   4.8437   52.4727   17.155   531   99.6392   114.270   4.8437   52.4727   17.135   17991   99.5876   33.0675   0.0983   26.0638   9.265   25278   99.5876   17.9070   0.0311   20.2940   11.97   25647   99.5876   361.9505   0.6894   247.9105   131.644   25264   99.5876   361.9505   0.6894   247.9105   131.644   25264   99.5876   341.5630   0.5218   88.3147   40.355   15888   99.5361   673.6840   0.6109   790.2653   146.766   15888   99.5361   137.8110   0.3861   191.4369   42.911   18274   99.5361   348.0135   4.7751   558.8275   337.481   1918   99.4845   20.1245   0.1336   3.2394   14.257   194.845   20.1245   0.1336   3.2394   14.257   14.255   99.4845   221.1840   5.8548   349.3276   65.426   99.4845   221.1840   5.8548   349.3276   65.426   65.25   99.4845   483.0040   5.6286   759.7738   135.93   1258   99.4845   484.830   3.3301   8.4739   24.777   25.538   99.4330   88.7140   1.0974   52.1067   20.033   20.411   194.842   99.4330   88.7140   1.0974   52.1067   20.033   20.411   20.99   23.99   23.99   24.777   25.538   99.4330   162.1815   0.01167   145.3141   35.446   39.4330   76.315   0.0219   22.8935   102.79   25.538   99.4330   162.1815   0.01167   145.3141   35.446   39.4330   76.315   0.0219   22.8935   102.79   25.538   99.4330   162.1815   0.01167   145.3141   35.446   39.4330   76.315   0.0219   22.8935   102.79   25.538   99.4330   162.1815   0.01167   145.3141   35.446   39.4330   76.315   0.0219   22.8935   102.79   39.4330   36.8625   4.8317   1627.0752   50.016   36.655   39.4344   37.665   39.4330   37.6355   39.3311   36.9752   36.6575   39.3314   35.4365   0.0898   19.0633   45.762   36.6575   39.3314   35.4365   0.0898   19.0633   45.762   36.6575   39.3314   35.4365   0.0898   19.0633   46.376   36.6575   39.3314   35.4365   0.0898   19.0683   43.43774						
1889   99.6392   60.6635   0.0403   46.7844   12.22					25.6337	
1889  99.6392  60.6635  0.0403  46.7844  12.22  16006  99.6392  125.6865  0.1011  112.7902  77.12  1791  18365  99.6392  115.6865  0.1011  112.7902  77.12  17991  99.5876  38.6675  0.0983  26.0638  9.266  25278  99.5876  17.9070  0.0311  20.2940  11.97  25647  99.5876  361.9505  0.6894  247.9105  131.644  23194  99.5876  313.3105  2.0584  77.0038  20.411  25264  99.5876  133.3105  2.0584  77.0038  20.411  25264  99.5876  41.5630  0.5218  88.3147  40.351  15888  99.5361  673.6840  0.6109  790.2653  146.762  12002  99.5361  137.8110  0.3861  191.4369  42.911  18274  99.5361  317.8110  0.3861  191.4369  42.911  18274  99.5361  317.8110  0.3861  31.3294  14.255  16649  99.4845  20.1245  0.1336  3.2394  14.255  16649  99.4845  216.8705  0.2199  259.9159  56.442  17.075  99.4845  211.1840  5.8548  349.3276  65.422  6525  99.4845  48.430040  5.6286  759.7738  135.933  11258  99.4330  88.7140  1.0974  52.1067  20.033  25411  99.4330  7.6315  0.0219  22.8935  102.799  259.9159  42.9715  391.099.4330  38.7140  1.0974  52.1067  20.033  25411  99.4330  7.6315  0.0219  22.8935  102.799  259.9159  42.9715  391.099.4330  38.7140  1.0974  52.1067  20.033  25411  99.4330  7.6315  0.0219  22.8935  102.799  259.9149  259.9159  259.91					100.6605	
18365   99.6392   114.270   4.8437   52.4727   17.15     18365   99.6392   114.2270   4.8437   52.4727   17.13     17991   99.5876   33.0675   0.0983   26.0638   9.26     25278   99.5876   37.9070   0.0311   20.2940   11.97     25647   99.5876   361.9505   0.6884   247.9105   131.64     23194   99.5876   133.3105   2.0584   77.0038   20.411     25264   99.5876   41.5630   0.5218   88.3147   40.35     15888   99.5361   673.6840   0.6109   790.2653   146.76     21002   99.5361   33.8110   0.3861   191.4369   42.91     18274   99.5361   348.0135   4.7751   558.8275   37.488     1918   99.4845   20.1245   0.1336   3.2394   14.25     16849   99.4845   211.1840   5.8548   349.3276   65.42     17075   99.4845   211.1840   5.8548   349.3276   65.42     17075   99.4845   483.0040   5.6286   759.7738   135.93     1258   99.4345   48.30040   5.6286   759.7738   135.93     1258   99.430   88.7140   1.0974   52.1067   20.03     3910   99.4330   76.315   0.0219   22.8935   102.79     3910   99.4330   162.1815   0.1167   145.3141   35.446     4642   99.4330   78.0675   0.2722   44.8844   21.656     24327   99.4330   37.6975   0.2722   44.8844   21.656     24327   99.4330   37.6975   0.2722   44.8844   21.656     24327   99.4330   37.6975   0.2722   44.8844   21.656     24327   99.4330   37.6975   0.2722   44.8844   21.656     24327   99.4330   37.6975   0.2722   44.8844   21.656     24327   99.4330   37.6975   0.2722   44.8844   21.656     24327   99.4330   37.5975   0.6555   23.1313   41.975     1958   99.4330   37.3915   0.6555   23.1313   41.975     1968   99.4330   37.3915   0.6555   23.1313   41.975     1968   99.4330   37.3915   0.6555   23.1313   41.975     1978   99.3814   95.7180   0.1739   126.6171   28.881     17083   99.3814   95.7180   0.1739   126.6171   28.881     17083   99.3814   95.615   0.2729   58.1091   28.604     3662   99.3814   35.4365   0.0898   19.668   34.845     24248   99.3814   35.4365   0.0898   19.668   34.345     24248   99.3814   35.4365   0.0898   19.668   34.345     24248   99.3814   36.6						
15353   99.6392   125.6865   0.1011   112.7902   77.12   531   99.6392   114.2270   4.8437   52.4727   17.13   17.991   99.5876   38.0675   0.0983   26.0638   9.26   25278   99.5876   17.9070   0.0311   20.2940   11.97   25647   99.5876   361.9505   0.6884   247.9105   131.64   23194   99.5876   133.3105   2.0564   77.0038   20.411   25264   99.5876   41.5630   0.5218   88.3147   40.351   15888   99.5361   673.6840   0.6109   790.2653   146.76   21002   99.5361   348.0135   4.7751   558.8275   137.481   191.4369   42.911   18274   99.5361   348.0135   4.7751   558.8275   137.481   191.69   99.4845   20.1245   0.1336   3.2394   14.251   16649   99.4845   216.8705   0.2199   259.9159   56.44   17075   99.4845   211.1840   5.8548   349.3276   65.42   11.258   99.4845   483.0040   5.6266   759.7738   135.93   11258   99.4830   48.4830   3.9301   8.4739   24.77   25538   99.4330   88.7140   1.0974   52.1067   20.033   3910   99.4330   162.1815   0.1167   145.3141   35.446   8661   99.4330   7.6315   0.0219   22.8935   102.794   23.27   99.4330   862.6415   566.5361   10.8047   59.91   11935   99.4330   76.0156   0.1167   145.3141   35.446   8661   99.4330   76.0156   0.1167   145.3141   35.446   8661   99.4330   76.0156   0.1167   145.3141   35.446   8661   99.4330   76.0156   0.1167   145.3141   35.446   8661   99.4330   76.0156   0.1167   145.3141   35.446   34.82   99.4330   76.0156   0.1167   145.3141   35.446   36.606   99.4330   362.6415   566.5361   10.8047   59.915   11935   99.4330   76.056   0.2722   44.8844   21.656   24.327   99.4330   987.6625   4.8317   1627.0752   502.013   1935   99.4330   362.6415   566.5361   10.8047   59.915   11935   99.4330   77.6625   4.8317   1627.0752   502.013   36.606   99.4330   360.6676   0.4589   56.2079   36.608   36.608   99.4330   36.8830   0.1343   62.5162   36.608   36.608   39.3304   36.8830   0.1343   62.5162   36.608   36.608   39.3304   36.605   36.606   33.8686   71.766   39.3814   39.4814   39.6066   33.8688   71.766   39.3814   39.3814   39.6066   33.8688					45.2072	
17991   99.5876   38.0675   0.0983   20.638   9.265				0.1011	112.7902	
1799   99.5876   38.0675   0.0983   26.0638   9.26				4.8437	52.4727	
25278 99.5876 17.9070 0.0311 20.2940 11.97 25647 99.5876 361.9505 0.6894 247.9105 131.644 23194 99.5876 133.3105 2.0564 77.0038 20.411 25264 99.5876 41.5630 0.5218 88.3147 40.351 15888 99.5361 673.6840 0.6109 790.2653 146.76 21002 99.5361 137.8110 0.3861 191.4369 42.911 18274 99.5361 348.0135 4.7751 558.8275 137.481 1918 99.4845 20.1245 0.1336 3.2394 14.251 16649 99.4845 21.1245 0.1336 3.2394 14.251 17075 99.4845 211.1840 5.8548 349.3276 65.422 6525 99.4845 483.0040 5.6286 759.7738 135.933 11258 99.4845 483.0040 5.6286 759.7738 135.933 11258 99.4845 48.4830 3.9301 8.4739 24.775 25538 99.4330 88.7140 1.0974 52.1067 20.033 25411 99.4330 7.6315 0.0219 22.8935 102.799 3910 99.4330 162.1815 0.1167 145.3141 35.446 8661 99.4330 682.6415 566.5361 10.8047 59.918 16482 99.4330 141.6685 0.3387 194.3194 41.768 24327 99.4330 987.6825 4.8317 1627.0752 244.8844 21.656 24327 99.4330 987.6825 4.8317 1627.0752 250.013 18462 99.4330 78.0675 0.2722 44.8844 21.656 24327 99.4330 987.6825 4.8317 1627.0752 250.013 1935 99.4330 987.6825 4.8317 1627.0752 250.013 19439 49.4330 987.6825 4.8317 1627.0752 50.2013 19439 49.4330 987.6825 4.8317 1627.0752 50.2013 19439 49.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 987.6825 4.8317 1627.0752 50.2013 1958 99.4330 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.4384 99.						
29647 99.5876 361.9505 0.6894 247.9105 131.648 23194 99.5876 133.3105 2.0584 77.0038 20.418 25264 99.5876 41.5630 0.5218 88.3147 40.355 15888 99.5361 673.6840 0.6109 790.2653 146.76 21002 99.5361 137.8110 0.3861 191.4369 42.918 16274 99.5361 348.0135 4.7751 558.8275 137.488 1918 99.4845 20.1245 0.1336 3.2394 14.255 16649 99.4845 216.8705 0.2199 259.9159 56.442 17075 99.4845 211.1840 5.8548 349.3276 65.428 6525 99.4845 483.0040 5.6286 759.7738 135.93 11258 99.4845 48.4830 3.9301 8.4739 24.772 25538 99.4330 88.7140 1.0974 52.1067 20.033 25411 99.4330 7.6315 0.0219 22.8935 102.794 8661 99.4330 162.1815 0.1167 145.3141 35.446 8661 99.4330 682.6415 566.5361 10.8047 59.918 16482 99.4330 141.6685 0.3387 194.3194 41.768 16482 99.4330 78.0675 0.2722 44.8844 21.656 24327 99.4330 80.76.765 0.2722 44.8844 21.656 24327 99.4330 80.76.765 0.2722 44.8844 21.656 24327 99.4330 80.8830 0.1343 62.5162 18.622 3474 99.4330 80.8830 0.1343 62.5162 18.622 3474 99.4330 80.8830 0.1343 62.5162 18.622 3474 99.4330 80.8830 0.1343 62.5162 18.622 3474 99.4330 60.6575 0.4599 56.2097 105.242 11935 99.4330 127.4906 2.1729 58.1091 28.604 8586 99.4330 80.8830 0.1343 62.5162 18.622 3474 99.4330 60.6575 0.4599 56.2097 105.242 17958 99.4330 127.4906 2.1729 58.1091 28.604 8586 99.4330 80.8830 0.1343 62.5162 18.622 3474 99.4330 60.6575 0.4599 56.2097 105.242 17958 99.4330 60.6575 0.4599 56.2097 105.242 17968 99.4330 60.6575 0.4599 56.2097 105.242 17968 99.4330 60.6575 0.4599 56.2097 105.242 17968 99.4330 60.6575 0.4599 56.2097 105.242 179798 99.4330 60.6575 0.4599 56.2097 105.242 17968 99.4330 60.6575 0.4599 56.2097 105.242 17968 99.4330 60.6575 0.4599 56.2097 105.242 17968 99.4330 60.6575 0.4599 56.2097 105.242 179798 99.4330 60.6575 0.4599 56.2097 105.242 17998 99.3814 95.7180 0.1739 126.6171 28.881 17083 99.3814 95.7180 0.1739 126.6171 28.881 17083 99.3814 95.7180 0.1739 126.6171 28.881 17083 99.3814 90.0066 3.38688 17.0666 2.38688 77.0668 2.9838 19.0863 99.3899 99.3814 90.6215 0.3415 57.5682 20.438 10.8662 99.3814 99.3299 90.66609 66.573 3.9068 8.8			17.9070	0.0311		
25194 99.5876 133.3105 2.0584 77.0038 20.411 25264 99.5876 41.5630 0.5218 88.3147 40.351 15888 99.5361 673.6840 0.6109 790.2653 21002 99.5361 137.8110 0.3861 191.4369 42.911 18274 99.5361 348.0135 4.7751 558.8275 137.481 1918 99.4845 20.1245 0.1336 3.2394 14.251 16649 99.4845 216.8705 0.2199 259.9159 56.441 17075 99.4845 211.1840 5.8548 349.3276 65.421 6525 99.4845 483.0040 5.6266 759.7738 135.933 11258 99.4845 483.0040 5.6266 759.7738 135.933 125538 99.4330 88.7140 1.0974 52.1067 20.033 25411 99.4330 7.6315 0.0219 22.8935 102.794 3910 99.4330 162.1815 0.1167 145.3141 35.446 8661 99.4330 682.6415 566.5361 10.8047 59.911 16482 99.4330 78.0675 0.2722 44.8844 21.656 24327 99.4330 987.6825 4.8317 1627.0752 250.015 11935 99.4330 127.4905 2.1729 58.1091 28.604 8586 99.4330 80.8830 0.1343 62.5162 18.628 3474 99.4330 80.8830 0.1343 62.5162 18.628 3474 99.4330 342.8520 6.1391 562.2097 65.242 17958 99.4330 60.6575 0.4589 56.2097 85.628 3802 99.3814 95.7180 0.1739 126.6171 28.881 17083 99.3814 94.0705 0.1407 68.1044 24.931 1016 99.3814 178.2220 0.7651 94.6033 45.422 24248 99.4330 60.6575 0.4589 56.2079 85.628 17083 99.3814 94.0705 0.1407 68.1044 24.931 1016 99.3814 178.2220 0.7651 94.6033 45.424 24248 99.3814 95.7180 0.1739 126.6171 28.881 17083 99.3814 95.7180 0.1739 126.6171 28.881 17083 99.3814 94.0705 0.1407 68.1044 24.931 1016 99.3814 59.5815 0.2199 84.6218 129.891 16081 99.3814 59.5815 0.2199 84.6218 129.891 16081 99.3814 59.5815 0.2199 84.6218 129.891 16081 99.3814 59.5815 0.2199 84.6218 129.891 16081 99.3814 59.5815 0.2199 84.6218 129.891 16081 99.3814 59.5815 0.2199 84.6218 129.891 16081 99.3814 90.6215 0.3415 57.5682 20.438 16081 99.3814 90.6215 0.3415 57.5682 20.438 16081 99.3814 90.6215 0.3415 57.5682 20.438 16081 99.3814 90.6215 0.3415 57.5682 20.438 16081 99.3814 90.6215 0.3415 57.5682 20.438 16081 99.3814 90.6215 0.3415 57.5682 20.438 16081 99.3814 90.6215 0.3415 57.5682 20.438 16081 99.3814 90.6215 0.3415 57.5682 20.438 16081 99.3299 14.0500 0.9164 18.6465 99.3299 14.0500 0.9164 18.6465 99.3299 14.0500 0.9			361.9505	0.6894		
1588   99.5361   673.6840   0.5218   88.3147   40.358   15888   99.5361   673.6840   0.6109   790.2653   146.764   146.764   146.764   191.3681   191.4369   42.911   18274   99.5361   348.0135   4.7751   558.8275   137.488   1918   99.4845   20.1245   0.1336   3.2394   14.258   16649   99.4845   216.8705   0.2199   259.9159   56.447   17075   99.4845   211.1840   5.8548   349.3276   65.428   17075   99.4845   483.0040   5.6286   759.7738   135.933   11258   99.4845   483.0040   5.6286   759.7738   135.933   12583   99.4330   88.7140   1.0974   52.1067   20.033   12583   99.4330   76.315   0.0219   22.8935   102.794   25538   99.4330   76.315   0.0219   22.8935   102.794   3910   99.4330   682.6415   566.5361   10.8047   59.916   16482   99.4330   682.6415   566.5361   10.8047   59.916   16482   99.4330   78.0675   0.2722   44.8844   21.656   24.227   99.4330   987.6825   4.8317   1627.0752   502.013   193.5   99.4330   127.4905   2.1729   58.1091   28.604   193.5   193.5   194.3194   41.766   193.5   43.444   99.4330   342.8520   6.1391   562.2097   105.242   17958   99.4330   342.8520   6.1391   562.2097   105.242   17958   99.4330   60.6575   0.4589   56.2079   85.628   3802   99.3814   95.7180   0.1739   126.6171   28.861   1016   99.3814   178.2220   0.7651   94.6033   45.424   2.1513   99.3814   94.0705   0.1407   68.1044   24.931   1016   99.3814   178.2220   0.7651   94.6033   45.424   2.2133   99.3814   94.0705   0.1407   68.1044   24.931   1016   99.3814   59.5815   0.2199   84.6218   129.891   1016   99.3814   59.5815   0.2199   84.6218   129.891   1016   99.3814   59.5815   0.2199   84.6218   129.891   1016   99.3814   59.5815   0.2199   84.6218   129.891   129.993   99.3814   96.6510   9.3126   469.3736   64.349   75.5829   36.5320   0.07651   94.6033   45.4242   2.233   99.3814   59.5815   0.2199   84.6218   129.891   10.8663   99.3299   36.5320   0.07651   34.6663   99.3299   36.5320   0.07651   34.6663   99.3299   36.6320   0.0760   39.1366   10.8663   99.3299   36.6320   0.0760   39.1366   10.				2.0584		
15888   99.5361   673.6840   0.6109   790.2653   146.762			41.5630	0.5218		40.3559
21002         99.5361         137.8110         0.3861         191.4369         42.915           18274         99.5361         348.0135         4.7751         558.8275         137.481           1918         99.4845         20.1245         0.1336         3.2394         14.255           16649         99.4845         216.8705         0.2199         259.9159         56.442           17075         99.4845         211.1840         5.8548         349.3276         65.426           6525         99.4845         483.0040         5.6286         759.7738         135.93           11258         99.4845         48.300         3.9301         8.4739         24.77           25538         99.4830         88.7140         1.0974         52.1067         20.03           25411         99.4330         162.1815         0.0219         22.8935         102.79           3910         99.4330         162.1815         0.0167         145.3141         35.446           3661         99.4330         141.6685         0.3387         194.3194         41.766           16482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330			673.6840	0.6109		
18274         99.5361         348.0135         4.7751         558.8275         137.486           1918         99.4845         20.1245         0.1336         3.2394         14.251           16649         99.4845         216.8705         0.2199         259.9159         56.426           17075         99.4845         211.1840         5.8548         349.3276         65.426           6525         99.4845         483.0040         5.6286         759.7738         135.933           11258         99.4845         48.4830         3.9301         8.4739         24.772           25538         99.4830         88.7140         1.0974         52.1067         20.035           25531         99.4330         7.6315         0.0219         22.8935         102.794           3910         99.4330         162.1815         0.1167         145.3141         35.466           8661         99.4330         682.6415         566.5361         10.8047         59.914           16482         99.4330         78.0675         0.2722         44.8844         21.652           24327         99.4330         127.4905         2.1729         58.1091         28.604           3586         99.4330 <td></td> <td></td> <td>137.8110</td> <td>0.3861</td> <td></td> <td></td>			137.8110	0.3861		
1918         99.4845         20.1245         0.1336         3.2394         14.257           16649         99.4845         216.8705         0.2199         259.9159         56.442           17075         99.4845         211.1840         5.8548         349.3276         65.425           6525         99.4845         483.0040         5.6286         759.7738         135.93           11258         99.4845         48.4830         3.9301         8.4739         24.772           25538         99.4330         76.315         0.0219         22.8935         102.793           3910         99.4330         162.1815         0.1167         145.3141         35.446           8661         99.4330         682.6415         566.5361         10.8047         59.915           16482         99.4330         78.0675         0.2722         44.8844         21.656           18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         342.8520         6.1391         1627.0752         502.013           11935         99.4330 <td></td> <td></td> <td>348.0135</td> <td>4.7751</td> <td></td> <td></td>			348.0135	4.7751		
16649         99.4845         216.8705         0.2199         259.9159         56.442           17075         99.4845         211.1840         5.8548         349.3276         65.425           6525         99.4845         483.0040         5.6286         759.7738         135.933           11258         99.4845         48.4830         3.9301         8.4739         24.772           25538         99.4330         88.7140         1.0974         52.1067         20.033           25411         99.4330         7.6315         0.0219         22.8935         102.792           3910         99.4330         162.1815         0.1167         145.3141         35.448           8661         99.4330         162.1815         0.1167         145.3141         35.448           16482         99.4330         141.6685         0.3387         194.3194         41.765           18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         187.6825         4.8317         1627.0752         502.013           11935         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330			20.1245	0.1336		
17075			216.8705	0.2199		
6525         99.4845         483.0040         5.6286         759.7738         135.93           11258         99.4845         48.4830         3.9301         8.4739         24.772           25538         99.4330         88.7140         1.0974         52.1067         20.033           25411         99.4330         7.6315         0.0219         22.8935         102.792           3910         99.4330         162.1815         0.1167         145.3141         35.446           8661         99.4330         682.6415         566.5361         10.8047         59.915           16482         99.4330         141.6685         0.3387         194.3194         41.765           18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         127.4905         2.1729         58.1091         28.604           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.976           3802         99.3814			211.1840	5.8548		
11258         99.4845         48.4830         3.9301         8.4739         24.772           25538         99.4330         88.7140         1.0974         52.1067         20.035           25411         99.4330         76.315         0.0219         22.8935         102.794           3910         99.4330         162.1815         0.0167         145.3141         35.446           8661         99.4330         682.6415         566.5361         10.8047         59.91           16482         99.4330         141.6685         0.3387         194.3194         41.765           18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         80.8830         0.1343         622.5162         18.628           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.976           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814			483.0040			
25538         99.4330         88.7140         1.0974         52.1067         20.035           25411         99.4330         7.6315         0.0219         22.8935         102.794           3910         99.4330         162.1815         0.1167         145.3141         35.446           8661         99.4330         162.6415         566.5361         10.8047         59.915           16482         99.4330         141.6685         0.3387         194.3194         41.765           24327         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         127.4905         2.1729         58.1091         28.604           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.972           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814			48.4830			
25411         99.4330         7.6315         0.0219         22.8935         102.792           3910         99.4330         162.1815         0.1167         145.3141         35.446           8661         99.4330         682.6415         566.5361         10.8047         59.915           16482         99.4330         141.6685         0.3387         194.3194         41.765           18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         987.6825         4.8317         1627.0752         502.013           11935         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.976           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1407         68.1044         24.931           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814 <td></td> <td></td> <td>88.7140</td> <td>1.0974</td> <td></td> <td></td>			88.7140	1.0974		
3910         99.4330         162.1815         0.1167         145.3141         35.446           8661         99.4330         682.6415         566.5361         10.8047         59.915           16482         99.4330         141.6685         0.3387         194.3194         41.765           18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         987.6825         4.8317         1627.0752         502.013           11935         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         80.8830         0.1343         62.5162         18.628           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.979           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814 <td></td> <td></td> <td>7.6315</td> <td>0.0219</td> <td></td> <td></td>			7.6315	0.0219		
8661         99.4330         682.6415         566.5361         10.8047         59.915           16482         99.4330         141.6685         0.3387         194.3194         41.765           18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         987.6825         4.8317         1627.0752         502.013           11935         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         80.8830         0.1343         62.5162         18.628           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.97           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814 <td></td> <td></td> <td>162.1815</td> <td></td> <td></td> <td></td>			162.1815			
16482         99.4330         141.6685         0.3387         194.3194         41.765           18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         987.6825         4.8317         1627.0752         502.013           11935         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         80.8830         0.1343         62.5162         18.628           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.979           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814			682.6415			
18482         99.4330         78.0675         0.2722         44.8844         21.656           24327         99.4330         987.6825         4.8317         1627.0752         502.013           11935         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         80.8830         0.1343         62.5162         18.628           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.979           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814			141.6685	0.3387		
24327         99.4330         987.6825         4.8317         1627.0752         502.013           11935         99.4330         127.4905         2.1729         58.1091         28.604           8586         99.4330         80.8830         0.1343         62.5162         18.628           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.65555         23.1313         41.979           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814 </td <td></td> <td></td> <td></td> <td>0.2722</td> <td></td> <td></td>				0.2722		
11935         99,4330         127,4905         2,1729         58,1091         28,604           8586         99,4330         80,8830         0,1343         62,5162         18,628           3474         99,4330         342,8520         6,1391         562,2097         105,242           17958         99,4330         73,3915         0,6555         23,1313         41,979           16954         99,4330         60,6575         0,4589         56,2079         85,628           3802         99,3814         95,7180         0,1739         126,6171         28,881           17083         99,3814         94,0705         0,1407         68,1044         24,931           1016         99,3814         178,2220         0,7651         94,6033         45,424           25133         99,3814         35,4365         0,0898         19,0683         16,376           24248         99,3814         59,5815         0,2199         84,6218         129,891           8662         99,3814         59,5815         0,2199         84,6218         129,891           20939         99,3814         296,6510         9,3126         469,3736         64,349           753         99,3814			987.6825	4.8317		
8586         99.4330         80.8830         0.1343         62.5162         18.626           3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.979           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         206.6510         9.3126         469.3736         64.349           753         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299			127.4905	2.1729		
3474         99.4330         342.8520         6.1391         562.2097         105.242           17958         99.4330         73.3915         0.6555         23.1313         41.979           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299			80.8830			
17958         99.4330         73.3915         0.6555         23.1313         41.979           16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         206.6510         9.3126         469.3736         64.349           753         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299			342.8520			
16954         99.4330         60.6575         0.4589         56.2079         85.628           3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299		99.4330	73.3915			
3802         99.3814         95.7180         0.1739         126.6171         28.881           17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         90.6215         0.3415         57.5682         20.438           16081         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299			60.6575	0.4589		
17083         99.3814         94.0705         0.1407         68.1044         24.931           1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000		99.3814	95.7180			
1016         99.3814         178.2220         0.7651         94.6033         45.424           25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         206.6510         9.3126         469.3736         64.349           753         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000		99.3814	94.0705			
25133         99.3814         35.4365         0.0898         19.0683         16.376           24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         90.6215         0.3415         57.5682         20.438           16081         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000			178.2220	0.7651		
24248         99.3814         59.5815         0.2199         84.6218         129.891           8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         90.6215         0.3415         57.5682         20.438           16081         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         71.6715         0.0092         45.3825         18.610			35.4365			
8662         99.3814         678.8710         609.6066         -33.8688         71.766           20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         90.6215         0.3415         57.5682         20.438           16081         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         71.6715         0.0092         45.3825         18.610			59.5815			
20939         99.3814         296.6510         9.3126         469.3736         64.349           753         99.3814         90.6215         0.3415         57.5682         20.438           16081         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         71.6715         0.0092         45.3825         18.610		99.3814	678.8710			
753         99.3814         90.6215         0.3415         57.5682         20.438           16081         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         71.6715         0.0092         45.3825         18.610			296.6510			
16081         99.3814         202.3560         7.3978         87.7021         67.093           2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         160.0000         122.4790         0.5190         61.0149         15.996           3486         100.0000         71.6715         0.0092         45.3825         18.610		99.3814	90.6215			
2119         99.3299         19.1290         0.0863         29.3608         8.836           734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         122.4790         0.5190         61.0149         15.996           3486         100.0000         71.6715         0.0092         45.3825         18,610		99.3814	202.3560			
734         99.3299         36.5320         0.0750         39.1366         10.868           20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         122.4790         0.5190         61.0149         15.996           3486         100.0000         71.6715         0.0092         45.3825         18.610						
20281         99.3299         44.0540         0.9164         18.6465         9.683           8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         122.4790         0.5190         61.0149         15.996           3486         100.0000         71.6715         0.0092         45.3825         18.610			36.5320			
8663         99.3299         946.6095         661.5373         -50.7499         160.678           18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         122.4790         0.519C         61.0149         15.996           3486         100.0000         71.6715         0.0092         45.3825         18.610						
18135         99.3299         204.7280         2.3278         139.0666         28.613           13504         100.0000         -2.8185         0.0813         23.0195         17.497           12367         100.0000         122.4790         0.5190         61.0149         15.996           3486         100.0000         71.6715         0.0092         45.3825         18.610			946.6095			
13504     100.0000     -2.8185     0.0813     23.0195     17.497       12367     100.0000     122.4790     0.5190     61.0149     15.996       3486     100.0000     71.6715     0.0092     45.3825     18.610						
12367         100.0000         122.4790         0.5190         61.0149         15.996           3486         100.0000         71.6715         0.0092         45.3825         18.610						
3486 100.0000 71.6715 0.0092 45.3825 18.610						
00.450						
	23452	100.0000	87.2960	0.1273		27.7784

LGC ID	: 3 hrs LDA Score	Mean Tox	100		•
12261	100.0000		SD Tox	Mean Nontox	SD Nontox
16447	100.0000				46.670
9629	100.0000			22.2409	30.826
7992				109.4844	36.426
11256	100.0000	164.3995		139.4257	42.554
4827	100.0000	15.6665	0.0049	45.2588	24.428
21522	100.0000	368.6650	0.0057	297.3386	72.862
	100.0000	-5.6725	0.4773	281.9593	145.106
1906	100.0000	296.1400	0.0721	260.3344	
4143	99.9485	211.6065	0.1181	163.5920	111.485
6364	99.9485	130.6750	0.0269	204.3970	41.441
8965	99.9485	-6.7810	0.0523	21.9504	58.965
19012	99.9485	859.4450	1.9898	456.8430	18.045
4102	99.9485	45.2145	0.0106	25.3158	117.170
24346	99.9485	22.2060	0.0057	22.7899	23.577
13886	99.9485	89.1165	0.0219		13.3460
11606	99.9485	38.8675	0.0389	70.9494	23.5754
9604	99.9485	1745.8500	7.3115	59.8457	25.586
8099	99.9485	-5.3630	0.0382	401.4725	410.1580
23756	99.9485	112.8855	0.0382	23.7230	13.6996
5486	99.9485	42.9570	0.0149	488.9448	451.6976
7852	99.9485	218.7985		-0.6565	26.3667
7584	99.9485	-11.1985	0.1337	311.1944	72.4066
23730	99.8969	38.6280	0.1435	52.0467	68.1599
14720	99.8969	104.1585	0.0354	24.8364	14.4108
12399	99.8969	215.2455	0.0884	50.4903	41.8844
7285	99.8969	247.7395	0.1605	145.4078	40.4092
5775	99.8969	152.3685	0.1167	216.2511	38.4607
6192	99.8969		1.5549	27.7251	47.4649
7193	99.8969	-354.8340	8.0441	237.4106	255.7853
22267	99.8969	20.8670	0.0311	2.5197	19.4278
5983	99.8969	130.1385	0.0926	85.0324	51.7028
3162	99.8969	487.2100	0.1839	583.5955	202.5020
2582	99.8969	366.2300	1.5005	200.6923	67.7833
2674		171.0265	0.5480	92.5514	34.7755
18188	99.8969	224.5095	0.0332	267.6288	131.5045
15089	99.8969	39.1870	0.0255	31.5260	17.8793
23644	99.8969	213.8270	0.3606	131.2459	49.1067
14028	99.8969	-25.2295	0.0983	36.3866	35.2960
6667	99.8454	193.4115	0.4264	123.9913	57.6787
	99.8454	71.0770	0.0424	91.2817	
13673	99.8454	50.4420	0.0255	28.8487	19.4419
8458	99.8454	266.1145	2.8235	166.1049	11.8323
24200	99.8454	779.5775	0.2510	653.9327	30.2839
10665	99.8454	284.4280	0.7693	162.6899	203.8749
12289	99.8454	40.3230	0.0792	22.4664	74.5278
23952	99.8454	15.6945	0.0686		15.4457
19121	99.8454	3057.4551	0.5289	45.1670	23.7826
7212	99.8454	70.1740	0.0438	3028.0362	555.0941
20345	99.8454	145.6510	1.1215	74.6855	32.5412
10004	99.8454	77.9140	0.0764	81.5308	23.2042
8109	99.7938	33.7350		53.1737	27.7288
22786	99.7938	799.4390	0.32 <del>69</del>	53.8145	17.8506
17291	99.7938	4720.8425	0.4737	625.2440	193.9831

Timepoint(s)	: 3 hrs	PANOLAMINE	Atty. I	Ref. 44921-5090-0	01-WO/210548
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
14352	99.7938	206.7885	0.0686	` .	
4163	99.7938				
21998	99.7938				49.2398
3557	99.7423	42.1170			96.4055
12829	99.7423		0.2828		24.0155
18427	99.7423	174.8815	0.2694	241.1290	56.8656
12999		28.6200	0.0877	9.9802	17.7337
547	99.7423	857.1445	7.8538	337.2493	308.4064
	99.7423	689.5490	0.4455	676.8199	101.5816
7122	99.7423	344.5180	0.5233	298.6755	
14722	99.7423	349.6955	0.2581	492.6213	105.2170
10182	99.7423	45.7590	0.2051		181.0495
17236	99.7423	747.2100		33.4329	103.8738
	30.7 (20)	171.2100	2.5428	429.2370	135.6359

LGC ID	6, 24 hrs LDA Score	Mean Tox	SD Tox	Indo-	
23282	96.6321			Mean Nontox	SD Nontox
15003	96.3731	292.5183	27.4198		
15002	95.6477			95.2474	
11955	94.7150		148.4186		188.54
14017	94.6114		26.0833	1038.0379	272.528
18274	94.1451	375.4566	93.6905	240.5996	73.690
25556	93.2124	68.8204	28.4677	559.7208	137.267
11745	93.1088	404.8954	5.6114	29.7573	31.867
17255	92.6425	83.6826	25.9654	531.2629	83.212
23574	92.6425	1552.3563	15.2779	51.0805	18.086
18509	92.2798	484.3571	72.2094	2097.5285	437.368
13051	92.2280	27.3324	63.9467	694.1347	146.520
862	92.2280	310.8466	3.6170	16.1123	6.445
20083	92.1762	48.1340	27.2636	418.1332	64.960
18290	92.0207		2.6821	40.3216	21.703
17570	91.7098	509.1194 307.3379	34.8874	332.0679	115.961
11953	91.6580		28.6175	209.2414	61.322
15166	91.6580	398.8276	77.9296	662.3780	184.817
16514	91.6062	514.5230	52.5308	739.6475	145.804
18378	91.0363	430.0497	48.1219	614.0355	129.495
25589	90.8290	128.7649	7.9406	165.6063	31.042
18686	90.8290	364.5660	41.5931	255.7049	60.322
11954		572.7926	104.2364	911.7203	228.829
16007	90.7772	1672.2456	175.0063	2344.3517	494.653
24598	90.2073	50.4853	6.4947	29.7826	22.926
25918	90.2073	315.7369	10.3925	264.4997	43.071
13323	90.0000	80.6966	8.3625	54.8994	39.375
25377	89.9482	223.7043	31.6749	139.5109	113.399
11531	89.8964	49.8599	12.7428	27.0748	15.411
18687	89.8520	1192.2064	583.2821	404.9046	287.440
11530	89.7927	485.6997	71.5381	738.1348	185.682
18480	89.6447	714.7133	319.9269	208.3621	168.4034
	89.5855	466.2059	97.7725	257.8981	127.8104
19710	89.4819	69.3371	11.2650	48.5251	23.1099
1529	89.4301	61.6946	2.7659	50.8535	13.3227
11994	89.3264	84.3529	10.8849	121.4100	
20848 18275	89.0674	1955.7463	153.6749	1610.9763	26.2193 277.7725
	88.9637	403.553€	32.5152	524.5248	96.3246
20925	88.9119	883.0746	122.1168	1306.5312	334.9510
20832	88.9119	1360.6574	100.1177	1774.1365	387.1552
1190	88.9119	29.0673	3.8404	16.4193	9.0588
20875	88.4974	458.3149	46.8834	689.7731	204.4667
18246	88.3420	45.6010	9.1258	23.0123	36.8751
22781	88.2902	190.9210	40.6469	123.2367	56.2668
15213	88.2902	36.7447	7.9841	18.4398	12.8703
16566	88.1347	46.9776	5.7708	33.5268	
8829	88.1347	349.8157	26.7008	268.0625	10.0833 71.0694
20938	88.0311	1613.9081	152.1232	2056.1340	
10888	87.9793	71.3309	11.1992	52.4854	353.1722
1258	87.8756	33.1121	5.3294	16.5840	31.1755
16468	87.8238	1024.4 <del>0</del> 16	27.1392	2021.7983	15.0523
1763	87.7202	125.3086	60.4036	109.4191	356.3830
25692	87.7202	264.4379	46.7915	173.7627	149.6196

mepoint(s): GC ID	LDA Score	Tax -	,	Ref. 44921-5090-	
			SD Tox	Mean Nontox	SD Nontox
1743			2.2076	20.7862	
2262			6.9616		10.928
9124		223.1137	7.9505		26.485
16340	87.2539	60.3917	9.4543	31.0146	42.734
17203	87.2539	1772.4377	199.6902	2512.4899	23.117
1048	87.1058	90.5180	37.1124	31.8054	721.474
425	87.0466	35.5210	6.0923		22.741
7207	87.0022	67.7761	21.4276	20.8300	11.633
9029	86.9948	334.8343	21.9516	32.6028	15.688
14015	86.8986	272.5329	107.2673	444.5613	106.2402
15011	86.8912	120.9673	17.9317	101.1813	67.1043
18569	86.8468	3045.8633	766.5001	84.6938	28.9688
21416	86.8394	157.8959	22.0795	1593.0368	600.009
20582	86.8394	361.1994	49.1565	110.5525	38.4310
20417	86.7876	307.6200	25.0861	493.3099	97.9212
17305	86.6839	3601.7647	221.6319	235.6386	62.5571
20628	86.6321	466.5057		4627.6390	1378.7428
11989	86.5803	50.2694	66.0002	316.5499	131.9943
25590	86.5285	73.1583	6.4633	35.6511	12.9634
20855	86.5285	569.9809	5.8480	59.0984	23.5690
623	86.5285	147.8191	39.3160	700.8075	122.7485
14621	86.4249		10.3632	164.9374	60.4766
18770	86.3731	132.9804	10.6645	169.2472	36.9981
17686	86.3212	556.1281	53.8248	688.1387	104.3536
20856	86.3212	963.0883	48.2210	1133.9716	219.4970
25716	86.2176	942.6401	51.6837	1096.2841	187.3694
1929	86.1658	1109.6887	150.5948	807.0937	362.0858
1427	86.0622	741.1960	62.4841	950.6275	205.9505
17759	86.0104	29.5961	5.8026	15.8735	10.9553
23710	85.9660	49.6866	10.8265	85.4551	36.7873
17159	85.9585	529.3191	73.5864	329.4104	100.0248
11966	85.9585	1260.6044	101.0225	1019.7509	246.1818
23011		305.8084	25.9266	381.2756	69.6767
16546	85.8031	39.4394	4.3848	29.7453	9.0599
20879	85.7513	172.7831	38.3790	261.2547	70.6676
449	85.7513	46.6570	7.3709	81.3752	45.6809
15291	85.7513	2997.3389	246.8743	3834.6812	1041.0001
20997	85.6477	47.0491	4.1811	35.9738	9.8753
450	85.5959	61.9484	5.9282	45.2079	15.5244
22670	85.5959	3128.0366	170.6099	3755.0537	786.3385
1061	85.4922	73.1264	6.9285	58.6469	22.3076
25686	85.4404	86.9340	22.3149	73.3214	45.3425
17564	85.4404	1035.4801	46.0477	972.7482	197.9158
	85.4404	322.3890	27.0546	415.0968	80.8663
17345	85.4404	189.0813	14.8041	150.9683	
3692	85.4404	173.2706	10.8216	175.4433	38.5857
17394	85.3886	446.1611	53.8995	355.1608	50.7958
15150	85.3886	111.2653	16.6139	154.2286	92.2841
16524	85.3886	27.0314	1.4365	24.0146	39.3321
3211	98.0311	66.6360	34.2891		6.6058
22077	97.0984	363.6396	107.5762	5.9667	17.9288
367	96.9430	94.7897	23.9348	163.4551	61.1284
21284	96.8912	62.8293	24.6617	27.9197	20.3222

GC ID	LDA Score	Mean Tox	SD Tox	Moon	T
320	96.7358			Mean Nontox	SD Nontox
6606			72.5440		
5876	96.1140		505.7537	1863.5623	759 462
24209	95.8031	91.4460	114.7470	2768.0950	622.989
13293	95.3886	229.8451	34.1551	2.7632	41.730
13227	95.3886	81.3164	22.0740	116.1949	53.175
14871	94.8705	215.3607	9.6413	138.7205	35.584
11404	94.7668	150.3903	41.5905	123.1735	34.293
2822	94.6114	91.8054	16.7821	104.6500	35.232
2765	94.1969	183.5886	9.6384	135.4241	26.861
17679	93.8860	343.9430	19.0895	115.0886	33.368
13786	93.4715	14.4553	34.0654	517.0982	116.274
2339	93.0570	306.7930	7.8845	74.7719	36.684
2292	92.7979	25.2096	10.9140	386.3540	75.605
5929	92.6943	209.0469	13.6850	-71.6174	71.018
7740	92.5389	428.8254	22.1540	137.3411	38.721
4891	92.4870	103.6429	45.4969	299.7705	66.908
15085	92.3834	743.4240	19.0689	57.8671	25.117
6731	92.2798	62.2046	45.8589	973.9295	173.861
23013	92.2280	444.5369	9.5695	36.2936	15.297
2479	92.1762	58.0911	41.6573	327.2587	66.848
4073	91.9689	644.9791	6.0372	36.3388	17.757
2140	91.9689	209.0921	74.1188	1029.5107	285.972
2210	91.7617	2139.1216	12.5349	304.0739	78.043
2085	91.7098	1261.3720	135.2739	2737.1711	440.8233
11363	91.3990	315.3564	78.2204	1731.5486	370.4574
16547	91.3990	461.0147	23.6801	210.2154	72.5573
4480	91.3990	41.1996	64.7025	725.5751	191.6030
3100	91.3990	794.9033	10.5207	7.3608	19.7165
22266	91.2953	343.4190	65.6045	1097.4930	215.417
12117	91.2435	441.3817	13.1320	288.1070	53.1166
17914	91.1399	202.8573	36.2464	591.7778	123.9976
8609	90.8808	86.1916	20.2436	329.1647	103.5805
24314	90.8290	42.9569	8.4037	54.0325	20.7432
6281	90.7772	257.7624	5.1119	27.7019	10.7034
12581	90.6736	68.4811	27.9984	361.0210	72.9734
21446	90.6218	132.5327	11.4932	46.8436	19.9619
18151	90.6218	257.7351	6.9337	103.4067	25.3453
8692	90.6218	134.0539	12.2031	331.2631	71.1854
7147	90.5181	853.3451	73.2045	294.2883	95.2647
2363	90.5181	1101.3957	41.3161	1022.9910	159.9812
12887	90.4145	510.7066	92.1394	1401.1085	254.0833
13929	90.3183	266.3954	47.6326	681.5103	136.1835
12583	90.3109	40.6801	67.2132	110.0210	47.6954
13826	90.3109	1059.8284	5.7975	28.6403	13.1969
15685	90.3109	915.3636	121.9072	1392.5923	237.9938
8180	90.2591	76.0079	83.4273	1260.3512	258.3780
13645	89.8964	142.6637	9.2527	43.5807	22.4886
3973	89.8446	60.4890	7.1546	108.4173	27.0982
6969	89.7927	399.7476	4.6992	44.4703	13.9335
2316	89.7927	164.8530	63.0653	581.1672	129.8956
21948	89.7927		11.1358	118.7672	37.2458
	55.7527	326.6289	16.6420	425.4622	91.7499

TABLE 5HH: PHENYLPROPANOLAMINE Timepoint(s): 6, 24 hrs			Atty.	Ref. 44921-5090-	01-WO/2105485
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
12450	89.7409	649.2902	71,1500		
16777		3862.9322	219.1471	4933.5552	
18104		00.0121	7.9853		
11086			9.1862		
12878			12.0559	81.3163	10.1.00
14013		123.6516	24.3626	53.6167	52.4413
19118		123.5876	6.3026	152.9155	
23296		187.5871	8.8887	231.0563	38.7801
3213	- 00.1001	232.0496	8.8971	257.7325	
17847	89.3264	764.5647	65.5905	989.3253	

meponia	s): 24 hrs			Ref. 44921-5090-0	1.00
SLGC ID		Mean Tox	SD Tox		SD Nontox
24472					
12253				23.7028	52.09
1316			0.6163		22.59
11857	99.3292	23.4130	1.7704	97.4638	67.63
12022	98.8648	13.3380	1.7736	49.2371	43.84
8098	98.7100	664.3467	13.1359	461.1968	23.75
21801	98.7100	275.7437	19.5469	159.9897	97.74
24875	98.2972	37.8720	0.2612	30.1976	36.23
5497	98.2972	65.3230	0.2242	64.6593	12.98
15975	98.0908	42.0350	0.3971	56.9127	17.39
21350	97.9360	13.7053	1.8179		24.76
7505	97.8844	144.1997	0.7750	45.0369	18.33
18317	97.8844	629.8513	5.9087	125.3235	24.60
17854	97.8844	327.4563	58.2752	634.9720	291.65
951	97.8844	44.4547	2.8004	161.6262	43.150
18402	97.8328	54.1813	3.2482	17.1017	14.024
17896	97.7812	22.5927	0.7072	27.5530	9.523
20421	97.5232	144.1200	12.2177	19.6479	15.698
15311	97.3684	32.9633	0.7168	86.3885	18.155
17530	97.3684	107.8800		48.1633	21.781
15364	97.3168	71.8460	0.6250	95.1970	23.912
16016	97.2652	33.4540	0.7089	58.6785	19.528
20600	97.2652	44.5330	0.5998	22.9672	8.171
17752	97.2136	81.6657	2.5682	21.3412	12.952
25070	97.0588	162.9857	14.7103	29.7740	15.568
501	97.0072	20.1930	1.0567	160.2047	36.899
1708	96.9040	44.4910	0.3634	25.8435	13.953
18621	96.8524	-5.7877	0.5296	54.3027	15.954
19512	96.8524	1588.0173	1.6834	34.6783	31.419
15077	96.8524		48.5040	1082.3959	326.474
20982	96.8008	97.6783	11.2089	49.3145	88.618
23042	96.6460	145.7583	7.6887	221.6117	51.032
18444	96.5944	197.3407	8.6586	106.7764	46.154
14285	96.5944	20.6473	1.0310	7.6059	66.513
11794	96.5944	25.4840	0.1620	23.6379	6.463
15136	96.5428	46.2100	3.1632	21.6649	12.3448
1467	96.5428	1155.0750	12.7427	1073.2833	274.6143
7594	96.4912	61.8283	16.5016	131.3942	30.130
15353	96.4912	28.0340	0.5483	21.6667	9.7468
16446	96.2848	28.4327	1.0063	19.3194	16.9895
23551	96.2848	38.8180	0.4042	34.9380	9.2352
15190	96.2332	46.8823	3.2267	18.8815	17.5348
17350		105.7410	2.7242	244.0274	340.9260
25793	96.2332	40.8510	2.3119	69.9725	23.8683
1028	96.1300	4.2637	0.8715	22.9080	13.7883
1376	96.0784	9.9707	0.5105	22.7991	17.4441
20056	95.9752	23.5600	0.5183	16.9839	5.9008
20818	95.9752	105.1077	5.6354	153.9815	29.3965
24718	95.9752	185.2633	5.4172	137.3185	39.7174
	95.9236	18.8950	0.6354	27.9234	8.9048
1323	95.9236	107.1023	4.0302	183.9743	78.7005
4500	95.8720	414.6623	43.8882	284.2921	53.4068
24617	95.8204	30.8503	15.5449	-5.4250	15.3317

TABLE 5II: ROSIGLITAZONE Timepoint(s): 24 hrs			Atty. Ref. 44921-5090-01-WO/210548			
GLGC ID	LDA Score	Mean Tox				
546	95.8204	194.8440		Mean Nontox	SD Nontox	
16681	95.8204				51.19	
4832	95.7172		5.1952		9.83	
983	95.6140				211.05	
8139	95.6140	128.6430	1.4157	119.2699	32.61	
19909	95.5108	23.1377	1.3032	12.1322	7.78	
16456	95.4592	21.1263	0.8218	35.7468	22.63	
15957	95.4592	255.4150	22.1686	159.3539	43.18	
20890		556.3827	29.7318	364.8595	103.23	
506	95.4592	118.9190	17.5009	61.3683	29.06	
16715	95.4076	15.0697	0.4476	21.5576	7.488	
18898	95.4076	38.3687	4.2783	15.5772		
	95.3560	54.2523	0.8445	62.3646	12.615	
22145	95.3560	98.1663	3.8046	62.9135	14.706	
24628	95.2528	447.0150	41.9194	312.6532	33.436	
18563	95.2528	49.5193	10.3168	25.7709	61.244	
104	95.2012	28.1137	0.7287		8.995	
22584	95.2012	57.9050	7.0705	36.4934	11.174	
19505	95.2012	75.6870	4.1889	30.3178	13.455	
15980	95.0464	125.0830	19.6528	49.6742	16.386	
17287	95.0464	64.3560	11.7193	77.0015	20.969	
4133	94.9948	143.7777		31.8702	12.466	
15748	94.9948	41.3827	8.5126	103.6586	20.976	
11982	94.9948	49.1207	1.3871	26.1896	12.076	
23871	94.9432	29.7637	0.9843	38.9172	13.534	
18949	94.9432	140.1103	0.6199	42.2141	22.888	
1822	94.9432		1.4782	151.1395	38.501	
22625	94.9432	21.5107	0.4403	23.7649	9.635	
957	94.8916	108.8400	12.9449	65.9630	32.196	
15511	94.8916	17.5493	1.1851	34.9745	22.7440	
24697	94.8916	526.8320	7.8951	512.3926	127.634	
15844	94.7368	190.7280	7.0129	155.0495	43.0660	
17508		39.7727	0.5520	39.7593	11.8411	
6892	94.7368	40.9170	1.0277	30.7312	10.7056	
22916	94.6852	80.6820	1.5026	68.3677	36.1805	
	94.6852	898.5600	35.8058	667.8349	138.1971	
21972	94.6336	169.8320	1.7219	166.5296		
15165	94.6336	220.2500	6.6959	179.3605	33.5529	
23705	94.5820	436.1430	70.3843	264.3237	54.2251	
19124	94.5304	80.5830	20.9013		68.1876	
16155	94.4788	20.0507	0.4562	26.8310	22.5233	
16082	94.4788	72.9257	14.5015	27.4904	16.4814	
10886	94.4788	29.2663	5.0680	37.5357	15.8036	
82	94.4788	8.3277	19.7431	89.4606	71.7197	
19667	94.4788	23.2083	1.2392	35.7844	13.6356	
24471	94.4272	124.0640		9.3084	14.6636	
15598	94.3756	445.8727	5.3375	89.1225	32.4936	
16675	94.3756	49.2383	97.3531	769.5472	158.9894	
1638	94.3756	98.9327	8.7158	23.6577	17.4757	
20647	94.3756	30.9327	5.8472	152.7614	49.9279	
9979	99.5872	30.8430	1.9821	15.5861	10.3438	
13266	99.4324	9.8250	0.0605	20.9416	12.0624	
10004	99.3808	36.1200	0.5561	95.0549	45.4090	
3547		44.3577	0.1781	53.2520	27.7615	
	99.1744	73.7057	4.8615	8.1680	17.5728	

Carrier   Carr		ŖOSIGLĮTAZ	ONE	Atty.	Ref. 44921-5090-0	01-WO/2105485
2055 99.1744 32.4663 0.2568 47.7918 16.545 23828 99.0712 59.2920 0.2020 58.3427 27.896 5996 99.0196 85.4693 0.1695 86.7945 25.270 16014 98.9164 106.4107 0.4908 81.6568 48.145 5513 98.9164 26.9637 0.0876 24.2733 19.971 7520 98.8648 39.0613 0.1274 38.8223 22.939 6821 98.7616 125.9117 0.9537 181.8108 52.340 2261 98.4004 4.0707 3.0124 46.7104 24.723 10233 98.3488 364.5093 5.9464 226.8268 103.4811 224146 98.2972 137.2997 2.0674 202.1487 49.6011 10900 98.2972 119.5810 0.5910 118.5750 39.436 3257 98.2456 51.7370 12.5256 198.1059 74.797 21508 98.1940 106.3280 2.5616 77.0680 16.558 11160 98.0392 48.3053 1.3174 83.3922 56.6098 23277 98.0392 48.3653 1.3174 83.3922 56.6098 23277 98.0392 68.8487 2.0289 30.8753 23.4437 11412 97.9360 159.9210 3.9050 85.4271 40.4725 7715 97.8844 13.0380 1.861 33.6916 11.9322 18811 97.7812 43.8537 0.5556 54.5499 2.2436 197.797.7912 43.8537 0.5556 54.5499 2.2436 199.09 97.9360 504.4400 8.5411 361.7481 93.5438 141412 97.9360 159.9210 3.9050 85.4271 40.4722 18811 97.7812 43.8537 0.5556 54.5499 2.24369 14901 97.5748 43.6537 0.5556 54.5499 2.24369 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2333 37.6604 14.2978 14901 97.5748 60.1213 1.2339 37.6604 14.2978 14901 97.5748 60.1213 1.2339 37.6604 14.2978 14901 97.5748 60.1213 1.2					*	
23828   99.0712   59.2920   0.2020   58.3427   27.896   5996   599.0196   52.4167   24.3389   556.9885   145.0941   6014   98.9164   106.4107   0.4908   81.6568   48.1455   6513   98.9164   26.9637   0.0876   24.2733   19.971   7520   98.8648   39.0613   0.1274   38.8223   22.339   6821   98.7616   125.9117   0.9537   181.8108   52.340   2261   98.7616   125.9117   0.9537   181.8108   52.340   2261   98.4004   4.0707   3.0124   46.7104   24.725   98.38   98.3488   364.5093   5.9464   226.8268   103.4811   10233   98.3488   46.7777   13.2959   142.1598   44.048   10233   98.3488   46.7777   13.2959   142.1598   44.048   24.028   26.0268   27.340   24.028   26.028   27.3997   2.0674   202.1487   49.6011   10900   98.2972   119.5810   0.5910   118.5750   39.4366   33.257   98.2456   51.7370   12.5226   198.1059   74.7974   21508   98.1940   106.3280   2.5616   77.0680   16.558   23277   98.0392   48.3053   1.3174   83.3922   56.8069   23277   98.0392   68.8497   2.0289   30.8753   23.443   12043   97.9876   306.3733   44.4038   128.5108   79.237   12043   97.9876   306.3733   44.4038   128.5108   79.237   14112   79.9360   504.4400   8.5411   361.7481   93.5431   1412   97.9360   504.4400   8.5411   361.7481   93.5431   1412   97.9360   504.4400   8.5411   361.7481   93.5431   1412   97.9360   159.9210   3.9050   85.4271   40.4722   2777   97.7812   43.8537   0.5556   54.5499   22.4362   22777   97.7812   43.8537   0.5556   54.5499   22.4362   22777   97.7812   43.8537   0.5556   54.5499   22.4362   22777   97.7812   40.950910   10.4442   1368.8336   415.2675   14.6674   97.5748   7.2960   0.8259   38.1981   31.5191   27.9748   7.2960   0.8259   38.1981   31.5191   27.9748   7.2960   0.8259   38.1981   31.5191   27.9748   7.2960   0.8259   38.1981   31.5191   27.5748   7.2960   0.8259   38.1981   31.5191   27.5748   7.2960   0.8259   38.1981   31.5191   27.5748   7.2960   0.8259   38.1981   31.5191   27.5748   7.2960   0.8259   38.1981   31.5191   27.5748   7.2960   0.8259   38.1981   31.5191   27.5748   27.5748					Mean Nontox	SD Nontox
2.5826         99.07196         85.4693         0.1695         86.7945         25.270           20924         99.0196         92.04167         24.3389         556.9585         145.0911           6014         98.9164         106.4107         0.4908         81.6568         48.145.51           5513         98.9164         26.9637         0.0876         24.2733         19.971           7520         98.8648         39.0613         0.1274         38.8223         22.939           6821         98.7616         125.9117         0.9537         181.8108         52.340           2261         98.4004         4.0707         3.0124         46.7104         24.725           9838         98.3488         364.5093         5.9464         226.8268         103.4811           10233         98.3484         46.7777         13.2959         142.1598         44.048           24146         98.2972         119.5810         0.5910         118.5750         39.436           3257         98.2456         51.7370         12.5226         198.1059         74.797           21508         98.1940         106.3280         2.5616         77.0880         16.558           11160         98.0					47.7918	16.5450
3990   99.0196   85.4693   0.1695   86.7945   25.270						
20924   99.0196   920.4167   24.3389   556.9585   145.091						
September   Sept						
3915   98.89648   39.0613   0.1274   38.8223   22.939					81.6568	
6821   98,7616   125,9117   0.9537   181,8108   52,3401					24.2733	
2261   98.4004   4.0707   3.0124   46.7104   24.7261     9838   98.3488   364.5093   5.9464   226.8268   103.4811     10233   98.3488   46.7777   13.2959   142.1598   44.0484     24146   98.2972   137.2997   2.0674   202.1487   49.6011     10900   98.2972   119.5810   0.5910   118.5750   39.4368     3257   98.2456   51.7370   12.5226   198.1059   74.7974     21508   98.1940   106.3280   2.5616   77.0680   16.5581     11160   98.0392   48.3053   1.3174   83.3922   56.6093     23277   98.0392   68.8487   2.0289   30.8753   23.4431     12043   97.9876   308.3733   44.4038   128.5108   79.4231     13412   97.9360   159.9210   3.9050   85.4271   40.4725     7715   97.8844   53.2420   8.7023   -0.2863   34.911     18811   97.7812   43.8537   0.5556   54.6499   22.4365     22737   97.7812   1095.0910   10.4442   1368.8336   415.2677     3353   97.7296   130.9480   1.4366   93.8077   27.0583     3669   97.6780   258.0857   1.5790   209.6585   63.3883     3625   97.6264   512.6547   10.0059   344.9622   125.2036     14901   97.5748   7.2960   0.8259   38.1981   31.5191     23998   97.5748   60.1213   1.2333   37.6604   14.2976     17664   97.5232   64.0910   0.4108   68.5611   29.4563     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23937   97.4716   41.8730   0.3260   51.9646   61.9768     23938   97.5748   60.1213   1.2333   37.6004   41.2977     2300   97.4716   41.8730   0.3260   51.9646   61.9768     23237   97.4200   551.6417   19.8714   365.3683   71.8291     23239   97.5748					38.8223	22.9392
9838 98.3488 364.5093 5.9464 226.8268 103.4811 10233 98.3488 46.7777 13.2959 142.1598 44.048 10233 98.3488 46.7777 13.2959 142.1598 44.048 10233 98.3488 46.7777 13.2959 142.1598 44.048 10590 98.2972 137.2997 2.0674 202.1487 49.6011 10900 98.2972 119.5810 0.5910 118.5750 39.436 3257 98.2456 51.7370 12.5226 198.1059 74.797 21508 98.1940 106.3280 2.5616 77.0680 16.558 11160 98.0392 48.3053 1.3174 83.3922 56.6093 23277 98.0392 68.8487 2.0289 30.8753 23.443 12043 97.9876 308.3733 44.4038 128.5108 79.423 11412 97.9360 159.9210 3.9050 85.4271 40.4725 7715 97.8844 13.0380 1.1861 33.6916 11.9325 6745 97.8844 53.2420 8.7023 -0.2863 34.9115 97.8844 53.2420 8.7023 -0.2863 34.9115 97.8844 53.2420 8.7023 -0.2863 34.9115 97.7812 43.8537 0.5556 54.5499 22.4363 22.737 97.7812 1095.0910 10.4442 1368.8336 415.2677 3353 97.7296 130.9480 1.4366 93.8077 27.0583 3625 97.6264 512.6547 10.0059 344.9622 125.2035 14901 97.5748 7.2960 0.8259 38.1981 31.5191 23998 97.5748 60.1213 1.2333 37.6604 14.2978 3316 97.5748 60.1213 1.2333 37.6604 14.2978 12590 97.4716 41.8730 0.3260 51.9646 16.9768 23937 97.4716 10.85207					181.8108	52.3404
99.3488						
24146         98.2972         137.2997         2.0674         202.1487         49.6011           10900         98.2972         119.5810         0.5910         118.5750         39.436           3257         98.2456         51.7370         12.5226         198.1059         74.797.           21508         98.1940         106.3280         2.5616         77.0680         16.558           11160         98.0392         48.3053         1.3174         83.3922         56.6098           23277         98.0392         68.8487         2.0299         30.8753         23.443           12043         97.9876         308.3733         44.4038         128.5108         79.423           3969         97.9360         159.9210         3.9050         85.4271         40.4722           7715         97.8844         13.0380         1.1861         33.6916         11.932           6745         97.8844         13.0380         1.1861         33.6916         11.932           22737         97.7812         49.8537         0.5556         54.5499         22.4362           3353         97.7296         130.9480         1.4366         93.8077         27.0583           3625         97.6264<						103.4810
10900   98.2972   119.5810   0.5910   118.5750   39.4366   3257   98.2456   51.7370   12.5226   198.1059   74.7974   21508   98.1940   106.3280   2.5616   77.0680   16.558   23277   98.0392   48.3053   1.3174   83.3922   56.6098   23277   98.0392   68.8487   2.0289   30.8753   23.443   12043   97.9876   308.3733   44.4038   128.5108   79.4231   3969   97.9360   504.4400   8.5411   361.7481   93.5438   11412   97.9360   159.9210   3.9050   85.4271   40.4725   4					142.1598	44.0484
10900   98.2972   119.5810   0.5910   118.5750   39.4366   3257   98.2456   51.7370   12.5226   198.1059   74.797   21508   98.1940   106.3280   2.5616   77.0680   16.558   11160   98.0392   48.3053   1.3174   83.3922   56.6098   23277   98.0392   68.8487   2.0289   30.8753   23.443   39.9876   308.3733   44.4038   128.5108   79.423   3969   97.9360   504.4400   8.5411   361.7481   93.5436   31.4142   97.9360   159.9210   3.9050   85.4271   40.4725   7715   97.8844   13.0380   1.1861   33.6916   11.9325   43.8537   0.5556   54.5499   22.4362   22737   97.7812   43.8537   0.5556   54.5499   22.4362   22737   97.7812   1095.0910   10.4442   1368.8336   415.2678   3353   97.7296   130.9480   1.4366   93.8077   27.0583   3625   97.6264   512.6547   10.0059   344.9622   125.2036   33998   97.5748   60.1213   1.2333   37.6604   14.2978   3316   97.5748   60.1213   1.2333   37.6604   14.2978   23998   97.5748   60.1213   1.2333   37.6604   14.2978   23937   97.4716   41.8730   0.3260   51.9646   16.9768   23937   97.4716   41.8730   0.3260   51.9646   16.9768   23937   97.4716   41.8730   0.3260   51.9646   16.9768   23237   97.4200   551.6447   19.8714   865.9790   172.2860   17.5748   97.4200   551.6447   19.8714   865.9790   172.2860   17.5748   97.4200   50.6007   12.7741   356.3683   79.5264   23237   97.4716   41.8730   0.3260   51.9646   16.9768   23237   97.4716   41.8673   0.3017   21.4351   24.0066   23237   97.4200   551.6447   19.8714   865.9790   172.2860   17.5749   17.2860   17.5749   17.2860   17.27741   356.3683   79.5265   17.590   17.2860   17.28						49.6015
3257         98.2456         51.7370         12.5226         198.1059         74.7974           21508         98.1940         106.3280         2.5616         77.0680         16.558           11160         98.0392         48.3053         1.3174         83.3922         56.6098           23277         98.0392         68.8487         2.0289         30.8753         23.443           12043         97.9876         308.3733         44.4038         128.5108         79.423           3969         97.9360         504.4400         8.5411         361.7481         93.543           11412         97.9360         159.9210         3.9050         85.4271         40.4722           7715         97.8844         13.0380         1.1861         33.6916         11.932           6745         97.8844         53.2420         8.7023         -0.2863         34.911           18811         97.7812         1095.0910         10.4442         1368.8336         415.2673           22737         97.7812         1095.0910         10.4442         1368.8336         72.70583           3625         97.6264         512.6547         10.0059         344.9622         125.2036           3625					118.5750	39.4364
21506   98.0394   106.3280   2.5616   77.0680   16.558     23277   98.0392   68.8487   2.0289   30.8753   23.443     12043   97.9876   308.3733   44.4038   128.5108   79.423     3969   97.9360   504.4400   8.5411   361.7481   93.5436     11412   97.9360   159.9210   3.9050   85.4271   40.4722     12043   97.9844   13.0380   1.1861   33.6916   11.932     13045   97.8844   13.0380   1.1861   33.6916   11.932     14141   97.9861   13.9380   1.1861   33.6916   11.932     18811   97.7812   43.8537   0.5556   54.5499   22.4362     22737   97.7812   1095.0910   10.4442   1368.8336   415.2676     3353   97.7296   130.9480   1.4366   93.8077   27.0563     34080   97.6780   258.0857   1.5790   209.6585   63.3883     3625   97.6264   512.6547   10.0059   344.9622   125.2036     14901   97.5748   7.2960   0.8259   38.1981   31.5191     23998   97.5748   60.1213   1.2333   37.6604   14.2976     3316   97.5748   81.3407   1.4270   55.7346   29.2755     17664   97.5232   64.0910   0.4108   68.5611   29.4563     12690   97.4716   41.8730   0.3260   51.9646   16.9768     23937   97.4716   14.6573   0.3017   21.4351   24.0086     23937   97.4716   14.6573   0.3017   21.4351   24.0086     23237   97.4200   551.6417   19.8714   865.9790   172.2860     7903   97.4200   551.6417   19.8714   865.9790   172.2860     7903   97.4200   551.6417   19.8714   865.9790   172.2860     7903   97.4200   551.6417   19.8714   865.9790   172.2860     17231   97.2652   55.3620   0.7405   38.8405   31.8456     17231   97.2652   19.9853   20.1603   162.0343   112.7268     22755   97.2136   69.1977   0.8980   94.8261   33.3201     12702   97.2652   19.9853   20.1603   162.0343   112.7268     22755   97.2136   69.1977   0.8980   94.8261   33.3201     13712   97.1400   23257   23267   1458.7760   282.3528     22755   97.2136   69.1977   0.8980   94.8261   33.3201     22755   97.2136   69.1977   0.8980   94.8261   33.3201     22755   97.2136   69.1977   0.8980   94.8261   33.3201     22755   97.2136   69.1977   0.8980   94.8261   33.3201     22755   97					198.1059	74.7974
1160   96.0392   48.3053   1.3174   83.3922   56.6098   23277   98.0392   68.8487   2.0289   30.8753   23.4431   3969   97.9876   308.3733   44.4038   128.5108   79.4231   3969   97.9360   504.4400   8.5411   361.7481   93.5438   11412   97.9360   159.9210   3.9050   85.4271   40.4725   40.472						16.5581
12043   97.9876   308.3733   44.4038   128.5108   79.4231					83.3922	56.6098
12043   97.9876   308.3733   44.4038   128.5108   79.4237   3969   97.9360   504.4400   8.5411   361.7481   93.5438   11412   97.9360   159.9210   3.9050   85.4271   40.4725					30.8753	23.4431
3969         97.9360         504.4400         8.5411         361.7481         93.5436           11412         97.9360         159.9210         3.9050         85.4271         40.4726           7715         97.8844         13.0380         1.1861         33.6916         11.9323           6745         97.8844         53.2420         8.7023         -0.2863         34.9115           18811         97.7812         43.8537         0.5556         54.5499         22.4362           22737         97.7812         1095.0910         10.4442         1368.8336         415.2673           3353         97.7296         130.9480         1.4366         93.8077         27.0583           4080         97.6780         258.0857         1.5790         209.6585         63.3883           3625         97.6264         512.6547         10.0059         344.9622         125.2036           14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2976           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664				44.4038	128.5108	
11412         97,9360         159,9210         3,9050         85,4271         40,4725           6745         97,8844         13,0380         1,1861         33,6916         11,9323           18811         97,7812         43,8537         0,5556         54,5499         22,4362           22737         97,7812         1095,0910         10,4442         1368,8336         415,2673           3353         97,7296         130,9480         1,4366         93,8077         27,0583           4080         97,6780         258,0857         1,5790         209,6585         63,3883           3625         97,6264         512,6547         10,0059         344,9622         125,2036           14901         97,5748         7,2960         0,8259         38,1981         31,5191           23998         97,5748         60,1213         1,2333         37,6604         14,2978           3316         97,5748         81,3407         1,4270         55,7346         29,2755           17664         97,5232         64,0910         0,4108         68,5611         29,4583           12690         97,4716         41,8730         0,3260         51,9646         16,9768           23937					361.7481	
6745         97.8844         13.0380         1.1861         33.6916         11.9323           6745         97.8844         53.2420         8.7023         -0.2863         34.9118           18811         97.7812         43.8537         0.5556         54.5499         22.4362           22737         97.7812         1095.0910         10.4442         1368.8336         415.2677           3353         97.7296         130.9480         1.4366         93.8077         27.0583           4080         97.6780         258.0857         1.5790         209.6585         63.3883           3625         97.6264         512.6547         10.0059         344.9622         125.2036           14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97					85.4271	
6745         97.8844         53.2420         8.7023         -0.2863         34.9116           18811         97.7812         195.0910         10.4442         1368.8336         415.2679           3353         97.7296         130.9480         1.4366         93.8077         27.0563           4080         97.6780         258.0857         1.5790         209.6585         63.3883           3625         97.6264         512.6547         10.0059         344.9622         125.2036           14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237 <td< td=""><td></td><td></td><td></td><td>1.1861</td><td>33.6916</td><td></td></td<>				1.1861	33.6916	
18811         97.7812         43.8537         0.5556         54.5499         22.4362           22737         97.7812         1095.0910         10.4442         1368.8336         415.2678           3353         97.7296         130.9480         1.4366         93.8077         27.0583           4080         97.6780         258.0857         1.5790         209.6585         63.3883           3625         97.6264         512.6547         10.0059         344.9622         125.2036           14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23337         97.4716         14.6573         0.3017         21.4351         24.0086           23037         97.4716         108.5207         2.6341         198.3327         102.5249           23237         <					-0.2863	
22/3/         97.7812         1095.0910         10.4442         1368.8336         415.2678           3353         97.7296         130.9480         1.4366         93.8077         27.0583           4080         97.6780         258.0857         1.5790         209.6585         63.3883           3625         97.6264         512.6547         10.0059         344.9622         125.2036           14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         <				0.5556		
3393         97.7296         130.9480         1.4366         93.8077         27.0583           4080         97.6780         258.0857         1.5790         209.6585         63.3883           3625         97.6264         512.6547         10.0059         344.9622         125.2036           14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14401         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463 <td< td=""><td></td><td></td><td></td><td>10.4442</td><td>1368.8336</td><td></td></td<>				10.4442	1368.8336	
4060         97.6780         258.0857         1.5790         209.6585         63.3883           3625         97.6264         512.6547         10.0059         344.9622         125.2036           14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         50.6007         12.7741         865.9790         172.2860           7903         <				1.4366		
3625         97.6264         512.6547         10.0059         344.9622         125.2036           14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         50.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289 <td< td=""><td></td><td></td><td></td><td>1.5790</td><td>209.6585</td><td></td></td<>				1.5790	209.6585	
14901         97.5748         7.2960         0.8259         38.1981         31.5191           23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         50.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8588           21754         97					344.9622	
23998         97.5748         60.1213         1.2333         37.6604         14.2978           3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592				0.8259	38.1981	
3316         97.5748         81.3407         1.4270         55.7346         29.2755           17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           17231				1.2333	37.6604	
17664         97.5232         64.0910         0.4108         68.5611         29.4583           12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102				1.4270	55.7346	
12690         97.4716         41.8730         0.3260         51.9646         16.9768           23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251				0.4108	68.5611	
23937         97.4716         14.6573         0.3017         21.4351         24.0086           14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           1024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755				0.3260	51.9646	
14101         97.4716         71.3150         0.8348         94.0315         25.2719           20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755				0.3017		
20106         97.4716         108.5207         2.6341         198.3327         102.5249           23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880				0.8348	94.0315	
23237         97.4200         551.6417         19.8714         865.9790         172.2860           14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273				2.6341	198.3327	102,5249
14463         97.4200         500.6007         12.7741         356.3683         79.5826           7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273         97.1620         2325.4020         280.9567         1458.7760         282.3528				19.8714		
7903         97.4200         44.3393         3.9227         17.2892         12.8793           23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273         97.1620         2325.4020         280.9567         1458.7760         282.3528				12.7741	356.3683	
23289         97.3684         68.7267         0.5748         77.1676         23.8858           21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273         97.1620         2325.4020         280.9567         1458.7760         282.3528				3.9227		
21754         97.3684         1274.0653         329.9235         636.6764         170.1959           13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273         97.1620         2325.4020         280.9567         1458.7760         282.3528				0.5748		
13592         97.2652         55.3620         0.7405         38.8405         31.8436           11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273         97.1620         2325.4020         280.9567         1458.7760         282.3528				329.9235		
11024         97.2652         23.1620         1.0596         14.5000         53.2536           17231         97.2652         145.6970         1.5258         161.5773         76.3897           12102         97.2652         19.9853         20.1603         162.0343         112.7268           6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273         97.1620         2325.4020         280.9567         1458.7760         282.3528				0.7405		
17231     97.2652     145.6970     1.5258     161.5773     76.3897       12102     97.2652     19.9853     20.1603     162.0343     112.7268       6251     97.2136     528.9010     2.2359     509.5125     98.0853       22755     97.2136     69.1977     0.8980     94.8261     33.3201       7880     97.2136     203.4163     15.0982     73.9560     59.7649       8273     97.1620     2325.4020     280.9567     1458.7760     282.3528       13712     97.1104     42.2872				1.0596		
12102     97.2652     19.9853     20.1603     162.0343     112.7268       6251     97.2136     528.9010     2.2359     509.5125     98.0853       22755     97.2136     69.1977     0.8980     94.8261     33.3201       7880     97.2136     203.4163     15.0982     73.9560     59.7649       8273     97.1620     2325.4020     280.9567     1458.7760     282.3528       13712     97.1104     42.2872     280.9567     1458.7760     282.3528			145.6970	1.5258		
6251         97.2136         528.9010         2.2359         509.5125         98.0853           22755         97.2136         69.1977         0.8980         94.8261         33.3201           7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273         97.1620         2325.4020         280.9567         1458.7760         282.3528           13712         97.1104         43.2872         282.3528			19.9853	20.1603		
22755     97.2136     69.1977     0.8980     94.8261     33.3201       7880     97.2136     203.4163     15.0982     73.9560     59.7649       8273     97.1620     2325.4020     280.9567     1458.7760     282.3528       13712     97.1104     43.2072     282.3528				2.2359		
7880         97.2136         203.4163         15.0982         73.9560         59.7649           8273         97.1620         2325.4020         280.9567         1458.7760         282.3528           13712         97.1104         43.2872         282.3528				0.8980		
8273 97.1620 2325.4020 280.9567 1458.7760 282.3528				15.0982		
13/12 97 1104 42 2072 0 004 1				280.9567		
49,55301 1/6.82/9	13712	97.1104	42.3873	3.3615	49.5530	
19005 97.0588 C1.4617 12.5572 32.5703 21.4578				12.5572		
4774 97.0588 298.2953 23.5386 179.0155 45.9753						
253/1 06 0556 50 4007 600	2534	96.9556	59.4027		47.0757	13.7709

TABLE 511:	ROSIGLITAZO	ONE :	Attv. I	Ref. 44921-5090-0	1-\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
Timepoint(	77 44 0/2/100-100				
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
19474		482.7043	4.7665	451.1035	171,2731
23929		119.9370	3.0490		
6829		71.9370	2.2959		
884		157.9607	1.5650	149.8314	
16668	96.8008	126.9523	2.9561	85.1508	
8124	96.8008	82.3080	7.0661	40.3686	
2456	96.8008	113.5797	6.5179	71.7085	
5002	96.7492	106.6370	1.0650	127.3864	25.2245
21604	96.7492	555.9780	80.8008	321.7814	84.0405
19467	96.7492	189.9040	11.3668	298.0918	72.6472
22439	96.7492	127.7150	17.7419		52.2231
3997	96.6460	50.1093	14.4782	139.3108	
10532	96.6460	97.7030	3.1952	70.9501	20.2826

Timepoint(s			• •	ef. 44921-5090-01	
22499	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
				18.2323	
1530	74.2041		33,4574		
11422	73.1898		29,2380		
15402	72.8374		59,4143		- 00.007
17217	71.9823	350.7624	83.8685		
1521	70.7964	98.4309	43.5447	63.7035	72.133
4473	70.4132	90.9636	22.7675	114.9192	29.510
9378	70.2415	100.9102	39.0637	114.9192	25.6330
17215	70.1358	140.3519	46.7323	135.8928	38.9239
5049	69.4194	653.5915	198.0143	173.9482	36.5854
19976	69.3990	40.2866	10.3838	761.5973	154.5657
24875	69.2614	21.6493	10.7901	50.3488	12.1908
11423	69.1954	157.6573	49.6884	32.1978	12.7463
23058	69.0237	232.9766	65.6118	214.8633	66.0918
20972	69.0010	845.8319	228.4433	295.2279	67.8701
15761	68.9464	23.3670	16.7164	1028.8737	206.7711
18655	68.7418	107.6260	62.1282	34.5911	14.8369
19650	68.4950	263.9817		167.7966	57.8838
8210	68.3631	57.4586	56.8728	325.8264	64.7982
21444	68.3597	136.5334	22.8477	80.0516	27.4342
1340	68.2733	1100.5494	82.1857	71.1793	38.0707
19279	68.2403	158.3076	220.9089	1290.4251	198.7156
10743	68.2199	139.7771	24.7864	179.0857	21.3291
20448	68.1937	200.0502	37.2153	170.4504	42.1306
17137	68.1414	656.8594	283.8492	54.1081	31.5035
16342	68.1414	29,4000	253.9941	892.0875	228.5328
20848	68.0470	28.4823	13.5937	36.5884	11.7237
10248	67.9470	1790.4577	279.1314	1568.6877	254.0128
13789	67.8560	380.7530	114.3829	294.6245	71.8207
6980	67.8105	35.6846	11.4824	49.3703	14.5261
16725	67.8083	119.7477	42.4442	154.0515	38.5185
23368	67.7832	21.0355	12.6859	13.3580	7.6181
12010		342.8849	89.3216	422.9070	86.0283
16123	67.7571	161.2940	37.9738	198.3717	49.9862
24362	67.7093	151.7510	84.6333	97.4968	34.5563
4339	67.6127	70.1349	21.0065	83.7830	19.9340
15379	67.5354	330.9076	59.9258	376.9540	58.0307
1271	67.3819	86.2432	32.6069	115.5606	35.7516
20177	67.3750	71.4633	17.5343	82.4708	14.7182
17296	67.3102	28.9418	16.2224	45.2501	
24763	67.2704	31.4375	8.7784	37.8552	18.6935
	67.2386	145.2555	55.4727	178.1109	8.0298
17601 25545	67.1385	177.2865	41.5957	208.3250	61.5849
	67.0726	292.3751	125.5411	360.7596	38.2134
16205	67.0123	1735.3080	245.2707	1528.1296	112.0516
10887	66.9805	67.1386	21.2123	91.3261	279.4525
20729	66.9566	698.2047	127.5898	788.2066	30.9001
16518	66.9543	1021.8743	506.7264		117.8244
18403	66.9339	2385.3237	624.8610	732.4187	169.6207
64	66.9032	97.8079	25.3021	2798.2098	541.7250
13092	66.7474	154.7147	56.2731	124.9819	33.1042
24234	66.7451	103.2255	54.4972	198.6891	54.3053
13574	66.6905	114.3515	29.1618	72.8244	23.1475
			43. ID [8]	98.1320	20.9062

LGC ID	s): All LDA Score	Kana -	<b>'</b> ?'		WO/21054
3692		Mean Tox	SD Tox	Mean Nontox	SD Nontox
15032					51.87
20734				39.5999	9.74
11352		145.0892		87.0347	26.78
16204		266.1557		311.6899	59.91
	66.4711	1406.6185		1244.8317	193.70
17218		313.9458	79.0318	376.5280	94.08
18360	66.4563	346.4218	85.2672	426.0018	103.28
1719	66.3949	156.4190	48.4436	192.6382	46.93
19048	66.3517	52.1643	20.6674	68.5798	24.81
16947	66.3460	64.6320	19.0932	77.9823	20.85
21722	66.3392	78.8460	28.5022	97.4257	24.56
19649	66.2733	77.2451	23.2617	99.7705	
15767	66.2687	185.6237	46.5275	222.2000	22.84
561	66.2516	430.8957	72.4243	495.6473	50.57
23300	66.2346	952.1552	173.8440	1085.2464	76.54
24662	66.1027	156.7100	39.5070	183.0955	163.24
25479	66.0254	1722.2655	325.7824	1991.8786	38.79
15468	66.0083	1436.5322	229.7038		338.85
11530	65.9230	382.9851	353.7153	1276.1137	212.91
8211	65.8912	828.4386	237.9910	177.7582	87.61
24873	65.8560	379.1240	64.7791	659.2601	154.160
19278	65.8173	90.0442	30.9386	435.5892	77.211
14580	65.7684	26.6497	11.7230	116.4107	38.56
1170	65.7479	90.3365	27.3135	32.3422	13.609
21069	65.6854	41.7827	10.6361	72.4629	17.715
4327	65.5387	108.9996	31.7510	51.4599	14.677
24419	65.5251	87.8761	57.7349	88.2913	26.489
11745	65.4910	479.0887	84.5144	60.3946	71.214
23715	65.4603	32.3760	54.2645	542.6919	79.862
13938	65.4421	77.6296	19.5470	6.1169	14.493
7164	65.4148	75.5764	21.5404	93.8024	22.406
25795	65.3875	278.7450	102.4319	94.6448	27.739
15410	65.3750	1163.7670		364.5919	132.050
15617	65.3625	22.0207	225.4294	1323.9725	212.685
15125	65.3568	73.4162	10.8451	13.6338	7.159
4448	65.3261	29.2971	25.4616	55.7064	17.431
24420	65.3238	1652.0605	10.2480	36.2998	10.458
3623	65.3034	30.9912	361.4076	1453.4235	277.236
17963	65.2818	191.6866	14.5403	40.3320	13.105
16485	65.2715	193.8563	68.4033	233.2032	76.865
10185	65.1976	26.7998	39.4326	223.3569	43.300
1731	65.1874	225.8634	12.4135	32.3165	9.794
17374	65.1567	249.3977	77.9986	280.1050	71.470
11966	65.1283	340.4083	41.6200	282.5205	59.828
15041	65.1123		61.8618	389.6810	68.3133
1841	65.0987	20.4580	12.9306	17.6363	22.8917
10016	65.0919	80.2937	32.1224	57.3336	25.8529
1715	65.0816	240.9787	88.2186	193.9152	52.6454
23780	65.0680	126.6321	32.8328	108.8386	24.9623
3225	65.0339	20.9706	12.2426	31.2656	15.8604
10015		31.0955	14.2829	41.2229	14.9068
25895	65.0259	254.6920	86.7035	210.1809	54.9484
	65.0237	8.6614	17.4251	20.4931	21.4915

mepoint(s	: GENERAL s): Ali		Auy. Re	ef. 44921-5090-01-	WO/21054
GC ID	LDA Score	Mean Tox			
1727				Mean Nontox	SD Nontox
23336					29.01
19326				70.2070	24.48
19022				-0.0020	20.48
25594	65.0009			109.1019	27.23
16192	65.0009	349.0339		385.2526	62.39
2448		34.5344		41.1047	9.98
22939	76.8158	74.2112	19.8277	100.7353	20.12
4479	75.1842	39.3657	41.2712	86.1641	33.98
9976	72.7248	228.3896	100.9083	145.1523	76.08
	72.2904	491.7338	202.1302	670.8533	145.10
22930	72.1870	217.4787	140.3171	357.4950	131.37
11426	71.7788	430.7607	141.9394	576.5768	141.74
12662	71.6128	59.2040	32.3768	90.8955	
22678	71.2171	240.9209	48.3079	298.3937	26.97
24171	70.7100	74.3770	22.6059	97.4837	55.48
13428	70.6986	65.2547	20.1172		23.26
19220	70.4223	343.5755	79.9381	81.4399	19.76
4909	70.4177	137.6288	51.9239	422.1556	68.54
7868	70.3188	100.1702	31.4308	192.9884	52.63
8820	70.0152	306.1685	131.6133	134.8450	36.80
15596	69.9209	921.6366		416.2712	114.10
4730	69.9209		213.7143	1113.8680	177.63
4253	69.8606	938.7402	250.0683	1105.9844	192.048
3304	69.8401	129.7892	40.9456	163.8501	34.988
11399		246.1395	57.3973	320.9397	79.598
2331	69.8231	121.1745	49.4948	160.5642	48.435
24051	69.7207	777.1228	653.0431	317.3893	197.511
11680	69.6184	117.0387	31.0186	150.0066	31.107
	69.4967	199.3478	39.9329	226.2258	34.275
14494	69.4353	196.4649	42.6964	232.1137	32.011
20953	69.3035	722.8413	152.7183	865.5185	121.507
2196	69.2204	369.0324	73.7154	314.7563	52.884
4285	69.1932	257.5456	74.2533	312.0967	
9633	69.1932	82.8350	45.8355	112.2171	54.700
21997	69.1886	265.5388	73.6475	343.0222	34.797
8619	69.1011	52.3146	29.2644		76.128
14095	68.9567	162.5993	39.5793	79.2878	29.770
9317	68.8577	589.7563	156.9397	193.2475	35.844
8917	68.8520	134.8922	40.7874	694.6903	135.016
22130	68.8475	180.4303	49.2285	174.6518	35.476
14776	68.7918	387.6523		222.9292	52.079
12435	68.7202	192.5566	82.4764	453.2932	75.435
16124	68.6792	324.6097	44.7331	237.4061	43.575
6550	68.6099		169.9924	212.2391	55.582
3043	68.5928	375.4099	91.4847	469.2689	93.3862
13826	68.5325	112.5273	35.1563	143.1731	30.392
5863		1219.1377	228.4679	1434.0857	217.1109
7785	68.4939	264.4685	63.6224	311.1134	54.025
2803	68.4166	18.3555	25.9962	36.4874	21.640
14700	68.3722	138.3072	54.9376	183.4522	45.2714
	68.3438	50.6679	20.6625	36.6629	13.091
15449	68.3245	247.3878	€2.7630	308.6923	71.0213
11897	68.2904	33.8856	11.4193	40.8550	10.4420
6263	68.2358	172.3906	45.0848	211.6096	45.1407

TABLE 5JJ	: GENERAL		Atty R	ef. 44921-5090-01	1410/040540
Timepoint(s		· ś	, my. 10	ci. 4402 i-0090-0 i	-770/210548
GLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
11246					
22081	68.2017	196.6991	49.8133		
6946		463.8221	106.1912	523.8894	92.4231
16599	68.1630	481.9139	159.4526		
11346	68.1198	86.2982	59.0297	133.2276	
12819	68.1096	432.2876	85.9746	504.2326	
22692	68.0971	432.0026		519.1002	92.5986
12117	68.0413	517.5391	142.7068	610.0512	100.0788
14654	67.9811	247.5209	89.6507	300.3160	111.6380
11696	67.9595	112.8963	44.9690	145.3375	70.1127
16752	67.9492	73.7208	50.4746	115.6206	40.0203
18251	67.9197	86.9313	23.1752	70.5075	50.0369
6758	67.8810	23.2318	13.6344	14.3589	16.0715
5668	67.8765	61.2483	34.8436	86.7686	9.5633
6645	67.8230	126.1081	28.5670	149.3772	31.1453
18206	67.8105	259.8077	52.0249	213.7398	32.0343
2373	67.7832	315.5731	87.4847	397.0314	49.5328
4855	67.7002	54.6195	21.2220	71.0632	82.1406
6686	67.6457	283.0167	56.5288	346.3295	20.0774
10650	67.6411	605.0163	199.5154	772.0382	55.6461
17524	67.6343	1027.3541	226.9904		226.1347
4052	67.5570	395.4532	97.6496	1192.6757	194.6795
4145	67.5354	1500.2723	281.6434	468.9675	87.9716
11752	67.5069	1644.3102	418.3417	1281.0845	292.0936
11424	67.5035	474.7738	132.3324	1893.5383	325.1941
			102.0024	609.3307	161.0273

i

i imepoint(s	): All	Tox Markers	•	ef. 44921-5090-0	1-WO/21054
	LDA Score	Mean Tox	SD Tox	Mean Nontox	ISD No.
22499	75.6185	34.2595	16.8535		SD Nontox
22321	75.1990	310.8506	167.1420		
20461	75.1842	62.7182	22.3949		
21975	74.9238	268.8610	123.7110		
1530	74.2041	156.4787		162.1553	50.783
15003	74.0688	321.4460	33.4574	199.8098	39.734
3431	73.4582	792.2635	390.6709	46.5067	36.325
15002	73.4241	432.4998	219.3143	591.5221	122.856
11422	73.1898	85.9764	364.4478	159.8612	50.372
18654	72.9079		29.2380	118.9154	30.094
15402	72.8374	152.9391	71.7638	231.9206	55.959
17217	71.9823	285.6013	59.4143	340.2954	57.451
16080	71.7594	350.7624	83.8685	419.1402	72.133
19710		67.3947	76.5776	7.1628	23.868
21657	71.7106	75.2188	37.0771	44.2077	
16081	71.5457	1185.4910	270.7155	902.5884	15.766
	71.4013	168.3883	130.2839	73.2613	167.237
6684	71.3603	27.7588	16.1172	44.4057	37.727
1892	71.3467	1642.8702	683.5585	1116.1400	15.453
21683	71.3410	97.1756	67.8425	40.2851	239.355
16312	71.1978	111.6100	72.4940		17.013
18313	70.9726	3376.8495	897.5373	60.1567	18.300
1521	70.7964	98.4309	43.5447	2652.8504	565.6103
20449	70.6133	292.2106	380.2844	63.7035	29.5109
15191	70.6076	788.2982	1133.4138	64.6547	57.5069
21239	70.5974	185.6163	105.8374	61.5220	171.1551
17736	70.5474	1035.4250		109.3490	45.4813
4473	70.4132	90.9636	693.2538	534.5436	180.7569
4130	70.3734	189.3837	22.7675	114.9192	25.6330
8829	70.2574	317.4360	78.0756	255.9001	68.0301
17394	70.2461	427.6224	76.4486	258.2476	63.7526
9378	70.2415		96.3789	339.9802	85.1111
17215	70.1358	100.9102	39.0637	135.8928	38.9239
21682	70.1062	140.3519	46.7323	173.9482	36.5854
22675	69.9914	28.3445	64.0469	-15.4356	55.3860
385		48.9600	30.0366	26.0113	14.6579
21443	69.7503	27.3961	21.3493	49.2124	21.8259
574	69.6662	280.4249	116.2170	189.4061	55.3624
5049	69.4842	742.571?	254.3230	573.4534	112.0019
19976	69.4194	653.5915	198.0143	761.5973	154.5657
1097	69.3990	40.2866	10.3838	50.3488	
	69.3091	238.2240	114.2269	318.9707	12.1908
24875	69.2614	21.6493	10.7901	32.1978	91.7227
11423	69.1954	157.6573	49.6884	214.8633	12.7463
21583	69.0397	324.4733	146.4239	275 2014	66.0918
23058	69.0237	232.9766	65.6118	375.2011	115.5780
1714	69.0135	148.3219	31.1826	295.2279	67.8701
20972	69.0010	845.8319	228.4433	182.1938	40.0553
15761	68.9464	23.3670	16.7164	1028.8737	206.7711
20983	68.8248	398.0834		34.5911	14.8369
18655	68.7418	107.6260	113.6422	498.4937	99.1120
3799	68.6906	462.7863	62.1282	167.7966	57.8838
4832	68.5496		191.9644	364.9625	81.7487
1435	68.5314	744.6212	207.4810	907.2128	199.1618
	33.3317	1107.3409	204.2324	959.6013	134.7527

Timepoint(s)			Atty. R	ef. 44921-5090-0	1-WO/2105485
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
19650	68.4950			325.8264	
8210	68.3631		22.8477	80.0516	
21444	68.3597		82.1857	71.1793	
1638	68.2801		39.2649	158.8515	
1340	68.2733	1100.5494	220.9089	1290.4251	
19279	68.2403	158.3076	24.7864	179.0857	
10743	68.2199	139.7771	37.2153	170.4504	21.3291
20448	68.1937	200.0502	283.8492	54.1081	
17137	68.1414	656.8594	253.9941	892.0875	31.5035
16342	68.1414	28.4823	13.5937	36.5884	
3430	68.1062	139.4883	47.9044		11.7237
21654	68.0948	281.9094	148.2317	102.3391	20.1371
2555	68.0675	67.1897	36.8268	188.9304	34.6117
20848	68.0470	1790.4577	279.1314	42.6112	17.2322
17735	68.0232	1689.5961	1092.4495	1568.6877	254.0128
10248	67.9470	380.7530		972.3470	298.9849
11114	67.9458	58.9010	114.3829	294.6245	71.8207
24235	67.8913	271.3439	70.0447	24.7929	11.4189
20868	67.8913	76.0247	126.9928	190.0143	48.7300
13789	67.8560		42.9611	43.2374	23.9546
18883	67.8196	35.6846	11.4824	49.3703	14.5261
6980	67.8105	95.9977	45.3994	63.0582	19.1063
16725		119.7477	42.4442	154.0515	38.5185
23368	67.8083	21.0355	12.6859	13.3580	7.6181
12010	67.7832	342.8849	89.3216	422.9070	86.0283
16123	67.7571	161.2940	37.9738	198.3717	49.9862
24362	67.7093	151.7510	84.6333	97.4968	34.5563
4339	67.6127	70.1349	21.0065	83.7830	19.9340
	67.5354	330.9076	59.9258	376.9540	58.0307
25705	67.5274	483.3095	205.7122	338.5691	79.1325
24219	67.5274	362.8953	136.9343	283.3848	55.6203
11153	67.4671	592.1088	210.2750	448.4556	122.6381
15379	67.3819	86.2432	32.6069	115.5606	35.7516
1271	67.3750	71.4633	17.5343	82.4708	14.7182
20433	67.3398	102.2437	66.1840	59.7421	20.5107
20177	67.3102	28.9418	16.2224	45.2501	18.6935
23731	67.2909	196.6788	64.7240	152.3782	36.4458
17296	67.2704	31.4375	8.7784	37.8552	8.0298
24763	67.2386	145.2555	55.4727	178.1109	
8597	67.1806	198.7026	63.6688	150.9571	61.5849
17601	67.1385	177.2865	41.5957	208.3250	30.9868
11865	67.1056	52.4406	19.9271	67.5548	38.2134
25545	67.0726	292.3751	125.5411	360.7596	18.2568
13646	67.0601	683.5205	181.4408		112.0516
16205	67.0123	1735.3080	245.2707	555.9496	143.0688
10887	66.9805	67.1386	21.2123	1528.1296	279.4525
5384	66.9703	102.7054	105.1552	91.3261	30.9001
20729	66.9566	698.2047		31.3045	36.3468
16518	66.9543	1021.8743	127.5898	788.2066	117.8244
1159	66.9521	85.6168	506.7264	732.4187	169.6207
18403	66.9339	2385.3237	27.9488	111.4484	30.7412
17734	66.9043	1608.1908	624.8610	2798.2098	541.7250
64	66.9032	97.8079	992.4403	936.8658	251.9332
·	33.0002	31.0019	25.3021	124.9819	33.1042

	): All LDA Score	Mean Tox	SD Tox	Mean Nontox	ICD N4
14185	66.8338	625.7184			SD Nonto
13092	66.7474		56.2731		
24234	66.7451				
13574	66.6905				
20869	66.6678				20.9
14989	66.6633	848.9285		55.4663	29.9
1760	66.6257	156.3426			139.9
10097	66.5984	104.9067		187.7109	39.8
3692	66.5893			123.0126	21.7
17401	66.5848	155.3092	29.6198	181.2876	51.8
15189	66.5791	853.6625		548.8353	114.9
15032	66.5382	677.1638	755.3909	270.6925	144.6
20734	66.5132	33.1735	8.9006	39.5999	9.7
11352		145.0892	98.4298	87.0347	26.7
16204	66.4768	266.1557	69.8218	311.6899	59.9
17218	66.4711	1406.6185	208.4569	1244.8317	193.7
	66.4677	313.9458	79.0318	376.5280	94.0
18360	66.4563	346.4218	85.2672	426.0018	103.2
1894	66.4427	204.3381	90.7458	137.8497	59.89
1719	66.3949	156.4190	48.4436	192.6382	46.93
244	66.3585	111.2471	93.3779	54.6692	
19048	66.3517	52.1643	20.6674	68.5798	21.8
16947	66.3460	64.6320	19.0932	77.9823	24.8
21722	66.3392	78.8460	28.5022	97.4257	20.85
958	66.3233	94.4035	32.8317	115:1819	24.56
20740	66.3096	566.3856	242.7529		31.72
19649	66.2733	77.2451	23.2617	429.8468	99.68
15767	66.2687	185.6237	46.5275	99.7705	22.84
561	66.2516	430.8957	72.4243	222.2000	50.57
23300	66.2346	952.1552	173.8440	495.6473	76.54
14184	66.1891	301.6652	151.3410	1085.2464	163.24
15540	66.1050	113.0405		207.8567	99.51
24662	66.1027	156.7100	134.6910	43.5299	17.57
17161	66.0777	329.7487	39.5070	183.0955	38.79
25479	66.0254	1722.2655	257.8396	182.3693	62.79
15468	66.0083	1436.5322	325.7824	1991.8786	338.85
20204	65.9526		229.7038	1276.1137	212.91
11530	65.9230	33.7880	16.9377	44.5225	12.89
1571	65.9128	382.9851	353.7153	177.7582	87.61
15935	65.8992	215.1553	90.6577	165.2073	40.66
8211	65.8912	60.7917	15.5263	74.6537	16.33
24873	65.8560	828.4386	237.9910	659.2601	154.16
19278	65.8173	379.1240	64.7791	435.5892	77.21
14580		90.0442	30.9386	116.4107	38.56
1170	65.7684	26.6497	11.7230	32.3422	13.60
20735	65.7479	90.3365	27.3135	72.4629	17.71
21069	65.7195	148.3225	96.1664	92.8798	26.78
8212	65.6854	41.7827	10.6361	51.4599	14.67
	65.6047	600.7557	164.8662	464.3623	104.14
1867	65.5399	728.2960	130.0766	636.9389	117.583
4327	65.5387	108.9996	31.7510	88.2913	
24419	65.5251	87.8761	57.7349	60.3946	26.489
11745	65.4910	479.0887	84.5144	542.6919	71.214
23715	65.4603	32.3760	54.2645	6.1169	79.862

TABLE 5KK: General Core Tox Markers Atty. Ref. 44921-5090-01-WO/210					
GLGC ID	LDA Score	Mean Tox.	SD Tox		
13938	65.4421				SD Nontox
20915	65.4296				22.406
23166	65.4284				81.981
20229	65.4250	56.3994		100:0070	24.922
7164	65.4148	75.5764		75.9754	22 746
25795	65.3875			94.6448	27.739
11531	65.3830			364.5919	132.050
15410	65.3750	699.7980		348.1907	133.404
15617	65.3625	1163.7670		1323.9725	212.685
15125	65.3568	22.0207	10.8451	13.6338	7.159
4448	65.3261	73.4162	25.4616	55.7064	17.431
24420		29.2971	10.2480	36.2998	10.458
1324	65.3238	1652.0605	361.4076	1453.4235	
3623	65.3204	545.2323	114.5703	620.8049	277.2360
17963	65.3034	30.9912	14.5403	40.3320	113.774
	65.2818	191.6866	68.4033	233.2032	13.1050
16485	65.2715	193.8563	39.4326	223.3569	76.865
25567	65.2511	104.1917	68.9794	61 4004	43.3008
10185	65.1976	26.7998	12.4135	61.4264	22.5819
11152	65.1965	292.1286	136.9697	32.3165	9.7942
1731	65.1874	225.8634	77.9986	202.8651	65.7325
19085	65.1851	64.1975	23.2243	280.1050	71.4705
17374	65.1567	249.3977		49.7426	9.5907
11483	65.1465	141.9201	41.6200	282.5205	59.8285
24783	65.1442	123.5962	75.6824	91.5787	30.8087
20743	65.1317	134.8016	30.1164	140.7204	30.2415
11966	65.1283	340.4083	31.2461	160.3544	25.4080
15041	65.1123	20.4580	61.8618	389.6810	68.3133
1841	65.0987		12.9306	17.6363	22.8917
15300	65.0964	80.2937	32.1224	57.3336	25.8529
24867	65.0953	362.0063	238.6042	227.2502	112.3115
10016	65.0919	41.6273	15.5508	53.9894	18.6980
1715	65.0816	240.9787	88.2186	193.9152	52.6454
23780		126.6321	32.8328	108.8386	24.9623
356	65.0680	20.9706	12.2426	31.2656	15.8604
9826	65.0418	81.3621	80.7823	33.5443	26.6137
	65.0339	31.0955	14.2829	41.2229	
10015 2629	65.0259	254.6920	86.7035	210.1809	14.9068
	65.0248	37.6718	38.3003	18.3119	54.9484
25895	65.0237	8.6614	17.4251	20.4931	7.1524
1727	65.0214	60.2738	36.8581	41.1555	21.4915
23336	65.0180	78.2744	21.6816		29.0110
19326	65.0168	65.5375	20.4478	96.2845	24.4844
19022	65.0066	95.9416	26.5834	53.0026	20.4891
25594	65.0009	349.0339	62.1185	109.1019	27.2374
16192	65.0009	34.5344		385.2526	62.3908
23964	78.2144	126.5579	9.0067	41.1047	9.9814
3207	77.0137	137.5633	41.9930	77.4694	22.1057
2448	76.8158	74.2112	99.9263	268.1614	78.1861
6606	75.2706	2778.3866	19.8277	100.7353	20.1242
22939	75.1842		1267.7231	1664.3804	379.8859
2583	74.9068	39.3657	41.2712	86.1641	33.9869
7362	74.8761	150.7627	119.1253	63.1029	22.4454
9059	73.8220	149.2298	45.9850	199.9303	42.5089
	13.0220	356.3773	96.3852	252.4288	64.5639

LGC ID LDA Score Mean Tox SD Tox Mean Nontox ISD Non							
3941		254.3828		Mean Nontox	SD Nontox		
5675		298.0814		168.0751			
13460		262.2853		127.8580	40.44		
4479	72.7248	228.3896	. 0.07 07	350.4144	56.42		
12946	72.5713	182.2626		145.1523	76.08		
14458	72.5599	65.5700	46.7070	225.9337	34.56		
3049	72.3109	405.9825	33.0872	36.6221	24.34		
9976	72.2904	491.7338	271.7365	217.2998	57.32		
22677	72.1904	258.0386	202.1302 131.7064	670.8533	145.10		
22930	72.1870	217.4787		137.4176	65.60		
23123	71.9698	416.7497	140.3171	357.4950	131.37		
5596	71.9505	108.4572	150.9988	301.3687	66.77		
2410	71.8208	37.3707	44.2477	155.3954	46.22		
11208	71.7936	438.5004	19.5481	20.8837	8.10		
11426	71.7788	430.7607	156.2798	307.8393	91.16		
11714	71.6628	561.7938	141.9394	576.5768	141.749		
12662	71.6128	59.2040	130.2066	690.4253	120.909		
22711	71.5912	190.7472	32.3768	90.8955	26.976		
22929	71.5855	475.6429	42.9075	237.9935	40.004		
2936	71.5855	58.5906	332.2278	785.2108	278.201		
15004	71.5116	639.3778	29.7154	77.3066	23.441		
5227	71.5070	195.6753	532.0518	267.6419	79.778		
5461	71.3910	169.5128	69.3480	141.6417	35.444		
3050	71.2307	167.4707	68.9620	108.3646	26.627		
22678	71.2171	240.9209	129.9994	74.5745	29.341		
14840	71.1978	37.0784	48.3079	298.3937	55.480		
15644	71.1375	1368.0130	27.3592	16.2933	9.190		
1754	71.1068	142.5430	384.5849	1057.4513	169.698		
15892	71.0158	116.6990	38.2508	188.2707	40.821		
21660	70.9396	2084.7781	87.7207	47.4806	32.203		
24171	70.7100	74.3770	602.4824	1503.6722	418.380		
13428	70.6986	65.2547	22.6059	97.4837	23.261		
17644	70.6872	396.1171	20.1172	81.4399	19.762		
21740	70.6690	366.4832	99.4881	464.4665	78.743		
22378	70.5542	232.3337	152.4895	260.6575	55.189		
3982	70.4507	212.0096	83.7080	281.5329	51.668		
22697	70.4394	293.2071	64.0922 178.9767	278.0007	64.053		
19220	70.4223	343.5755		436.8873	143.0992		
4909	70.4177	137.6288	79.9381	422.1556	68.546		
5969	70.3939	524.5497	51.9239	192.9884	52.638		
7868	70.3188	100.1702	159.7548	408.3575	98.7308		
16	70.1790	1542.4920	31.4308	134.8450	36.8073		
17320	70.1460	238.4803	400.2563	1158.2518	239.3993		
8820	70.0152	306.1685	68.2936	178.0873	42.0592		
15596	69.9209	921.6366	131.6133	416.2712	114.1028		
4730	69.9209	938.7402	213.7143	1113.8680	177.6359		
4253	69.8606	129.7892	250.0683	1105.9844	192.0489		
3304	69.8401	246.1395	40.9456	163.8501	34.9888		
11399	69.8231	121.1745	57.3973	320.9397	79.5986		
2331	69.7207		49.4948	160.5642	48.4350		
13029	69.6605	284 7117	853.5437	317.3893	197.5116		
24051	69.6184	284.7117	151.2432	188.3711	57.9521		
		117.0387	31.0186	150.0066	31.1072		

SLGC ID	LDA Score	Mean Tox	SD Tox	Mean Nontox	CD Novi
18744	69.5945	135.8172	, P		SD Nontox
24028	69.5240	307.6217			
11680	69.4967		39.9329	392.1102	
10227	69.4433				
14494	69.4353			810.0097	170.53
20953	69.3035	722.8413		232.1137	32.01
5867	69.2921	149.7650		865.5185	121.50
16596	69.2602	247.6911	33.7458 77.9596	122.5807	27.93
7760	69.2318	302.7767		330.0640	78.300
2196	69.2204	369.0324	73.0101	358.5221	59.480
4285	69.1932	257.5456	73.7154	314.7563	52.884
9633	69.1932		74.2533	312.0967	54.700
21997	69.1886	82.8350	45.8355	112.2171	34.797
9166	69.1590	265.5388	73.6475	343.0222	76.128
17361	69.1340	113.8603	69.0179	54.2985	30.579
15197	69.1272	73.5384	29.8482	101.2109	29.249
2852		257.4820	70.1225	321.7657	55.545
8619	69.1113	341.3036	143.6284	447.7942	126.275
8938	69.1011	52.3146	29.2644	79.2878	29.770
14095	69.0897	41.6969	30.7637	78.2492	32.624
	68.9567	162.5993	39.5793	193.2475	35.844
3822	68.9498	926.8186	312.3629	700.4526	155.896
22212	68.9191	48.6413	16.3801	34.9544	19.983
18473	68.8782	262.0640	95.1634	191.9001	58.326
22898	68.8611	141.4675	90.2036	77.8919	32.232
9317	68.8577	589.7563	156.9397	694.6903	135.016
8917	68.8520	134.8922	40.7874	174.6518	35.476
22130	68.8475	180.4303	49.2285	222.9292	
3003	68.8282	135.2772	102.8554	58.5761	52.079
14776	68.7918	387.6523	82.4764	453.2932	44.525
6166	68.7690	250.6880	100.7962	336.0125	75.435
4874	68.7361	109.2814	60.0379	152.9358	83.662
6548	68.7236	307.2205	137.4010	199.8153	49.109
12435	68.7202	192.5566	44.7331	237.4061	58.242
13310	68.6860	341.7250	99.9780	257.6428	43.575
16124	68.6792	324.6097	169.9924		73.8299
10549	68.6735	40.2321	22.3612	212.2391	55.582
14464	68.6599	93.1297	53.5168	23.7656	11.245
15556	68.6371	588.6597	170.6522	143.4925	53.698
6550	68.6099	375.4099	91.4847	733.8417	143.5701
3043	68.5928	112.5273	35.1563	469.2689	93.3862
13826	68.5325	1219.1377	228.4679	143.1731	30.3926
12664	68.5212	84.8834		1434.0857	217.1109
21766	68.5200	144.2476	36.9411	118.8635	29.6834
19184	68.5189	45.0610	48.3863	101.4527	28.6385
5863	68.4939	264.4685	41.2248	14.0365	19.8994
6982	68.4586	45.3718	63.6224	311.1134	54.0255
21796	68.4370		58.1904	9.0022	11.6442
7785	68.4166	344.1850	140.6693	254.3082	68.7033
24237	68.4041	18.3555	25.9962	36.4874	21.6407
22899	68.3984	321.6027	150.3749	212.4182	72.2063
2803	68.3722	71.9333	49.5082	39.0086	26.1443
14700		138.3072	54.9376	183.4522	45.2714
14700	68.3438	50.6679	20.6625	36.6629	13.0915

	LDA Score	Mean Tox	SD Tox	Mean Nontox	len N
22626	68.3427	155.7964			SD Nonto
23978	68.3279	152.6187	43.5701		
15449	68.3245	247.8878			
11897	68.2904	33.8856		308.6923	
6263	68.2358	172.3906	46.0848	40.8550	
11246	68.2028	91.1100	26.1558	211.6096	
22081	68.2017	196.6991	49.8133	113.3934	27.
6946	68.1960	463.8221	106.1912	238.1235	42.4
16599	68.1630	481.9139	159.4526	523.8894	92.4
15283	68.1459	350.7587		608.6746	132.
7315	68.1448	34.1667	73.8419	296.6933	65.3
11346	68.1198	86.2982	46.4857	6.3470	17.7
12819	68.1096	432.2876	59.0297	133.2276	58.5
22692	68.0971	432.0026	85.9746	504.2326	92.5
18507	68.0686	631.2803	111.8651	519.1002	100.0
12117	68.0413	517.5391	150.0123	485.8802	116.3
14654	67.9811	247.5209	142.7068	610.0512	111.€
11242	67.9743		89.6507	300.3160	70.1
11696	67.9595	60.8831	36.0013	36.1544	16.9
16752	67.9492	112.8963	44.9690	145.3375	40.0
16533	67.9356	73.7208	50.4746	115.6206	50.0
18251	67.9197	384.8170	134.7857	291.2660	70.3
6758	67.8810	86.9313	23.1752	70.5075	16.0
5668	67.8765	23.2318	13.6344	14.3589	9.5
4861		61.2483	34.8436	86.7686	31.1
6645	67.8321	140.7460	51.4468	180.7381	41.4
2539	67.8230	126.1081	28.5670	149.3772	32.0
18206	67.8196	49.7049	46.1090	15.8238	22.4
22615	67.8105	259.8077	52.0249	213.7398	49.5
2373	67.7969	129.6028	185.4675	34.7554	33.0
7749	67.7832	315.5731	87.4847	397.0314	82.14
	67.7764	1258.3134	278.6021	1117.5030	188.5
1287	67.7446	522.6697	143.8574	637.2558	128.89
4855	67.7002	54.6195	21.2220	71.0632	20.0
4154	67.6934	261.8141	94.0689	204.3082	51.80
6585	67.6650	1146.6529	693.6719	647.8214	276.32
23963	67.6604	75.4752	34.4528	55.7581	29.72
22765	67.6593	48.48C4	47.6731	18.4176	11.57
6686	67.6457	283.0167	56.5288	346.3295	
3014	67.6445	209.8156	101.6757	259.7456	55.64
10650	67.6411	605.0163	199.5154	772.0382	64.83
17524	67.6343	1027.3541	226.9904	1192.6757	226.13
4052	67.5570	395.4532	97.6496	468.9675	194.67
8012	67.5558	40.1688	16.7176	27.3498	87.97
4145	67.5354	1500.2723	281.6434		11.27
17950	67.5331	61.5713	28.9890	1281.0845	292.09
11752	67.5069	1644.3102	418.3417	38.8838	14.85
11424	67.5035	474.7738	132.3324	1893.5383 609.3307	325.19

SLGC ID	LDA Score	Mean Toy		Ref. 44921-5090-0	
18135	85.1153		SD Tox	Mean Nontox	SD Nontox
10015	84.4864	109.7176 307.2109			
19101	81.7610				63 919
574	81.6038				48.194
24623	81.4990	868.6018			155.275
10016	81.4990	150.4577		. 02.4100	32.510
11352	81.0797	255.3307	40.9017	201.4507	62.854
8386	80.7128	238.0028		302.5550	63.580
22739	80.6604	191.6506		319.8779	112.270
23731	80.5031	288.6301	32.0748	361,3413	61.574
1510	80.1363	208.2056	35.9154	159.3211	45.058
18108		10.4589	25.8256	47.1716	33.701
21443	79.9266	186.5162	19.2195	157.6083	24.195
15185	79.4549	278.9396	65.4947	` 205.5944	75.504
21709	79.2977	1191.3623	205.4639	927.9137	185.000
15629	79.0881	379.8018	93.7882	251.8914	56.121
20917	79.0356	35.2703	17.2408	60.6819	30.015
18043	78.5115	92.9927	17.2303	127.6081	
	78.4591	95.0253	23.7170	62.4319	31.169 21.372
25802	78.3019	827.0513	147.1717	597.0436	
11423	78.1447	137.3237	37.3896	204.2398	152.134
15379	78.1447	68.1402	20.2105	109.5535	66.534
7196	78.0398	218.5551	37.3309	169.1407	36.732
20856	77.9350	920.0494	90.0732	1098.4819	42.7482
10185	77.6730	16.8177	9.9618	31.4369	186.9935
17108	77.5681	108.6139	26.7864	137.8878	10.3328
8597	77.5681	196.5452	33.9961	158.3220	27.1458
15886	77.3585	473.4446	52.3190	404.9769	41.6170
20778	77.3061	52.1464	7.7314	62.5674	96.7858
11635	77.1488	105.4547	29.3018		13.1215
2689	76.8868	155.2587	17.7492	135.9076	28.7605
15741	76.7296	213.3656	39.0040	180.5665	32.8832
12347	76.5199	80.9177	15.4050	294.8905	82.3313
1283	76.5199	67.8683	22.4825	105.6893	37.4992
692	76.5199	184.3874	42.8530	110.9277	40.2613
20740	76.4675	767.3149	291.8238	136.3400	35.4832
11387	76.2579	38.4384	13.7943	445.5906	133.9981
243	76.2055	773.9058	141.3403	60.3757	18.4692
1745	76.2055	15.3793	7.6469	619.1436	112.2056
17920	76.1006	159.4769	22.2002	28.1031	13.7895
8384	76.1006	51.3825	14.2583	194.6245	58.2811
18957	75.9958	757.8179	109.3794	97.5901	53.4359
13646	75.8910	676.2628	111.7638	915.5492	163.8856
15706	75.7862	24.5906	7.0316	577.1817	157.9653
1942	75.7338	101.1933	43.7219	36.7932	11.9603
24469	75.7338	948.2668	237.3070	44.5242	32.3307
21102	75.7338	141.3676		819.7597	143.6278
20249	75.6813	30.2006	41.2766	100.6470	36.9067
1791	75.6289	101.6522	20.4935	56.9048	24.6832
11350	75.3145	34.4875	14.2226	124.6235	26.7114
3799	75.2621	523.5803	12.3894	63.9145	29.9663
13974	75.2096	651.4240	197.0155	380.1915	112.2063
20986	75.0524		118.8780	537.7303	145.4884
	. 0.0024	82.5788	26.3473	143.8036	78.5875

	LDA Score	Mean Tox	SD Tox	Mean Nontox	SD Nontox
16177	75.0000				
4472	74.9476	11.5361			
8212	74.7904	547.3333			
167	74.7904	450.3721		493.9779	
8596	74.7904	208.7893		587.7048	
8200	74.7379	45.1388		156.1137	53.92
2882	74.7379	464.8075		32.1794	17.440
16871	74.6855	57.6114		567.8139	134.10
15347	74.5807	107.5588		83.2232	23.95
1310	74.5807	124.4094		81.7974	33.78
15125	74.5283	77.9493		150.5538	31.42
17086	74.4759		21.7589	58.5298	19.797
2150	74.4235	258.0716	40.7148	207.6230	48.510
20984	74.4235	124.7298	33.6883	153.2660	33.224
5998		512.0872	89.2280	660.8973	153.97
21809	74.3711	80.2265	25.9044	108.2507	32.372
25710	74.3711	47.6884	8.9429	61.3223	17.297
	74.2138	120.7997	70.3191	66.2559	70.047
21421	74.2138	36.1153	11.6675	47.8754	
25547	74.1614	233.1962	107.9455	357.9659	14.342
1383	74.1614	147.4641	19.1658	162.2522	128.639
349	74.1090	149.7719	18.5362	177.6972	44.148
15849	74.0566	171.2254	58.8615	275.9202	36.200
15697	74.0566	91.9489	11.0971		143.240
17159	74.0566	1323.5028	203.4722	78.8023	25.108
17612	73.7945	136.9738	29.7617	1015.7870	243.512
24428	73.7421	103.1922	25.2810	184.9652	54.238
21840	73.7421	427.7531	74.4946	79.8971	19.943
15510	73.7421	231.8466		526.4060	123.207
19177	73.6897	64.8991	44.2767	281.7326	54.446
24107	73.6373	97.4100	24.4287	89.0352	27.970
14554	73.5849	75.4516	40.5221	110.0648	28.194
25379	73.5325	265.7183	13.1010	100.9108	27.678
15767	73.5325	203.7 183	60.6464	189.6822	49.055
20985	73.4801	173.4103	26.5105	214.5572	52.0656
25594	73.4277	86.3309	36.4701	95.2842	22.7042
19894		309.3353	59.2185	377.8568	64.1453
10071	73.4277	310.4214	135.1212	188.4120	63.2929
13151	73.3753	395.4896	137.1970	263.7735	107.1199
17212	73.3753	2714.7755	598.6401	2181.2875	567.1612
20092	73.3753	107.5611	17.5468	132.2912	35.3210
	73.3229	20.8556	6.3050	34.3316	18.0096
20515	73.2704	84.0794	12.1683	101.9885	22.0912
13926	73.2704	37.5504	8.4762	48.6142	
25365	73.1656	26.6963	9.5167	47.8513	12.4977
5065	73.1656	35.7989	9.9797	47.9983	34.0213
16330	73.1132	203.4242	27.4716	172.4242	13.0662
23854	73.0608	846.9536	120.8130		33.3735
24420	73.0084	1707.2664	471.1667	708.7908	174.9077
15244	73.0084	15.8128	4.8813	1500.5725	304.1412
2757	90.4612	1394.3556	259.9027	23.6694	9.2592
6548	86.5828	482.3749	178.7265	804.5697	235.2406
24171	85.9539	55.8309	14.5413	210.7078	73.1549
		VU.UUU31	14 5/17/1	93.8863	25.5174

LGC ID	LDA Score	100	- u		1 0,2,00
7846		Mean Tox	SD Tox		SD Nontox
6037	83.4382		25,0190	45.1187	
13622	82.9665		16.1603	80.4229	
21816	82.9665		76,6283		10.00
	82.9140	325.1390	68.8148	239.4026	
4168	82.7568	74.0096	24.8449	110.7782	
22914	82.6520	1799.6522	315,7989	2446.7836	22.40
13664	82.0755	68.2059	8.9533	69.0762	478.95
23978	81.4990	124.2453	24.0576	167.6789	35.22
9454	81.2893	26.4989	33.4200	40.8179	33.18
22484	80.9224	74.5881	19.8437	49.1110	23.93
3014	80.9224	154.3853	48.4023	250.2939	19.67
13296	80.9224	120.8284	40.0001	198.2065	75.11
6897	79.9790	170.1049	32.0611	232.1324	56.06
4330	79.8742	806.9655	381.4427		59.21
23822	79.8742	133.8473	112.7870	449.5732	123.38
23015	79.7170	123.1848	48.7067	319.2932	145.27
19840	79.7170	1671.9778	299.7040	77.3003	20.77
17003	79.5597	92.5409	49.1633	1348.2181	316.517
12946	79.4025	155.2430	34.5710	101.8845	29.182
3904	79.3501	232.2479	56.7419	219.4671	41.764
3332	78.8784	382.2983	62.5836	134.3438	93.937
9485	78.6164	55.9292	45.7132	304.7896	65.941
2321	78.6164	78.8396	29.1136	54.4030	25.915
14434	78.3543	54.1851	10.2485	61.0074	17.643
23428	78.1971	715.2545		72.9447	25.995
20924	78.1447	410.4444	140.8607	516.5359	137.334
20038	78.1447	147.3998	95.4891	560.8658	145.659
6946	77.9874	381.3689	30.8322	199.9446	50.959
24022	77.9874	75.2621	98.9321	512.4703	102.137
6509	77.8826	30.4987	19.1818	102.1569	27.057
6489	77.8826	190.7523	24.7422	0.6097	30.319
3250	77.7254	670.2989	40.0632	256.2544	52.042
17363	77.6730	431.3331	218.5471	434.6725	153.524
24310	77.6205	426.9662	42.8836	527.6242	94.1476
5795	77.5681	415.6309	135.6242	306.1028	92.5617
16756	77.4109	170.4001	137.6263	548.9514	130.988
12435	77.3585	163.8264	34.0036	135.6609	30.9771
12399	77.3061		43.3651	230.6378	47.8400
18473	77.2537	205.5457	48.7213	144.4195	39.4832
12662	76.9916	321.1359	96.9679	202.9609	69.2027
6226	76.8868	54.9449	27.1251	85.9728	31.3064
19006	76.8344	248.0906	60.6504	172.4560	54.6165
3143	76.8344	1498.6855	335.8005	1055.0046	326.8376
3982	76.8344	258.8920	63.6545	323.6245	81.6914
5206	76.7820	177.5016	56.3794	268.5876	71.5952
18529	76.6771	93.5909	65.7977	111.3791	39.7002
4770	76.6771	408.7730	80.3108	289.0741	76.2198
19195	76.4675	231.7275	47.6269	171.2552	44.3775
7117		2261.7617	542.8825	1640.1981	380.3353
21539	76.4675	112.8620	21.9993	142.7610	28.4806
14884	76.4151	608.7199	92.4545	519.8072	103.6568
13758	76.2055	50.1086	17.2257	74.0682	26.0532
37.90	76.1530	30.3706	11.4064	44.7867	12.0964

3'		RE AGENTS	Atty. R	ef. 44921-5090-0	1-WO/2105485
		Mean Tox	SD Tox	Mean Nontox	SD Nontox
11355		102.1000	76.3592	110.7182	42.9662
5732	. 0.000	120.0007	33.4845	153.8469	
15365	75.8910	1198.6604	348.4301		00.0.02

3	Treatment and			Atty, Re	f. 44921-5090-01-WO/2105
Toxin and Group	Compound	Dosage		1.10.01	
	1 intraperitoneal	(mg/kg)	(mg/ml)	Males	Sacrifice
Cyclophosphamide	injection on Day 1				
1	Saline				
2		0	0	5	6 hours post-dose
3	Cyclophosphamide	20	2	5	6 hours post-dose
4	Cyclophosphamide	200	20	5	6 hours post-dose
5	Saline	0	0	5	24 hours post-dose
6	Cyclophosphamide	20	2	5	24 hours post-dose
7	Cyclophosphamide	200	20	5	24 hours post-dose
8	Saline	0	0	5	48 hours post-dose
9	Cyclophosphamide	20	2	5	48 hours post-dose
10	Cyclophosphamide	200	20	5	48 hours post-dose
11	Saline	0	0	5	
12	Cyclophosphamide	20	2	5	Day 8
	Cyclophosphamide	200	20	5	Day 8
B N JA	V	4	<b>y</b>		Day 8
				,	*** ** **
	Daily I.p. injection exce	pt			
	for day of sacrifice	1	1		
	(groups 1-3 injected on	i			
osfamide	day of sacrifice)	[	ļ		
1	Saline	0	0		01
2	Ifosfamide	5	0.5	5	6 hours post-dose
3	Ifosfamide	100	10		6 hours post-dose
4	Saline	0	10	5	6 hours post-dose
5	Ifosfamide	5	0.5	5	24 hours post-dose
6	Ifosfamide	100	10	5	24 hours post-dose
7	Saline	0	0	5	24 hours post-dose
8	Ifosfamide	5		5	48 hours post-dose
9	Ifosfamide	100	0.5	5	48 hours post-dose
10	Saline	0	10	5	48 hours post-dose
11	Ifosfamide		0	5	Day 6
12	Ifosfamide	5	0.5	5	Day 6
	nosiamide	100	10	5	Day 6
36.	- CA 3,	· · · · · · · · · · · · · · · · · · ·		ўз. — 1	A A
	Added to drinking water,	ľ			
	continuous until	1	1	1	
noxidil	sacrifice (changed daily)	mg/L	1	1	
1	Orinte (changed daily)				
2	Drinking water Minoxidil	0		5	6 hours post-dose
3		12		5	6 hours post-dose
4	Minoxidil	120		5	6 hours post-dose
5	Drinking water	0		5	24 hours post-dose
6	Minoxidil	12		5	24 hours post-dose
. 7	Minoxidil	120		5	24 hours post-dose
8	Drinking water	0		5	Day 15
9	Minoxidil	12		5	Day 15
,	Minoxidil	120		5	Day 15
The second secon	Un injection				
Italazino		Dosage	Conc.	T	
		(mg/kg)	(mg/ml)		
$\frac{1}{2}$	Saline	0	0	5	6 hours = act 1
2	Hydralazine HCI	2.5	1.25	5	6 hours post-dose 6 hours post-dose

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	Treatment and	Dosage	Conc.	f. 44921-5090-01-WO/2105	
Toxin and Group	Compound .:	(mg/kg)	(mg/ml)	No. of Males	Sacrifice
3	Hydralazine HCI	25	12.5	5	
4	Saline	0	0	5	6 hours post-dose
5	Hydralazine HCI	2.5	1.25	5	24 hours post-dose
6	Hydralazine HCl	25	12.5	5	24 hours post-dose
7	Saline	0	0		24 hours post-dose
8	Hydralazine HCI	2.5		5	Day 3
9	Hydralazine HCl	25	1.25	5	Day 3
9 3 G	The state of the s		12.5	5	Day 3
	daily oral gavage, but	1 64	· · ·	ě,	
	not on day of sacrifice				
BI-QT	(except groups 1-3)	1	ĺ		
1	(except groups 1-3)				
2	0.5% natrosol	0	0	4	6 hrs post-dose
3	BI-QT	10	1.0	4	6 hrs post-dose
	BI-QT	50	5.0	4	6 hrs post-dose
4	0.5% natrosol	0	0	4	
5	BI-QT	10	1.0	4	24 hrs post-dose
6	BI-QT	50	5.0	4	24 hrs post-dose
77	0.5% natrosol	0	0		24 hrs post-dose
8	BI-QT	10		4	Day 3
9	BI-QT	50	1.0	4	Day 3
10	0.5% natrosol		5.0	4	Day 3
11	BI-QT	0	0	4	Day 7
12		10	1.0	4	Day 7
13	BI-QT	50	5.0	4	Day 7
14	0.5% natrosol	0	0	4	Day 14
15	Bl-QT	10	1.0	4	Day 14
985	BI-QT	50	5.0	4	Day 14
		•	· 12	7	Day 14
	Daily subcutaneous				**
	injection, but not on day				
landon t	of sacrifice (except				
lenbuterol	groups 1-3)				
1	Saline	0	0.00		0.1
2	Clenbuterol	0.4	0.00	5	6 hrs post-dose
3	Clenbuterol	4.0	2.27		6 hrs post-dose
4	Saline	0		5	6 hrs post-dose
5	Clenbuterol	5.4	0.00	5	24 hrs post-dose
6	Clenbuterol		0.23	5	24 hrs post-dose
7	Saline	4.0	2.27	5	24 hrs post-dose
8	Clenbuterol	0	0.00	5	Day 6
9		0.4	0.23	5	Day 6
10	Clenbuterol	4.0	2.27	5	Day 6
11	Saline	0	0.00	5	Day 15
12	Clenbuterol	0.4	0.23	5	Day 15
12	Clenbuterol	4.0	2.27	5	Day 15
<del></del>	<u> </u>		, ,		
madere - I	1 subcutaneous	T			<u></u>
proterenol	injection on Day 1				
1	Sterile water	0	0	5	2 h
2	Isoproterenol	0.05	0.05		3 hrs post-dose
3	Isoproterenoi	<u>ਹ.ਰਹ</u>		5	3 hrs post-dose
4	Sterile water	0.5	∂.5	5	3 hrs post-dose
5	Isoproterenol	0.05	0.05	5	6 hrs post-dose
					6 hrs post-dose

Toxin and Group 6 7 8 9	Treatment and Compound Isoproterenol	Dosage (mg/kg)	Conc.	11101 01	f. 44921-5090-01-WO/210
7 8 9	Isoproterenol		(mg/ml)	Males	Sacrifice
8 9		0.5	0.5	5	
9	Sterile water	0	0	5	6 hrs post-dose
	Isoproterenol	0.05	0.05	5	24 hrs post-dose
	Isoproterenol	0.5	0.5	5	24 hrs post-dose
5'	<u> </u>	:			24 hrs post-dose
Moroninanh ein -	1 subcutaneous			1 54	
Norepinephrine	injection on Day 1	1	1	1	1
<del></del>	Sterile water	0	0	5	
2	Norepinephrine	0.05	0.05	5	3 hrs post-dose
3	Norepinephrine	0.5	0.5	5	3 hrs post-dose
4	Sterile water	0	0.0	5	3 hrs post-dose
5	Norepinephrine	0.05	0.05	5	6 hrs post-dose
6	Norepinephrine	0.5	0.5	5	6 hrs post-dose
7	Sterile water	0.0	0.5	5	6 hrs post-dose
8	Norepinephrine	0.05	0.05		24 hrs post-dose
9	Norepinephrine	0.5	0.05	5	24 hrs post-dose
		- 0.0	1 0.5		24 hrs post-dose
	1 subcutaneous	T	1 15	<u>, , , , , , , , , , , , , , , , , , , </u>	
pinephrine	injection on Day 1				
1	Sterile water	0	10	<del> </del>	
2	Epinephrine	0.1		5	3 hrs post-dose
3	Epinephrine	1 1	0.1	5	3 hrs post-dose
4	Sterile water	0	1	5	3 hrs post-dose
5	Epinephrine	0.1	0	5	6 hrs post-dose
6	Epinephrine		0.1	5	6 hrs post-dose
7	Sterile water	1 1	1	5	6 hrs post-dose
8	Epinephrine	0	0	5	24 hrs post-dose
9	Epinephrine	0.1	0.1	5	24 hrs post-dose
est wa	A N 13 14	11	1 1	5	24 hrs post-dose
riamycin (Doxorubicin	1 intravenous injection	<u> </u>	T		
1)	on Day 1				
1	Saline				
2	Doxorubicin HCI	0	0	5	6 hours post-dose
3	Doxorubicin HCl	1.3	0.64	5	6 hours post-dose
4	Saline	12.8	6.4	5	6 hours post-dose
5	Doxorubicin HCI	0	0	5	24 hours post-dose
6	Doxorubicin HCI	1.3	0.64	5	24 hours post-dose
7	Saline	12.8	6.4	5	24 hours post-dose
8	Doxorubicin HCI	0	0	5	Day 6
9	Doxorubicin HCI	1.3	0.64	5	Day 6
10	Saline	12.8	6.4	5	Day 6
11	Doxorubicin HCI	0	0	5	Day 8
12		1.3	0.64	5	Day 8
	Doxorubicin HCI	12.8	6.4	5	Day 8
	Intravenous bolus on		ε,		
	Day 1				
1				1	
<u>:</u>	Saline	0	0	5	3 hrs post-dose
3	Amphotericin B	0.25	0.125	5	3 hrs post-dose
4	Amphotericin B	2.5	1.25	7	3 hrs post-dose
5	Saline Amphotericin B	0	0	5	6 hrs post-dose

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Toxin and Group	Treatment and	Dosage	Conc.	No. of	f. 44921-5090-01-WO/210
	Compound	(mg/kg)	(mg/ml)	Males	Sacrifice
6	Amphotericin B	2.5	1.25	7	
7	Saline	0	0	5	6 hrs post-dose
8	Amphotericin B	0.25	0.125	5	24 hrs post-dose
9	Amphotericin B	2.5	1.25	7	24 hrs post-dose
12.25		<i>3</i> € 5.			24 hrs post-dose
The same of the same	intravenous injection or	1	T	·	
Elprubicin	Day 1				
1	Saline	0	0	5	Chan
2	Epirubicin	1.2	0.6	5	6 hours post-dose
3	Epirubicin	12	6	5	6 hours post-dose
4	Saline	0	0	5	6 hours post-dose
5	Epirubicin	1.2	0.6	5	24 hours post-dose
6	Epirubicin	12	6	5	24 hours post-dose
7	Saline	0	1 0	5	24 hours post-dose
8	Epirubicin	1.2	0.6		Day 6
9	Epirubicin	12	6	5	Day 6
10	Saline	0	0	5	Day 6
11	Epirubicin	1.2	0.6	5	Day 8
12	Epirubicin	12	6	5	Day 8
	A 18 8 18			5	Day 8
	intrapeitoneal injection		ré Ā	***	
henylpropanolamine	on Day 1	1	1		
1	Saline	0	<del> </del>		
2	Phenylpropanolamine	8	0	5	3 hrs post-dose
3	Phenylpropanolamine		0.8	5	3 hrs post-dose
4	Saline	80	8	5	3 hrs post-dose
5	Phenylpropanolamine	0	0	5	6 hrs post-dose
6	Phenylpropanolamine	8	0.8	5	6 hrs post-dose
7	Saline	80	8	5	6 hrs post-dose
8	Phenylpropanolamine	0	0	5	24 hrs post-dose
9	Phenylpropanolamine	8	0.8	5	24 hrs post-dose
2* 14	1 nenyipropanolamine	80	8	5	24 hrs post-dose
	5 daily doses of oral			- 19-2 - 18-2	33 8 8
siglitazone	gavage				
1	0				
2	1% methylcellulose	0	0	5	· 6 hours post-dose
3	Rosiglitazone	18	1.8	5	6 hours post-dose
4	Rosiglitazone	180	18	5	6 hours post-dose
5	1% methylcellulose	0	0	5	24 hours post-dose
6	Rosiglitazone	18	1.8	5	24 hours post-dose
7	Rosiglitazone	180	18	5	24 hours post-dose
8	1% methylcellulose	0	0	5	Day 8
9	Rosiglitazone	18	1.8	5	Day 8
10	Rosiglitazone	180	18	5	Day 8
11	1% methylcellulose	0	0	5	Day 15
12	Rosiglitazone	18	1.8	5	
14	Rosiglitazone	180	18	5	Day 15